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OM nucleic - nucleic search, using sw model

Run on: May 18, 2005, 19:27:08 ; Search time 21134 Seconds
(without alignments)
11738.938 Million cell updates/sec

Title: US-10-680-287A-2
Perfect score: 5120
Sequence: 1 actaaagcgccgccgccgcg.....aaacttaattttgtaaaaca 5120

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
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9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	5120	100.0	5120	6	AR567476	AR567476 Sequence
2	5120	100.0	5120	6	AX277523	AX277523 Sequence
3	5120	100.0	5120	6	AX418087	AX418087 Sequence
4	5118.4	100.0	5120	6	AR567475	AR567475 Sequence
5	5118.4	100.0	5120	6	AX277522	AX277522 Sequence
6	5118.4	100.0	5120	6	AX418086	AX418086 Sequence
7	5094.8	99.5	5099	6	CQ870240	CQ870240 Sequence
8	5091.6	99.4	5135	6	AX658229	AX658229 Sequence
9	5091.6	99.4	5135	9	AF077820	AF077820 Homo sapi
10	5077.4	99.2	5100	6	AX821900	AX821900 Sequence
11	5077.4	99.2	5100	9	AF064548	AF064548 Homo sapi
12	5053.4	98.7	5098	6	AR305075	AR305075 Sequence
13	5053.4	98.7	5098	6	AR309179	AR309179 Sequence
14	5053.4	98.7	5098	6	BD105986	BD105986 Novel LDL
15	5048.8	98.6	5135	6	CQ870242	CQ870242 Sequence
16	5014.2	97.9	5059	9	AB017498	AB017498 Homo sapi
17	4935.4	96.4	4970	6	CQ722758	CQ722758 Sequence
18	4927.4	96.2	5022	6	AR305086	AR305086 Sequence
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45	3965.8	77.5	5166	10	BC011374	BC011374 Mus muscu

ALIGNMENTS

RESULT 1
AR567476
LOCUS AR567476 5120 bp DNA linear PAT 08-OCT-2004
DEFINITION Sequence 2 from patent US 6780609.
ACCESSION AR567476
VERSION AR567476.1 GI:53985258
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 5120)
AUTHORS Carulli,J.P., Little,R.D., Recker,R.R. and Johnson,M.L.
TITLE High bone mass gene of 1.1q13.3
JOURNAL Patent: US 6780609-A 2 24-AUG-2004;
FEATURES Location/Qualifiers
source 1. .5120
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN

Query Match 100.0%; Score 5120; DB 6; Length 5120;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         61 GCCGGACAACATGGAGGCAGCGCCGCCCGGGCCGCCGTGGCCGCTGCTGCTGCTGCTGCT 120
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Db         61 GCCGGACAACATGGAGGCAGCGCCGCCCGGGCCGCCGTGGCCGCTGCTGCTGCTGCTGCT 120

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Qy       1321 CCCCGATGGCATCGCGGTCGACTGGGTGGCCCGAAACCTCTACTGGACCGACACGGGCAC 1380
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Qy       4261 CTTCGTCATGGGTGGTGTCTATTTTGTGTGCCAGCGCGTGGTGTGCCAGCGCTATGCGGG 4320
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Qy       4321 GGCCAACGGGCCCTTCCCGCACGAGTATGTCAGCGGGACCCCGCACGTGCCCCTCAATTT 4380
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Qy       4381 CATAGCCCCGGGCGGTTCCCAGCATGGCCCCTTCACAGGCATCGCATGCGGAAAGTCCAT 4440
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Qy       4501 CGTCACAGGGGCCTCGTCCAGCAGCTCGTCCAGCACGAAGGCCACGCTGTACCCGCCGAT 4560
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Db       4621 CTCTTCAAACATTCCGGCCACTGCGAGACCGTACAGGCCCTACATCATTCGAGGAATGGC 4680

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Qy       4801 CACGCCCCACAGCCAGTACCTGTCGGCGGAGGACAGCTGCCCGCCCTCGCCCGCCACCGA 4860
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Qy       4981 AAAAAATATATTTTATGATTTAAAAAATAAATATAATTGGGATTTTAAAAACATGAGAAA 5040
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Qy       5101 AAACTTAATTTTGTAAAACA 5120
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Db       5101 AAACTTAATTTTGTAAAACA 5120


RESULT 2
AX277523
LOCUS       AX277523               5120 bp    DNA     linear   PAT 01-NOV-2001
DEFINITION  Sequence 2 from Patent WO0177327.
ACCESSION   AX277523
VERSION     AX277523.1  GI:16604716
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Carulli,J.P., Little,R.D., Recker,R.R. and Johnson,M.L.
  TITLE     The high bone mass gene of 11q13.3
  JOURNAL   Patent: WO 0177327-A 2 18-OCT-2001;
            Genome Therapeutics Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .5120
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                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             100.0%;  Score 5120;  DB 6;  Length 5120;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 5120;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ACTAAAGCGCCGCCGCCGCGCCATGGAGCCCGAGTGAGCGCGGCGCGGGCCCGTCCGGCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ACTAAAGCGCCGCCGCCGCGCCATGGAGCCCGAGTGAGCGCGGCGCGGGCCCGTCCGGCC 60

Qy         61 GCCGGACAACATGGAGGCAGCGCCGCCCGGGCCGCCGTGGCCGCTGCTGCTGCTGCTGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCCGGACAACATGGAGGCAGCGCCGCCCGGGCCGCCGTGGCCGCTGCTGCTGCTGCTGCT 120

Qy        121 GCTGCTGCTGGCGCTGTGCGGCTGCCCGGCCCCCGCCGCGGCCTCGCCGCTCCTGCTATT 180
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Db        121 GCTGCTGCTGGCGCTGTGCGGCTGCCCGGCCCCCGCCGCGGCCTCGCCGCTCCTGCTATT 180

Qy        181 TGCCAACCGCCGGGACGTACGGCTGGTGGACGCCGGCGGAGTCAAGCTGGAGTCCACCAT 240
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Db        181 TGCCAACCGCCGGGACGTACGGCTGGTGGACGCCGGCGGAGTCAAGCTGGAGTCCACCAT 240

Qy        241 CGTGGTCAGCGGCCTGGAGGATGCGGCCGCAGTGGACTTCCAGTTTTCCAAGGGAGCCGT 300
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Db        241 CGTGGTCAGCGGCCTGGAGGATGCGGCCGCAGTGGACTTCCAGTTTTCCAAGGGAGCCGT 300

Qy        301 GTACTGGACAGACGTGAGCGAGGAGGCCATCAAGCAGACCTACCTGAACCAGACGGGGGC 360
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Db        301 GTACTGGACAGACGTGAGCGAGGAGGCCATCAAGCAGACCTACCTGAACCAGACGGGGGC 360

Qy        361 CGCCGTGCAGAACGTGGTCATCTCCGGCCTGGTCTCTCCCGACGGCCTCGCCTGCGACTG 420
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Qy        421 GGTGGGCAAGAAGCTGTACTGGACGGACTCAGAGACCAACCGCATCGAGGTGGCCAACCT 480
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Qy        541 CTTGGACCCCGCTCACGGGTACATGTACTGGACAGACTGGGTTGAGACGCCCCGGATTGA 600
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Qy        601 GCGGGCAGGGATGGATGGCAGCACCCGGAAGATCATTGTGGACTCGGACATTTACTGGCC 660
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Db        601 GCGGGCAGGGATGGATGGCAGCACCCGGAAGATCATTGTGGACTCGGACATTTACTGGCC 660

Qy        661 CAATGGACTGACCATCGACCTGGAGGAGCAGAAGCTCTACTGGGCTGACGCCAAGCTCAG 720
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Db        661 CAATGGACTGACCATCGACCTGGAGGAGCAGAAGCTCTACTGGGCTGACGCCAAGCTCAG 720

Qy        721 CTTCATCCACCGTGCCAACCTGGACGGCTCGTTCCGGCAGAAGGTGGTGGAGGGCAGCCT 780
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Db        721 CTTCATCCACCGTGCCAACCTGGACGGCTCGTTCCGGCAGAAGGTGGTGGAGGGCAGCCT 780

Qy        781 GACGCACCCCTTCGCCCTGACGCTCTCCGGGGACACTCTGTACTGGACAGACTGGCAGAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACGCACCCCTTCGCCCTGACGCTCTCCGGGGACACTCTGTACTGGACAGACTGGCAGAC 840

Qy        841 CCGCTCCATCCATGCCTGCAACAAGCGCACTGGGGGGAAGAGGAAGGAGATCCTGAGTGC 900
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Db        841 CCGCTCCATCCATGCCTGCAACAAGCGCACTGGGGGGAAGAGGAAGGAGATCCTGAGTGC 900

Qy        901 CCTCTACTCACCCATGGACATCCAGGTGCTGAGCCAGGAGCGGCAGCCTTTCTTCCACAC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        961 TCGCTGTGAGGAGGACAATGGCGGCTGCTCCCACCTGTGCCTGCTGTCCCCAAGCGAGCC 1020
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Qy       1021 TTTCTACACATGCGCCTGCCCCACGGGTGTGCAGCTGCAGGACAACGGCAGGACGTGTAA 1080
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Qy       1081 GGCAGGAGCCGAGGAGGTGCTGCTGCTGGCCCGGCGGACGGACCTACGGAGGATCTCGCT 1140
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Db       1081 GGCAGGAGCCGAGGAGGTGCTGCTGCTGGCCCGGCGGACGGACCTACGGAGGATCTCGCT 1140

Qy       1141 GGACACGCCGGACTTCACCGACATCGTGCTGCAGGTGGACGACATCCGGCACGCCATTGC 1200
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Qy       1201 CATCGACTACGACCCGCTAGAGGGCTATGTCTACTGGACAGATGACGAGGTGCGGGCCAT 1260
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Qy       1261 CCGCAGGGCGTACCTGGACGGGTCTGGGGCGCAGACGCTGGTCAACACCGAGATCAACGA 1320
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Qy       1321 CCCCGATGGCATCGCGGTCGACTGGGTGGCCCGAAACCTCTACTGGACCGACACGGGCAC 1380
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             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       1741 CATCTACTGGACTGACTGGCAGCGCCGCAGCATCGAGCGGGTGCACAAGGTCAAGGCCAG 1800
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Db       1981 GAAGACCTGCATCGTGCCTGAGGCCTTCTTGGTCTTCACCAGCAGAGCCGCCATCCACAG 2040

Qy       2041 GATCTCCCTCGAGACCAATAACAACGACGTGGCCATCCCGCTCACGGGCGTCAAGGAGGC 2100
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Qy       2101 CTCAGCCCTGGACTTTGATGTGTCCAACAACCACATCTACTGGACAGACGTCAGCCTGAA 2160
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Qy       2161 GACCATCAGCCGCGCCTTCATGAACGGGAGCTCGGTGGAGCACGTGGTGGAGTTTGGCCT 2220
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Db       2761 CTCCCGCCAGGATGGCCTCAATGACTGTATGCACAACAACGGGCAGTGTGGGCAGCTGTG 2820

Qy       2821 CCTTGCCATCCCCGGCGGCCACCGCTGCGGCTGCGCCTCACACTACACCCTGGACCCCAG 2880
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Db       2821 CCTTGCCATCCCCGGCGGCCACCGCTGCGGCTGCGCCTCACACTACACCCTGGACCCCAG 2880

Qy       2881 CAGCCGCAACTGCAGCCCGCCCACCACCTTCTTGCTGTTCAGCCAGAAATCTGCCATCAG 2940
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Db       2881 CAGCCGCAACTGCAGCCCGCCCACCACCTTCTTGCTGTTCAGCCAGAAATCTGCCATCAG 2940

Qy       2941 TCGGATGATCCCGGACGACCAGCACAGCCCGGATCTCATCCTGCCCCCTGCATGGACTGAG 3000
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2941 TCGGATGATCCCGGACGACCAGCACAGCCCGGATCTCATCCTGCCCCTGCATGGACTGAG 3000

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Db       3001 GAACGTCAAAGCCATCGACTATGACCCACTGGACAAGTTCATCTACTGGGTGGATGGGCG 3060

Qy       3061 CCAGAACATCAAGCGAGCCAAGGACGACGGGACCCAGCCCTTTGTTTTGACCTCTCTGAG 3120
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Db       3061 CCAGAACATCAAGCGAGCCAAGGACGACGGGACCCAGCCCTTTGTTTTGACCTCTCTGAG 3120

Qy       3121 CCAAGGCCAAAACCCAGACAGGCAGCCCCACGACCTCAGCATCGACATCTACAGCCGGAC 3180
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Db       3121 CCAAGGCCAAAACCCAGACAGGCAGCCCCACGACCTCAGCATCGACATCTACAGCCGGAC 3180

Qy       3181 ACTGTTCTGGACGTGCGAGGCCACCAATACCATCAACGTCCACAGGCTGAGCGGGGAAGC 3240
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Db       3181 ACTGTTCTGGACGTGCGAGGCCACCAATACCATCAACGTCCACAGGCTGAGCGGGGAAGC 3240

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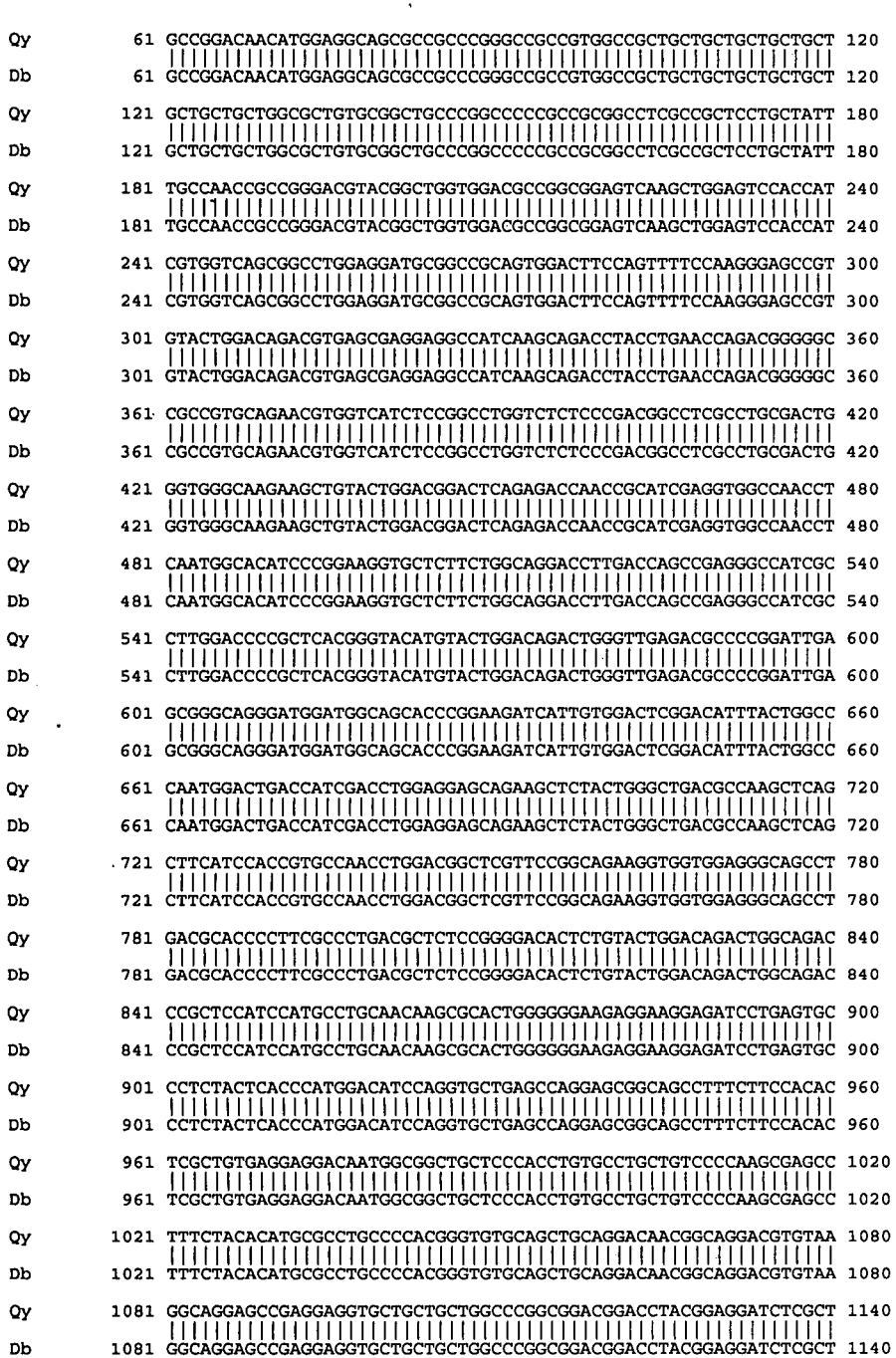
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ACCESSION AX418087
VERSION AX418087.1 GI:21523101
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ORGANISM Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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AUTHORS Carulli,J.P., Little,R.D., Recker,R.R. and Johnson,M.L.
TITLE Regulating lipid levels via the Zmax1 or HBM gene
JOURNAL Patent: WO 0192891-A 2 06-DEC-2001;
Genome Therapeutics Corporation (US) ; Creighton University School of Medicine (US)
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ORIGIN

Query Match 100.0%; Score 5120; DB 6; Length 5120;
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Db      4021 CGACGGCGAGGCAGACTGTCAGGACCGCTCAGACGAGGTGGACTGTGACGCCATCTGCCT 4080
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Db      4261 CTTCGTCATGGGTGGTGTCTATTTTGTGTGCCAGCGCGTGGTGTGCCAGCGCTATGCGGG 4320
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Db      4321 GGCCAACGGGCCCTTCCCGCACGAGTATGTCAGCGGGACCCCGCACGTGCCCCTCAATTT 4380
Qy      4381 CATAGCCCCGGGCGGTTCCCAGCATGGCCCCTTCACAGGCATCGCATGCGGAAAGTCCAT 4440
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Qy       4441 GATGAGCTCCGTGAGCCTGATGGGGGGCCGGGGCGGGGTGCCCCTCTACGACCGGAACCA 4500
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Qy       4501 CGTCACAGGGGCCTCGTCCAGCAGCTCGTCCAGCACGAAGGCCACGCTGTACCCGCCGAT 4560
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Qy       4621 CTCTTCAAACATTCCGGCCACTGCGAGACCGTACAGGCCCTACATCATTCGAGGAATGGC 4680
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Qy       4681 GCCCCCGACGACGCCCTGCAGCACCGACGTGTGTGACAGCGACTACAGCGCCAGCCGCTG 4740
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Db       4681 GCCCCCGACGACGCCCTGCAGCACCGACGTGTGTGACAGCGACTACAGCGCCAGCCGCTG 4740

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Qy       4981 AAAAAATATATTTTATGATTTAAAAAATAAATATAATTGGGATTTTAAAAACATGAGAAA 5040
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Qy       5041 TGTGAACTGTGATGGGGTGGGCAGGGCTGGGAGAACTTTGTACAGTGGAGAAATATTTAT 5100
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RESULT 4
AR567475
LOCUS       AR567475                5120 bp    DNA     linear   PAT 08-OCT-2004
DEFINITION  Sequence 1 from patent US 6780609.
ACCESSION   AR567475
VERSION     AR567475.1  GI:53985257
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 5120)
  AUTHORS   Carulli,J.P., Little,R.D., Recker,R.R. and Johnson,M.L.
  TITLE     High bone mass gene of 1.1q13.3
  JOURNAL   Patent: US 6780609-A 1 24-AUG-2004;
FEATURES             Location/Qualifiers
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                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match           100.0%;  Score 5118.4;  DB 6;  Length 5120;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 5119;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
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Qy          1 ACTAAAGCGCCGCCGCCGCGCCATGGAGCCCGAGTGAGCGCGGCGCGGGCCCGTCCGGCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ACTAAAGCGCCGCCGCCGCGCCATGGAGCCCGAGTGAGCGCGGCGCGGGCCCGTCCGGCC 60

Qy         61 GCCGGACAACATGGAGGCAGCGCCGCCCGGGCCGCCGTGGCCGCTGCTGCTGCTGCTGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCCGGACAACATGGAGGCAGCGCCGCCCGGGCCGCCGTGGCCGCTGCTGCTGCTGCTGCT 120

Qy        121 GCTGCTGCTGGCGCTGTGCGGCTGCCCGGCCCCCGCCGCGGCCTCGCCGCTCCTGCTATT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCTGCTGCTGGCGCTGTGCGGCTGCCCGGCCCCCGCCGCGGCCTCGCCGCTCCTGCTATT 180

Qy        181 TGCCAACCGCCGGGACGTACGGCTGGTGGACGCCGGCGGAGTCAAGCTGGAGTCCACCAT 240
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Db        181 TGCCAACCGCCGGGACGTACGGCTGGTGGACGCCGGCGGAGTCAAGCTGGAGTCCACCAT 240

Qy        241 CGTGGTCAGCGGCCTGGAGGATGCGGCCGCAGTGGACTTCCAGTTTTCCAAGGGAGCCGT 300
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Db        241 CGTGGTCAGCGGCCTGGAGGATGCGGCCGCAGTGGACTTCCAGTTTTCCAAGGGAGCCGT 300

Qy        301 GTACTGGACAGACGTGAGCGAGGAGGCCATCAAGCAGACCTACCTGAACCAGACGGGGGC 360
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Db        301 GTACTGGACAGACGTGAGCGAGGAGGCCATCAAGCAGACCTACCTGAACCAGACGGGGGC 360

Qy        361 CGCCGTGCAGAACGTGGTCATCTCCGGCCTGGTCTCTCCCGACGGCCTCGCCTGCGACTG 420
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Db        361 CGCCGTGCAGAACGTGGTCATCTCCGGCCTGGTCTCTCCCGACGGCCTCGCCTGCGACTG 420

Qy        421 GGTGGGCAAGAAGCTGTACTGGACGGACTCAGAGACCAACCGCATCGAGGTGGCCAACCT 480
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Qy        481 CAATGGCACATCCCGGAAGGTGCTCTTCTGGCAGGACCTTGACCAGCCGAGGGCCATCGC 540
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Qy        541 CTTGGACCCCGCTCACGGGTACATGTACTGGACAGACTGGGTTGAGACGCCCCGGATTGA 600
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Qy        601 GCGGGCAGGGATGGATGGCAGCACCCGGAAGATCATTGTGGACTCGGACATTTACTGGCC 660
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Qy        661 CAATGGACTGACCATCGACCTGGAGGAGCAGAAGCTCTACTGGGCTGACGCCAAGCTCAG 720
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Qy        721 CTTCATCCACCGTGCCAACCTGGACGGCTCGTTCCGGCAGAAGGTGGTGGAGGGCAGCCT 780
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Db        721 CTTCATCCACCGTGCCAACCTGGACGGCTCGTTCCGGCAGAAGGTGGTGGAGGGCAGCCT 780

Qy        781 GACGCACCCCTTCGCCCTGACGCTCTCCGGGGACACTCTGTACTGGACAGACTGGCAGAC 840
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Qy        901 CCTCTACTCACCCATGGACATCCAGGTGCTGAGCCAGGAGCGGCAGCCTTTCTTCCACAC 960
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Db        901 CCTCTACTCACCCATGGACATCCAGGTGCTGAGCCAGGAGCGGCAGCCTTTCTTCCACAC 960

Qy        961 TCGCTGTGAGGAGGACAATGGCGGCTGCTCCCACCTGTGCCTGCTGTCCCCAAGCGAGCC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TCGCTGTGAGGAGGACAATGGCGGCTGCTCCCACCTGTGCCTGCTGTCCCCAAGCGAGCC 1020

Qy       1021 TTTCTACACATGCGCCTGCCCCACGGGTGTGCAGCTGCAGGACAACGGCAGGACGTGTAA 1080
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Qy      1081 GGCAGGAGCCGAGGAGGTGCTGCTGCTGGCCCGGCGGACGGACCTACGGAGGATCTCGCT 1140
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Qy      1141 GGACACGCCGGACTTCACCGACATCGTGCTGCAGGTGGACGACATCCGGCACGCCATTGC 1200
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Qy      1201 CATCGACTACGACCCGCTAGAGGGCTATGTCTACTGGACAGATGACGAGGTGCGGGCCAT 1260
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Qy      1381 GGACCGCATCGAGGTGACGCGCCTCAACGGCACCTCCCGCAAGATCCTGGTGTCGGAGGA 1440
Db      1381 GGACCGCATCGAGGTGACGCGCCTCAACGGCACCTCCCGCAAGATCCTGGTGTCGGAGGA 1440

Qy      1441 CCTGGACGAGCCCCGAGCCATCGCACTGCACCCCGTGATGGGCCTCATGTACTGGACAGA 1500
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Qy      1501 CTGGGGAGAGAACCCTAAAATCGAGTGTGCCAACTTGGATGGGCAGGAGCGGCGTGTGCT 1560
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Qy      1561 GGTCAATGCCTCCCTCGGGTGGCCCAACGGCCTGGCCCTGGACCTGCAGGAGGGGAAGCT 1620
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Qy      1681 GCGGACCCTCCTGGAGGACAAGCTCCCGCACATTTTCGGGTTCACGCTGCTGGGGGACTT 1740
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Qy      1741 CATCTACTGGACTGACTGGCAGCGCCGCAGCATCGAGCGGGTGCACAAGGTCAAGGCCAG 1800
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Qy      1801 CCGGGACGTCATCATTGACCAGCTGCCCGACCTGATGGGGCTCAAAGCTGTGAATGTGGC 1860
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Qy      1861 CAAGGTCGTCGGAACCAACCCGTGTGCGGACAGGAACGGGGGGTGCAGCCACCTGTGCTT 1920
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Qy      1921 CTTCACACCCCACGCAACCCGGTGTGGCTGCCCCATCGGCCTGGAGCTGCTGAGTGACAT 1980
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Qy      1981 GAAGACCTGCATCGTGCCTGAGGCCTTCTTGGTCTTCACCAGCAGAGCCGCCATCCACAG 2040
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Qy      2041 GATCTCCCTCGAGACCAATAACAACGACGTGGCCATCCCGCTCACGGGCGTCAAGGAGGC 2100
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Qy      2101 CTCAGCCCTGGACTTTGATGTGTCCAACAACCACATCTACTGGACAGACGTCAGCCTGAA 2160
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Qy      2161 GACCATCAGCCGCGCCTTCATGAACGGGAGCTCGGTGGAGCACGTGGTGGAGTTTGGCCT 2220
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Qy      2221 TGACTACCCCGAGGGCATGGCCGTTGACTGGATGGGCAAGAACCTCTACTGGGCCGACAC 2280
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Qy      2281 TGGGACCAACAGAATCGAAGTGGCGCGGCTGGACGGGCAGTTCCGGCAAGTCCTCGTGTG 2340
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Qy      2341 GAGGGACTTGGACAACCCGAGGTCGCTGGCCCTGGATCCCACCAAGGGCTACATCTACTG 2400
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Qy      2401 GACCGAGTGGGGCGGCAAGCCGAGGATCGTGCGGGCCTTCATGGACGGGACCAACTGCAT 2460
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Qy      2701 GAACCGCACCCTCATCCAGGGCCACCTGGACTTCGTGATGGACATCCTGGTGTTCCACTC 2760
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Qy      2821 CCTTGCCATCCCCGGCGGCCACCGCTGCGGCTGCGCCTCACACTACACCCTGGACCCCAG 2880
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Qy      3421 GGTGGTGGACAACACACTGGGCAAGCTGTTCTGGGTGGACGCGGACCTGAAGCGCATTGA 3480
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Db      3601 CGAGCGTGTGGAGAAGACCACCGGGGACAAGCGGACTCGCATCCAGGGCCGTGTCGCCCA 3660
Qy      3661 CCTCACTGGCATCCATGCAGTGGAGGAAGTCAGCCTGGAGGAGTTCTCAGCCCACCCATG 3720
Db      3661 CCTCACTGGCATCCATGCAGTGGAGGAAGTCAGCCTGGAGGAGTTCTCAGCCCACCCATG 3720
Qy      3721 TGCCCGTGACAATGGTGGCTGCTCCCACATCTGTATTGCCAAGGGTGATGGGACACCACG 3780
Db      3721 TGCCCGTGACAATGGTGGCTGCTCCCACATCTGTATTGCCAAGGGTGATGGGACACCACG 3780
Qy      3781 GTGCTCATGCCCAGTCCACCTCGTGCTCCTGCAGAACCTGCTGACCTGTGGAGAGCCGCC 3840
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Qy      3841 CACCTGCTCCCCGGACCAGTTTGCATGTGCCACAGGGGAGATCGACTGTATCCCCGGGGC 3900
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Qy      3901 CTGGCGCTGTGACGGCTTTCCCGAGTGCGATGACCAGAGCGACGAGGAGGGCTGCCCCGT 3960
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Qy      4201 AGACGACAGCCCGGCCCACAGCAGTGCCATCGGGCCCGTCATTGGCATCATCCTCTCTCT 4260
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Qy      4321 GGCCAACGGGCCCTTCCCGCACGAGTATGTCAGCGGGACCCCGCACGTGCCCCTCAATTT 4380
Db      4321 GGCCAACGGGCCCTTCCCGCACGAGTATGTCAGCGGGACCCCGCACGTGCCCCTCAATTT 4380
Qy      4381 CATAGCCCCGGGCGGTTCCCAGCATGGCCCCTTCACAGGCATCGCATGCGGAAAGTCCAT 4440
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Qy      4561 CCTGAACCCGCCGCCCTCCCCGGCCACGGACCCCTCCCTGTACAACATGGACATGTTCTA 4620
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Db      5101 AAACTTAATTTTGTAAAACA 5120
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RESULT 5
AX277522
LOCUS       AX277522               5120 bp    DNA     linear   PAT 01-NOV-2001
DEFINITION  Sequence 1 from Patent WO0177327.
ACCESSION   AX277522
VERSION     AX277522.1  GI:16604715
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Carulli,J.P., Little,R.D., Recker,R.R. and Johnson,M.L.
  TITLE     The high bone mass gene of 11q13.3
  JOURNAL   Patent: WO 0177327-A 1 18-OCT-2001;
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FEATURES             Location/Qualifiers
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                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match           100.0%;  Score 5118.4;  DB 6;  Length 5120;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 5119;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ACTAAAGCGCCGCCGCCGCGCCATGGAGCCCGAGTGAGCGCGGCGCGGGCCCGTCCGGCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ACTAAAGCGCCGCCGCCGCGCCATGGAGCCCGAGTGAGCGCGGCGCGGGCCCGTCCGGCC 60

Qy         61 GCCGGACAACATGGAGGCAGCGCCGCCCGGGCCGCCGTGGCCGCTGCTGCTGCTGCTGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        121 GCTGCTGCTGGCGCTGTGCGGCTGCCCGGCCCCCGCCGCGGCCTCGCCGCTCCTGCTATT 180
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Qy        181 TGCCAACCGCCGGGACGTACGGCTGGTGGACGCCGGCGGAGTCAAGCTGGAGTCCACCAT 240
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Qy        241 CGTGGTCAGCGGCCTGGAGGATGCGGCCGCAGTGGACTTCCAGTTTTCCAAGGGAGCCGT 300
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Qy        301 GTACTGGACAGACGTGAGCGAGGAGGCCATCAAGCAGACCTACCTGAACCAGACGGGGGC 360
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Qy        661 CAATGGACTGACCATCGACCTGGAGGAGCAGAAGCTCTACTGGGCTGACGCCAAGCTCAG 720
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Qy        841 CCGCTCCATCCATGCCTGCAACAAGCGCACTGGGGGGAAGAGGAAGGAGATCCTGAGTGC 900
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Qy        901 CCTCTACTCACCCATGGACATCCAGGTGCTGAGCCAGGAGCGGCAGCCTTTCTTCCACAC 960
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Qy       1081 GGCAGGAGCCGAGGAGGTGCTGCTGCTGGCCCGGCGGACGGACCTACGGAGGATCTCGCT 1140
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Qy       2821 CCTTGCCATCCCCGGCGGCCACCGCTGCGGCTGCGCCTCACACTACACCCTGGACCCCAG 2880
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Db       2821 CCTTGCCATCCCCGGCGGCCACCGCTGCGGCTGCGCCTCACACTACACCCTGGACCCCAG 2880
Qy       2881 CAGCCGCAACTGCAGCCCGCCCACCACCTTCTTGCTGTTCAGCCAGAAATCTGCCATCAG 2940
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2881 CAGCCGCAACTGCAGCCCGCCCACCACCTTCTTGCTGTTCAGCCAGAAATCTGCCATCAG 2940
Qy       2941 TCGGATGATCCCGGACGACCAGCACAGCCCGGATCTCATCCTGCCCCTGCATGGACTGAG 3000
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Db       2941 TCGGATGATCCCGGACGACCAGCACAGCCCGGATCTCATCCTGCCCCTGCATGGACTGAG 3000
Qy       3001 GAACGTCAAAGCCATCGACTATGACCCACTGGACAAGTTCATCTACTGGGTGGATGGGCG 3060
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Qy       3181 ACTGTTCTGGACGTGCGAGGCCACCAATACCATCAACGTCCACAGGCTGAGCGGGGAAGC 3240
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Qy       3541 TCTGGGCCTGACCATCCTTGGCAAGCATCTCTACTGGATCGACCGCCAGCAGCAGATGAT 3600
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Qy       3781 GTGCTCATGCCCAGTCCACCTCGTGCTCCTGCAGAACCTGCTGACCTGTGGAGAGCCGCC 3840
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Db       3781 GTGCTCATGCCCAGTCCACCTCGTGCTCCTGCAGAACCTGCTGACCTGTGGAGAGCCGCC 3840
Qy       3841 CACCTGCTCCCCGGACCAGTTTGCATGTGCCACAGGGGAGATCGACTGTATCCCCGGGGC 3900
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Qy       3901 CTGGCGCTGTGACGGCTTTCCCGAGTGCGATGACCAGAGCGACGAGGAGGGCTGCCCCGT 3960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       4021 CGACGGCGAGGCAGACTGTCAGGACCGCTCAGACGAGGTGGACTGTGACGCCATCTGCCT 4080
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Db       4021 CGACGGCGAGGCAGACTGTCAGGACCGCTCAGACGAGGTGGACTGTGACGCCATCTGCCT 4080
Qy       4081 GCCCAACCAGTTCCGGTGTGCGAGCGGCCAGTGTGTCCTCATCAAACAGCAGTGCGACTC 4140
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Qy       4141 CTTCCCCGACTGTATCGACGGCTCCGACGAGCTCATGTGTGAAATCACCAAGCCGCCCTC 4200
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Qy       4201 AGACGACAGCCCGGCCCACAGCAGTGCCATCGGGCCCGTCATTGGCATCATCCTCTCTCT 4260
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Qy       4261 CTTCGTCATGGGTGGTGTCTATTTTGTGTGCCAGCGCGTGGTGTGCCAGCGCTATGCGGG 4320
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Qy       4321 GGCCAACGGGCCCTTCCCGCACGAGTATGTCAGCGGGACCCCGCACGTGCCCCTCAATTT 4380
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Qy       4381 CATAGCCCCGGGCGGTTCCCAGCATGGCCCCTTCACAGGCATCGCATGCGGAAAGTCCAT 4440
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Qy       4681 GCCCCCGACGACGCCCTGCAGCACCGACGTGTGTGACAGCGACTACAGCGCCAGCCGCTG 4740
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Qy       4741 GAAGGCCAGCAAGTACTACCTGGATTTGAACTCGGACTCAGACCCCTATCCACCCCCACC 4800
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Qy       4801 CACGCCCCACAGCCAGTACCTGTCGGCGGAGGACAGCTGCCCGCCCTCGCCCGCCACCGA 4860
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Qy       4861 GAGGAGCTACTTCCATCTCTTCCCGCCCCCTCCGTCCCCCTGCACGGACTCATCCTGACC 4920
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Qy       4921 TCGGCCGGGCCACTCTGGCTTCTCTGTGCCCCTGTAAATAGTTTTAAATATGAACAAAGA 4980
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Qy       4981 AAAAAATATATTTTATGATTTAAAAAATAAATATAATTGGGATTTTAAAAACATGAGAAA 5040
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Qy       5041 TGTGAACTGTGATGGGGTGGGCAGGGCTGGGAGAACTTTGTACAGTGGAGAAATATTTAT 5100
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Qy       5101 AAACTTAATTTTGTAAAACA 5120
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Db       5101 AAACTTAATTTTGTAAAACA 5120


RESULT 6
AX418086
LOCUS       AX418086               5120 bp    DNA     linear   PAT 18-JUN-2002
DEFINITION  Sequence 1 from Patent WO0192891.
ACCESSION   AX418086
VERSION     AX418086.1  GI:21523100
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Carulli,J.P., Little,R.D., Recker,R.R. and Johnson,M.L.
  TITLE     Regulating lipid levels via the Zmax1 or HBM gene
  JOURNAL   Patent: WO 0192891-A 1 06-DEC-2001;
            Genome Therapeutics Corporation (US) ; Creighton University School
            of Medicine (US)
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match           100.0%;  Score 5118.4;  DB 6;  Length 5120;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 5119;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ACTAAAGCGCCGCCGCCGCGCCATGGAGCCCGAGTGAGCGCGGCGCGGGCCCGTCCGGCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ACTAAAGCGCCGCCGCCGCGCCATGGAGCCCGAGTGAGCGCGGCGCGGGCCCGTCCGGCC 60

Qy         61 GCCGGACAACATGGAGGCAGCGCCGCCCGGGCCGCCGTGGCCGCTGCTGCTGCTGCTGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCCGGACAACATGGAGGCAGCGCCGCCCGGGCCGCCGTGGCCGCTGCTGCTGCTGCTGCT 120

Qy        121 GCTGCTGCTGGCGCTGTGCGGCTGCCCGGCCCCCGCCGCGGCCTCGCCGCTCCTGCTATT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCTGCTGCTGGCGCTGTGCGGCTGCCCGGCCCCCGCCGCGGCCTCGCCGCTCCTGCTATT 180

Qy        181 TGCCAACCGCCGGGACGTACGGCTGGTGGACGCCGGCGGAGTCAAGCTGGAGTCCACCAT 240
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Db        181 TGCCAACCGCCGGGACGTACGGCTGGTGGACGCCGGCGGAGTCAAGCTGGAGTCCACCAT 240

Qy        241 CGTGGTCAGCGGCCTGGAGGATGCGGCCGCAGTGGACTTCCAGTTTTCCAAGGGAGCCGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CGTGGTCAGCGGCCTGGAGGATGCGGCCGCAGTGGACTTCCAGTTTTCCAAGGGAGCCGT 300

Qy        301 GTACTGGACAGACGTGAGCGAGGAGGCCATCAAGCAGACCTACCTGAACCAGACGGGGGC 360
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Db        301 GTACTGGACAGACGTGAGCGAGGAGGCCATCAAGCAGACCTACCTGAACCAGACGGGGGC 360

Qy        361 CGCCGTGCAGAACGTGGTCATCTCCGGCCTGGTCTCTCCCGACGGCCTCGCCTGCGACTG 420
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Db        361 CGCCGTGCAGAACGTGGTCATCTCCGGCCTGGTCTCTCCCGACGGCCTCGCCTGCGACTG 420

Qy        421 GGTGGGCAAGAAGCTGTACTGGACGGACTCAGAGACCAACCGCATCGAGGTGGCCAACCT 480
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Qy        481 CAATGGCACATCCCGGAAGGTGCTCTTCTGGCAGGACCTTGACCAGCCGAGGGCCATCGC 540
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Qy        541 CTTGGACCCCGCTCACGGGTACATGTACTGGACAGACTGGGTTGAGACGCCCCGGATTGA 600
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Qy        601 GCGGGCAGGGATGGATGGCAGCACCCGGAAGATCATTGTGGACTCGGACATTTACTGGCC 660
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Qy        661 CAATGGACTGACCATCGACCTGGAGGAGCAGAAGCTCTACTGGGCTGACGCCAAGCTCAG 720
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Db        661 CAATGGACTGACCATCGACCTGGAGGAGCAGAAGCTCTACTGGGCTGACGCCAAGCTCAG 720

Qy        721 CTTCATCCACCGTGCCAACCTGGACGGCTCGTTCCGGCAGAAGGTGGTGGAGGGCAGCCT 780
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Db        721 CTTCATCCACCGTGCCAACCTGGACGGCTCGTTCCGGCAGAAGGTGGTGGAGGGCAGCCT 780

Qy        781 GACGCACCCCTTCGCCCTGACGCTCTCCGGGGACACTCTGTACTGGACAGACTGGCAGAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACGCACCCCTTCGCCCTGACGCTCTCCGGGGACACTCTGTACTGGACAGACTGGCAGAC 840

Qy        841 CCGCTCCATCCATGCCTGCAACAAGCGCACTGGGGGGAAGAGGAAGGAGATCCTGAGTGC 900
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Db        841 CCGCTCCATCCATGCCTGCAACAAGCGCACTGGGGGGAAGAGGAAGGAGATCCTGAGTGC 900
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Db        901 CCTCTACTCACCCATGGACATCCAGGTGCTGAGCCAGGAGCGGCAGCCTTTCTTCCACAC 960
Qy        961 TCGCTGTGAGGAGGACAATGGCGGCTGCTCCCACCTGTGCCTGCTGTCCCCAAGCGAGCC 1020
Db        961 TCGCTGTGAGGAGGACAATGGCGGCTGCTCCCACCTGTGCCTGCTGTCCCCAAGCGAGCC 1020
Qy       1021 TTTCTACACATGCGCCTGCCCCACGGGTGTGCAGCTGCAGGACAACGGCAGGACGTGTAA 1080
Db       1021 TTTCTACACATGCGCCTGCCCCACGGGTGTGCAGCTGCAGGACAACGGCAGGACGTGTAA 1080
Qy       1081 GGCAGGAGCCGAGGAGGTGCTGCTGCTGGCCCGGCGGACGGACCTACGGAGGATCTCGCT 1140
Db       1081 GGCAGGAGCCGAGGAGGTGCTGCTGCTGGCCCGGCGGACGGACCTACGGAGGATCTCGCT 1140
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Qy       1321 CCCCGATGGCATCGCGGTCGACTGGGTGGCCCGAAACCTCTACTGGACCGACACGGGCAC 1380
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Qy       1501 CTGGGGAGAGAACCCTAAAATCGAGTGTGCCAACTTGGATGGGCAGGAGCGGCGTGTGCT 1560
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Qy       1741 CATCTACTGGACTGACTGGCAGCGCCGCAGCATCGAGCGGGTGCACAAGGTCAAGGCCAG 1800
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Qy       1861 CAAGGTCGTCGGAACCAACCCGTGTGCGGACAGGAACGGGGGGTGCAGCCACCTGTGCTT 1920
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Qy       1921 CTTCACACCCCACGCAACCCGGTGTGGCTGCCCCATCGGCCTGGAGCTGCTGAGTGACAT 1980
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Db       1921 CTTCACACCCCACGCAACCCGGTGTGGCTGCCCCATCGGCCTGGAGCTGCTGAGTGACAT 1980
Qy       1981 GAAGACCTGCATCGTGCCTGAGGCCTTCTTGGTCTTCACCAGCAGAGCCGCCATCCACAG 2040
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Qy       2041 GATCTCCCTCGAGACCAATAACAACGACGTGGCCATCCCGCTCACGGGCGTCAAGGAGGC 2100
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Qy       2161 GACCATCAGCCGCGCCTTCATGAACGGGAGCTCGGTGGAGCACGTGGTGGAGTTTGGCCT 2220
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Qy       2221 TGACTACCCCGAGGGCATGGCCGTTGACTGGATGGGCAAGAACCTCTACTGGGCCGACAC 2280
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Qy       2581 GCGGGTCGTGATTGCCGACGATCTCCCGCACCCGTTCGGTCTGACGCAGTACAGCGATTA 2640
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Qy       2641 TATCTACTGGACAGACTGGAATCTGCACAGCATTGAGCGGGCCGACAAGACTAGCGGCCG 2700
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Qy       3061 CCAGAACATCAAGCGAGCCAAGGACGACGGGACCCAGCCCTTTGTTTTGACCTCTCTGAG 3120
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             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3481 GAGCTGTGACCTGTCAGGGGCCAACCGCCTGACCCTGGAGGACGCCAACATCGTGCAGCC 3540

Qy       3541 TCTGGGCCTGACCATCCTTGGCAAGCATCTCTACTGGATCGACCGCCAGCAGCAGATGAT 3600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3541 TCTGGGCCTGACCATCCTTGGCAAGCATCTCTACTGGATCGACCGCCAGCAGCAGATGAT 3600

Qy       3601 CGAGCGTGTGGAGAAGACCACCGGGGACAAGCGGACTCGCATCCAGGGCCGTGTCGCCCA 3660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       3661 CCTCACTGGCATCCATGCAGTGGAGGAAGTCAGCCTGGAGGAGTTCTCAGCCCACCCATG 3720
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Db       3661 CCTCACTGGCATCCATGCAGTGGAGGAAGTCAGCCTGGAGGAGTTCTCAGCCCACCCATG 3720

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Db       3781 GTGCTCATGCCCAGTCCACCTCGTGCTCCTGCAGAACCTGCTGACCTGTGGAGAGCCGCC 3840

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Qy       4021 CGACGGCGAGGCAGACTGTCAGGACCGCTCAGACGAGGTGGACTGTGACGCCATCTGCCT 4080
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Qy       4441 GATGAGCTCCGTGAGCCTGATGGGGGGCCGGGGCGGGGTGCCCCTCTACGACCGGAACCA 4500
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RESULT 7
CQ870240
LOCUS CQ870240 5099 bp DNA linear PAT 13-SEP-2004
DEFINITION Sequence 661 from Patent WO2004074320.

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ACCESSION   CQ870240
VERSION     CQ870240.1  GI:51999859
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Morris,D.W., Morris,D.W. and Malandro,M.S.
  TITLE     Novel therapeutic targets in cancer
  JOURNAL   Patent: WO 2004074320-A 661 02-SEP-2004;
            Sagres Discovery, Inc. (US)
FEATURES             Location/Qualifiers
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                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             99.5%;  Score 5094.8;  DB 6;  Length 5099;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 5096;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         23 ATGGAGCCCGAGTGAGCGCGGCGCGGGCCCGTCCGGCCGCCGGACAACATGGAGGCAGCG 82
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGAGCCCGAGTGAGCGCGGCGCGGGCCCGTCCGGCCGCCGGACAACATGGAGGCAGCG 60

Qy         83 CCGCCCGGGCCGCCGTGGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGGCGCTGTGCGGC 142
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Qy        203 CTGGTGGACGCCGGCGGAGTCAAGCTGGAGTCCACCATCGTGGTCAGCGGCCTGGAGGAT 262
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Qy        263 GCGGCCGCAGTGGACTTCCAGTTTTCCAAGGGAGCCGTGTACTGGACAGACGTGAGCGAG 322
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Qy        383 TCCGGCCTGGTCTCTCCCGACGGCCTCGCCTGCGACTGGGTGGGCAAGAAGCTGTACTGG 442
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Qy        623 ACCCGGAAGATCATTGTGGACTCGGACATTTACTGGCCCAATGGACTGACCATCGACCTG 682
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Qy        683 GAGGAGCAGAAGCTCTACTGGGCTGACGCCAAGCTCAGCTTCATCCACCGTGCCAACCTG 742
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Db        721 GACGGCTCGTTCCGGCAGAAGGTGGTGGAGGGCAGCCTGACGCACCCCTTCGCCCTGACG 780

Qy        803 CTCTCCGGGGACACTCTGTACTGGACAGACTGGCAGACCCGCTCCATCCATGCCTGCAAC 862
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Qy        863 AAGCGCACTGGGGGGAAGAGGAAGGAGATCCTGAGTGCCCTCTACTCACCCATGGACATC 922
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Qy        923 CAGGTGCTGAGCCAGGAGCGGCAGCCTTTCTTCCACACTCGCTGTGAGGAGGACAATGGC 982
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        983 GGCTGCTCCCACCTGTGCCTGCTGTCCCCAAGCGAGCCTTTCTACACATGCGCCTGCCCC 1042
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Db        961 GGCTGCTCCCACCTGTGCCTGCTGTCCCCAAGCGAGCCTTTCTACACATGCGCCTGCCCC 1020

Qy       1043 ACGGGTGTGCAGCTGCAGGACAACGGCAGGACGTGTAAGGCAGGAGCCGAGGAGGTGCTG 1102
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Qy       1223 GGCTATGTCTACTGGACAGATGACGAGGTGCGGGCCATCCGCAGGGCGTACCTGGACGGG 1282
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Db       1201 GGCTATGTCTACTGGACAGATGACGAGGTGCGGGCCATCCGCAGGGCGTACCTGGACGGG 1260

Qy       1283 TCTGGGGCGCAGACGCTGGTCAACACCGAGATCAACGACCCCGATGGCATCGCGGTCGAC 1342
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Qy       1463 GCACTGCACCCCGTGATGGGCCTCATGTACTGGACAGACTGGGGAGAGAACCCTAAAATC 1522
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Qy       1883 TGTGCGGACAGGAACGGGGGGTGCAGCCACCTGTGCTTCTTCACACCCCACGCAACCCGG 1942
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Qy       1943 TGTGGCTGCCCCATCGGCCTGGAGCTGCTGAGTGACATGAAGACCTGCATCGTGCCTGAG 2002
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Qy       2243 GTTGACTGGATGGGCAAGAACCTCTACTGGGCCGACACTGGGACCAACAGAATCGAAGTG 2302
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Db       2221 GTTGACTGGATGGGCAAGAACCTCTACTGGGCCGACACTGGGACCAACAGAATCGAAGTG 2280

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Qy       2663 CTGCACAGCATTGAGCGGGCCGACAAGACTAGCGGCCGGAACCGCACCCTCATCCAGGGC 2722
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Qy       2723 CACCTGGACTTCGTGATGGACATCCTGGTGTTCCACTCCTCCCGCCAGGATGGCCTCAAT 2782
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Qy       2783 GACTGTATGCACAACAACGGGCAGTGTGGGCAGCTGTGCCTTGCCATCCCCGGCGGCCAC 2842
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Db       2761 GACTGTATGCACAACAACGGGCAGTGTGGGCAGCTGTGCCTTGCCATCCCCGGCGGCCAC 2820

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             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2821 CGCTGCGGCTGCGCCTCACACTACACCCTGGACCCCAGCAGCCGCAACTGCAGCCCGCCC 2880

Qy       2903 ACCACCTTCTTGCTGTTCAGCCAGAAATCTGCCATCAGTCGGATGATCCCGGACGACCAG 2962
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Db       2941 CACAGCCCGGATCTCATCCTGCCCCTGCATGGACTGAGGAACGTCAAAGCCATCGACTAT 3000

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Qy       3203 ACCAATACCATCAACGTCCACAGGCTGAGCGGGGAAGCCATGGGGGTGGTGCTGCGTGGG 3262
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Qy       3323 AACATGCAGGACCGGGCAGCCAAGATCGAACGCGCAGCCCTGGACGGCACCGAGCGCGAG 3382
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Qy       3383 GTCCTCTTCACCACCGGCCTCATCCGCCCTGTGGCCCTGGTGGTGGACAACACACTGGGC 3442
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Qy       3443 AAGCTGTTCTGGGTGGACGCGGACCTGAAGCGCATTGAGAGCTGTGACCTGTCAGGGGCC 3502
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RESULT 8
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DEFINITION  Sequence 145 from Patent WO03000928.
ACCESSION   AX658229
VERSION     AX658229.1  GI:29160770
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Poulsen,H.S., Pedersen,N., Mortensen,S., Sorensen,S.B.,
            Petersen,M.W. and Elsner,H.I.
  TITLE     Methods for identification of cancer cell surface molecules and
            cancer specific promoters, and therapeutic uses thereof
  JOURNAL   Patent: WO 03000928-A 145 03-JAN-2003;
            Odin Medical A/S (DK)
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ORIGIN

  Query Match             99.4%;  Score 5091.6;  DB 6;  Length 5135;
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  Matches 5094;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

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Qy       3248 GTGGTGCTGCGTGGGGACCGCGACAAGCCCAGGGCCATCGTCGTCAACGCGGAGCGAGGG 3307
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Db       3266 GTGGTGCTGCGTGGGGACCGCGACAAGCCCAGGGCCATCGTCGTCAACGCGGAGCGAGGG 3325

Qy       3308 TACCTGTACTTCACCAACATGCAGGACCGGGCAGCCAAGATCGAACGCGCAGCCCTGGAC 3367
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3326 TACCTGTACTTCACCAACATGCAGGACCGGGCAGCCAAGATCGAACGCGCAGCCCTGGAC 3385

Qy       3368 GGCACCGAGCGCGAGGTCCTCTTCACCACCGGCCTCATCCGCCCTGTGGCCCTGGTGGTG 3427
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Db       3386 GGCACCGAGCGCGAGGTCCTCTTCACCACCGGCCTCATCCGCCCTGTGGCCCTGGTGGTG 3445

Qy       3428 GACAACACACTGGGCAAGCTGTTCTGGGTGGACGCGGACCTGAAGCGCATTGAGAGCTGT 3487
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Qy       3488 GACCTGTCAGGGGCCAACCGCCTGACCCTGGAGGACGCCAACATCGTGCAGCCTCTGGGC 3547
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Db       3506 GACCTGTCAGGGGCCAACCGCCTGACCCTGGAGGACGCCAACATCGTGCAGCCTCTGGGC 3565

Qy       3548 CTGACCATCCTTGGCAAGCATCTCTACTGGATCGACCGCCAGCAGCAGATGATCGAGCGT 3607
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Db       3566 CTGACCATCCTTGGCAAGCATCTCTACTGGATCGACCGCCAGCAGCAGATGATCGAGCGT 3625

Qy       3608 GTGGAGAAGACCACCGGGGACAAGCGGACTCGCATCCAGGGCCGTGTCGCCCACCTCACT 3667
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3626 GTGGAGAAGACCACCGGGGACAAGCGGACTCGCATCCAGGGCCGTGTCGCCCACCTCACT 3685

Qy       3668 GGCATCCATGCAGTGGAGGAAGTCAGCCTGGAGGAGTTCTCAGCCCACCCATGTGCCCGT 3727
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Db       3686 GGCATCCATGCAGTGGAGGAAGTCAGCCTGGAGGAGTTCTCAGCCCACCCATGTGCCCGT 3745

Qy       3728 GACAATGGTGGCTGCTCCCACATCTGTATTGCCAAGGGTGATGGGACACCACGGTGCTCA 3787
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Db       3746 GACAATGGTGGCTGCTCCCACATCTGTATTGCCAAGGGTGATGGGACACCACGGTGCTCA 3805

Qy       3788 TGCCCAGTCCACCTCGTGCTCCTGCAGAACCTGCTGACCTGTGGAGAGCCGCCCACCTGC 3847
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Qy       3848 TCCCCGGACCAGTTTGCATGTGCCACAGGGGAGATCGACTGTATCCCCGGGGCCTGGCGC 3907
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Qy       3908 TGTGACGGCTTTCCCGAGTGCGATGACCAGAGCGACGAGGAGGGCTGCCCCGTGTGCTCC 3967
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Qy       3968 GCCGCCCAGTTCCCCTGCGCGCGGGGTCAGTGTGTGGACCTGCGCCTGCGCTGCGACGGC 4027
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Qy       4028 GAGGCAGACTGTCAGGACCGCTCAGACGAGGTGGACTGTGACGCCATCTGCCTGCCCAAC 4087
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Qy       4088 CAGTTCCGGTGTGCGAGCGGCCAGTGTGTCCTCATCAAACAGCAGTGCGACTCCTTCCCC 4147
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Db       4106 CAGTTCCGGTGTGCGAGCGGCCAGTGTGTCCTCATCAAACAGCAGTGCGACTCCTTCCCC 4165

Qy       4148 GACTGTATCGACGGCTCCGACGAGCTCATGTGTGAAATCACCAAGCCGCCCTCAGACGAC 4207
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4166 GACTGTATCGACGGCTCCGACGAGCTCATGTGTGAAATCACCAAGCCGCCCTCAGACGAC 4225

Qy       4208 AGCCCGGCCCACAGCAGTGCCATCGGGCCCGTCATTGGCATCATCCTCTCTCTCTTCGTC 4267
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4226 AGCCCGGCCCACAGCAGTGCCATCGGGCCCGTCATTGGCATCATCCTCTCTCTCTTCGTC 4285

Qy       4268 ATGGGTGGTGTCTATTTTGTGTGCCAGCGCGTGGTGTGCCAGCGCTATGCGGGGGCCAAC 4327
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Db       4286 ATGGGTGGTGTCTATTTTGTGTGCCAGCGCGTGGTGTGCCAGCGCTATGCGGGGGCCAAC 4345

Qy       4328 GGGCCCTTCCCGCACGAGTATGTCAGCGGGACCCCGCACGTGCCCCTCAATTTCATAGCC 4387
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4346 GGGCCCTTCCCGCACGAGTATGTCAGCGGGACCCCGCACGTGCCCCTCAATTTCATAGCC 4405

Qy       4388 CCGGGCGGTTCCCAGCATGGCCCCTTCACAGGCATCGCATGCGGAAAGTCCATGATGAGC 4447
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Qy       4448 TCCGTGAGCCTGATGGGGGGCCGGGGCGGGGTGCCCCTCTACGACCGGAACCACGTCACA 4507
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Qy       4508 GGGGCCTCGTCCAGCAGCTCGTCCAGCACGAAGGCCACGCTGTACCCGCCGATCCTGAAC 4567
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Db       4526 GGGGCCTCGTCCAGCAGCTCGTCCAGCACGAAGGCCACGCTGTACCCGCCGATCCTGAAC 4585

Qy       4568 CCGCCGCCCTCCCCGGCCACGGACCCCTCCCTGTACAACATGGACATGTTCTACTCTTCA 4627
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Qy       4628 AACATTCCGGCCACTGCGAGACCGTACAGGCCCTACATCATTCGAGGAATGGCGCCCCCG 4687
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Qy       4688 ACGACGCCCTGCAGCACCGACGTGTGTGACAGCGACTACAGCGCCAGCCGCTGGAAGGCC 4747
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Qy       4748 AGCAAGTACTACCTGGATTTGAACTCGGACTCAGACCCCTATCCACCCCCACCCACGCCC 4807
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Qy       4808 CACAGCCAGTACCTGTCGGCGGAGGACAGCTGCCCGCCCTCGCCCGCCACCGAGAGGAGC 4867
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Qy       4988 ATATTTTATGATTTAAAAAATAAATATAATTGGGATTTTAAAAACATGAGAAATGTGAAC 5047
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Db       5006 ATATTTTATGATTTAAAAAATAAATATAATTGGGATTTTAAAAACATGAGAAATGTGAAC 5065

Qy       5048 TGTGATGGGGTGGGCAGGGCTGGGAGAACTTTGTACAGTGGAGAAATATTTATAAACT 5105
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Db      1046 ACATGCGCCTGCCCCACGGGTGTGCAGCTGCAGGACAACGGCAGGACGTGTAAGGCAGGA 1105
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Qy      1148 CCGGACTTCACCGACATCGTGCTGCAGGTGGACGACATCCGGCACGCCATTGCCATCGAC 1207
Db      1166 CCGGACTTCACCGACATCGTGCTGCAGGTGGACGACATCCGGCACGCCATTGCCATCGAC 1225
Qy      1208 TACGACCCGCTAGAGGGCTATGTCTACTGGACAGATGACGAGGTGCGGGCCATCCGCAGG 1267
Db      1226 TACGACCCGCTAGAGGGCTATGTCTACTGGACAGATGACGAGGTGCGGGCCATCCGCAGG 1285
Qy      1268 GCGTACCTGGACGGGTCTGGGGCGCAGACGCTGGTCAACACCGAGATCAACGACCCCGAT 1327
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Qy      1388 ATCGAGGTGACGCGCCTCAACGGCACCTCCCGCAAGATCCTGGTGTCGGAGGACCTGGAC 1447
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Qy      1568 GCCTCCCTCGGGTGGCCCAACGGCCTGGCCCTGGACCTGCAGGAGGGGAAGCTCTACTGG 1627
Db      1586 GCCTCCCTCGGGTGGCCCAACGGCCTGGCCCTGGACCTGCAGGAGGGGAAGCTCTACTGG 1645
Qy      1628 GGAGACGCCAAGACAGACAAGATCGAGGTGATCAATGTTGATGGGACGAAGAGGCGGACC 1687
Db      1646 GGAGACGCCAAGACAGACAAGATCGAGGTGATCAATGTTGATGGGACGAAGAGGCGGACC 1705
Qy      1688 CTCCTGGAGGACAAGCTCCCGCACATTTTCGGGTTCACGCTGCTGGGGGACTTCATCTAC 1747
Db      1706 CTCCTGGAGGACAAGCTCCCGCACATTTTCGGGTTCACGCTGCTGGGGGACTTCATCTAC 1765
Qy      1748 TGGACTGACTGGCAGCGCCGCAGCATCGAGCGGGTGCACAAGGTCAAGGCCAGCCGGGAC 1807
Db      1766 TGGACTGACTGGCAGCGCCGCAGCATCGAGCGGGTGCACAAGGTCAAGGCCAGCCGGGAC 1825
Qy      1808 GTCATCATTGACCAGCTGCCCGACCTGATGGGGCTCAAAGCTGTGAATGTGGCCAAGGTC 1867
Db      1826 GTCATCATTGACCAGCTGCCCGACCTGATGGGGCTCAAAGCTGTGAATGTGGCCAAGGTC 1885
Qy      1868 GTCGGAACCAACCCGTGTGCGGACAGGAACGGGGGGTGCAGCCACCTGTGCTTCTTCACA 1927
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Qy      1928 CCCCACGCAACCCGGTGTGGCTGCCCCATCGGCCTGGAGCTGCTGAGTGACATGAAGACC 1987
Db      1946 CCCCACGCAACCCGGTGTGGCTGCCCCATCGGCCTGGAGCTGCTGAGTGACATGAAGACC 2005
Qy      1988 TGCATCGTGCCTGAGGCCTTCTTGGTCTTCACCAGCAGAGCCGCCATCCACAGGATCTCC 2047
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Qy      2348 TTGGACAACCCGAGGTCGCTGGCCCTGGATCCCACCAAGGGCTACATCTACTGGACCGAG 2407
Db      2366 TTGGACAACCCGAGGTCGCTGGCCCTGGATCCCACCAAGGGCTACATCTACTGGACCGAG 2425
Qy      2408 TGGGGCGGCAAGCCGAGGATCGTGCGGGCCTTCATGGACGGGACCAACTGCATGACGCTG 2467
Db      2426 TGGGGCGGCAAGCCGAGGATCGTGCGGGCCTTCATGGACGGGACCAACTGCATGACGCTG 2485
Qy      2468 GTGGACAAGGTGGGCCGGGCCAACGACCTCACCATTGACTACGCTGACCAGCGCCTCTAC 2527
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Qy      2528 TGGACCGACCTGGACACCAACATGATCGAGTCGTCCAACATGCTGGGTCAGGAGCGGGTC 2587
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Qy      2588 GTGATTGCCGACGATCTCCCGCACCCGTTCGGTCTGACGCAGTACAGCGATTATATCTAC 2647
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Qy      2648 TGGACAGACTGGAATCTGCACAGCATTGAGCGGGCCGACAAGACTAGCGGCCGGAACCGC 2707
Db      2666 TGGACAGACTGGAATCTGCACAGCATTGAGCGGGCCGACAAGACTAGCGGCCGGAACCGC 2725
Qy      2708 ACCCTCATCCAGGGCCACCTGGACTTCGTGATGGACATCCTGGTGTTCCACTCCTCCCGC 2767
Db      2726 ACCCTCATCCAGGGCCACCTGGACTTCGTGATGGACATCCTGGTGTTCCACTCCTCCCGC 2785
Qy      2768 CAGGATGGCCTCAATGACTGTATGCACAACAACGGGCAGTGTGGGCAGCTGTGCCTTGCC 2827
Db      2786 CAGGATGGCCTCAATGACTGTATGCACAACAACGGGCAGTGTGGGCAGCTGTGCCTTGCC 2845
Qy      2828 ATCCCCGGCGGCCACCGCTGCGGCTGCGCCTCACACTACACCCTGGACCCCAGCAGCCGC 2887
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Qy      3008 AAAGCCATCGACTATGACCCACTGGACAAGTTCATCTACTGGGTGGATGGGCGCCAGAAC 3067
Db      3026 AAAGCCATCGACTATGACCCACTGGACAAGTTCATCTACTGGGTGGATGGGCGCCAGAAC 3085
Qy      3068 ATCAAGCGAGCCAAGGACGACGGGACCCAGCCCTTTGTTTTGACCTCTCTGAGCCAAGGC 3127
Db      3086 ATCAAGCGAGCCAAGGACGACGGGACCCAGCCCTTTGTTTTGACCTCTCTGAGCCAAGGC 3145
Qy      3128 CAAAACCCAGACAGGCAGCCCCACGACCTCAGCATCGACATCTACAGCCGGACACTGTTC 3187
Db      3146 CAAAACCCAGACAGGCAGCCCCACGACCTCAGCATCGACATCTACAGCCGGACACTGTTC 3205
Qy      3188 TGGACGTGCGAGGCCACCAATACCATCAACGTCCACAGGCTGAGCGGGGAAGCCATGGGG 3247
Db      3206 TGGACGTGCGAGGCCACCAATACCATCAACGTCCACAGGCTGAGCGGGGAAGCCATGGGG 3265
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Qy       3248 GTGGTGCTGCGTGGGGACCGCGACAAGCCCAGGGCCATCGTCGTCAACGCGGAGCGAGGG 3307
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Db       3266 GTGGTGCTGCGTGGGGACCGCGACAAGCCCAGGGCCATCGTCGTCAACGCGGAGCGAGGG 3325

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Qy       3368 GGCACCGAGCGCGAGGTCCTCTTCACCACCGGCCTCATCCGCCCTGTGGCCCTGGTGGTG 3427
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Db       3506 GACCTGTCAGGGGCCAACCGCCTGACCCTGGAGGACGCCAACATCGTGCAGCCTCTGGGC 3565

Qy       3548 CTGACCATCCTTGGCAAGCATCTCTACTGGATCGACCGCCAGCAGCAGATGATCGAGCGT 3607
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Db       3566 CTGACCATCCTTGGCAAGCATCTCTACTGGATCGACCGCCAGCAGCAGATGATCGAGCGT 3625

Qy       3608 GTGGAGAAGACCACCGGGGACAAGCGGACTCGCATCCAGGGCCGTGTCGCCCACCTCACT 3667
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3626 GTGGAGAAGACCACCGGGGACAAGCGGACTCGCATCCAGGGCCGTGTCGCCCACCTCACT 3685

Qy       3668 GGCATCCATGCAGTGGAGGAAGTCAGCCTGGAGGAGTTCTCAGCCCACCCATGTGCCCGT 3727
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Qy       3728 GACAATGGTGGCTGCTCCCACATCTGTATTGCCAAGGGTGATGGGACACCACGGTGCTCA 3787
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Qy       3788 TGCCCAGTCCACCTCGTGCTCCTGCAGAACCTGCTGACCTGTGGAGAGCCGCCCACCTGC 3847
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Qy       3848 TCCCCGGACCAGTTTGCATGTGCCACAGGGGAGATCGACTGTATCCCCGGGGCCTGGCGC 3907
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Qy       3908 TGTGACGGCTTTCCCGAGTGCGATGACCAGAGCGACGAGGAGGGCTGCCCCGTGTGCTCC 3967
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Qy       3968 GCCGCCCAGTTCCCCTGCGCGCGGGGTCAGTGTGTGGACCTGCGCCTGCGCTGCGACGGC 4027
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       4028 GAGGCAGACTGTCAGGACCGCTCAGACGAGGTGGACTGTGACGCCATCTGCCTGCCCAAC 4087
             |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db       4046 GAGGCAGACTGTCAGGACCGCTCAGACGAGGCGGACTGTGACGCCATCTGCCTGCCCAAC 4105

Qy       4088 CAGTTCCGGTGTGCGAGCGGCCAGTGTGTCCTCATCAAACAGCAGTGCGACTCCTTCCCC 4147
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4106 CAGTTCCGGTGTGCGAGCGGCCAGTGTGTCCTCATCAAACAGCAGTGCGACTCCTTCCCC 4165

Qy       4148 GACTGTATCGACGGCTCCGACGAGCTCATGTGTGAAATCACCAAGCCGCCCTCAGACGAC 4207
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4166 GACTGTATCGACGGCTCCGACGAGCTCATGTGTGAAATCACCAAGCCGCCCTCAGACGAC 4225

Qy       4208 AGCCCGGCCCACAGCAGTGCCATCGGGCCCGTCATTGGCATCATCCTCTCTCTCTTCGTC 4267
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       4268 ATGGGTGGTGTCTATTTTGTGTGCCAGCGCGTGGTGTGCCAGCGCTATGCGGGGGCCAAC 4327
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Qy       4388 CCGGGCGGTTCCCAGCATGGCCCCTTCACAGGCATCGCATGCGGAAAGTCCATGATGAGC 4447
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Qy       4448 TCCGTGAGCCTGATGGGGGGCCGGGGCGGGGTGCCCCTCTACGACCGGAACCACGTCACA 4507
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Qy       4508 GGGGCCTCGTCCAGCAGCTCGTCCAGCACGAAGGCCACGCTGTACCCGCCGATCCTGAAC 4567
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Qy       4568 CCGCCGCCCTCCCCGGCCACGGACCCCTCCCTGTACAACATGGACATGTTCTACTCTTCA 4627
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Qy       4808 CACAGCCAGTACCTGTCGGCGGAGGACAGCTGCCCGCCCTCGCCCGCCACCGAGAGGAGC 4867
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Qy       5048 TGTGATGGGGTGGGCAGGGCTGGGAGAACTTTGTACAGTGGAGAAATATTTATAAACT 5105
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RESULT 10
AX821900
LOCUS       AX821900               5100 bp    DNA     linear   PAT 10-DEC-2003
DEFINITION  Sequence 28 from Patent WO03068961.
ACCESSION   AX821900
VERSION     AX821900.1  GI:39725121
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Andrews,P.A., Walsh,J.A. and Gokhale,P.A.
  TITLE     Method to modify differentiation of pluripotential stem cells
  JOURNAL   Patent: WO 03068961-A 28 21-AUG-2003;
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FEATURES             Location/Qualifiers
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                     /mol_type="unassigned DNA"
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                     /db_xref="taxon:9606"
ORIGIN

  Query Match           99.2%;  Score 5077.4;  DB 6;  Length 5100;
  Best Local Similarity  99.9%;  Pred. No. 0;
  Matches 5092;  Conservative    0;  Mismatches    6;  Indels    1;  Gaps    1;

Qy         23 ATGGAGCCCGAGTGAGCGCGGCGCGGGCCCGTCCGGCCGCCGGACAACATGGAGGCAGCG 82
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGAGCCCGAGTGAGCGCGGCGCGGGCCCGTCCGGCCGCCGGACAACATGGAGGCAGCG 60

Qy         83 CCGCCCGGGCCGCCGTGGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGGCGCTGTGCGGC 142
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Qy        203 CTGGTGGACGCCGGCGGAGTCAAGCTGGAGTCCACCATCGTGGTCAGCGGCCTGGAGGAT 262
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Qy        323 GAGGCCATCAAGCAGACCTACCTGAACCAGACGGGGGCCGCCGTGCAGAACGTGGTCATC 382
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Qy        683 GAGGAGCAGAAGCTCTACTGGGCTGACGCCAAGCTCAGCTTCATCCACCGTGCCAACCTG 742
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Qy        923 CAGGTGCTGAGCCAGGAGCGGCAGCCTTTCTTCCACACTCGCTGTGAGGAGGACAATGGC 982
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Qy       1103 CTGCTGGCCCGGCGGACGGACCTACGGAGGATCTCGCTGGACACGCCGGACTTCACCGAC 1162
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Qy       1283 TCTGGGGCGCAGACGCTGGTCAACACCGAGATCAACGACCCCGATGGCATCGCGGTCGAC 1342
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Qy       1403 CTCAACGGCACCTCCCGCAAGATCCTGGTGTCGGAGGACCTGGACGAGCCCCGAGCCATC 1462
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Qy      2123 TCCAACAACCACATCTACTGGACAGACGTCAGCCTGAAGACCATCAGCCGCGCCTTCATG 2182
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Qy      2183 AACGGGAGCTCGGTGGAGCACGTGGTGGAGTTTGGCCTTGACTACCCCGAGGGCATGGCC 2242
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Qy      2243 GTTGACTGGATGGGCAAGAACCTCTACTGGGCCGACACTGGGACCAACAGAATCGAAGTG 2302
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Qy      2303 GCGCGGCTGGACGGGCAGTTCCGGCAAGTCCTCGTGTGGAGGGACTTGGACAACCCGAGG 2362
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Qy      2723 CACCTGGACTTCGTGATGGACATCCTGGTGTTCCACTCCTCCCGCCAGGATGGCCTCAAT 2782
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Qy      2903 ACCACCTTCTTGCTGTTCAGCCAGAAATCTGCCATCAGTCGGATGATCCCGGACGACCAG 2962
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Db      2881 ACCACCTTCTTGCTGTTCAGCCAGAAATCTGCCATCAGTCGGATGATCCCGGACGACCAG 2940

Qy      2963 CACAGCCCGGATCTCATCCTGCCCCTGCATGGACTGAGGAACGTCAAAGCCATCGACTAT 3022
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Db      2941 CACAGCCCGGATCTCATCCTGCCCCTGCATGGACTGAGGAACGTCAAAGCCATCGACTAT 3000

Qy      3023 GACCCACTGGACAAGTTCATCTACTGGGTGGATGGGCGCCAGAACATCAAGCGAGCCAAG 3082
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Qy      3143 CAGCCCCACGACCTCAGCATCGACATCTACAGCCGGACACTGTTCTGGACGTGCGAGGCC 3202
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Qy      3203 ACCAATACCATCAACGTCCACAGGCTGAGCGGGGAAGCCATGGGGGTGGTGCTGCGTGGG 3262
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Qy      3263 GACCGCGACAAGCCCAGGGCCATCGTCGTCAACGCGGAGCGAGGGTACCTGTACTTCACC 3322
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ACCESSION   AF064548
VERSION     AF064548.1  GI:3641526
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
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  AUTHORS   Hey,P.J., Twells,R.C., Phillips,M.S., Yusuke,Nakagawa., Brown,S.D.,
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            Metzker,M.L., Todd,J.A. and Hess,J.F.
  TITLE     Cloning of a novel member of the low-density lipoprotein receptor
            family
  JOURNAL   Gene 216 (1), 103-111 (1998)
  MEDLINE   98382578
   PUBMED   9714764
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  AUTHORS   Hey,P.J., Twells,R.C.J., Phillips,M.S., Nakagawa,Y., Brown,S.D.,
            Kawaguchi,Y., Cox,R., Xie,G., Dugan,V., Hammond,H., Metzker,M.L.,
            Todd,J.A. and Hess,J.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-MAY-1998) Human Genetics, Merck Research Lab,
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ORIGIN

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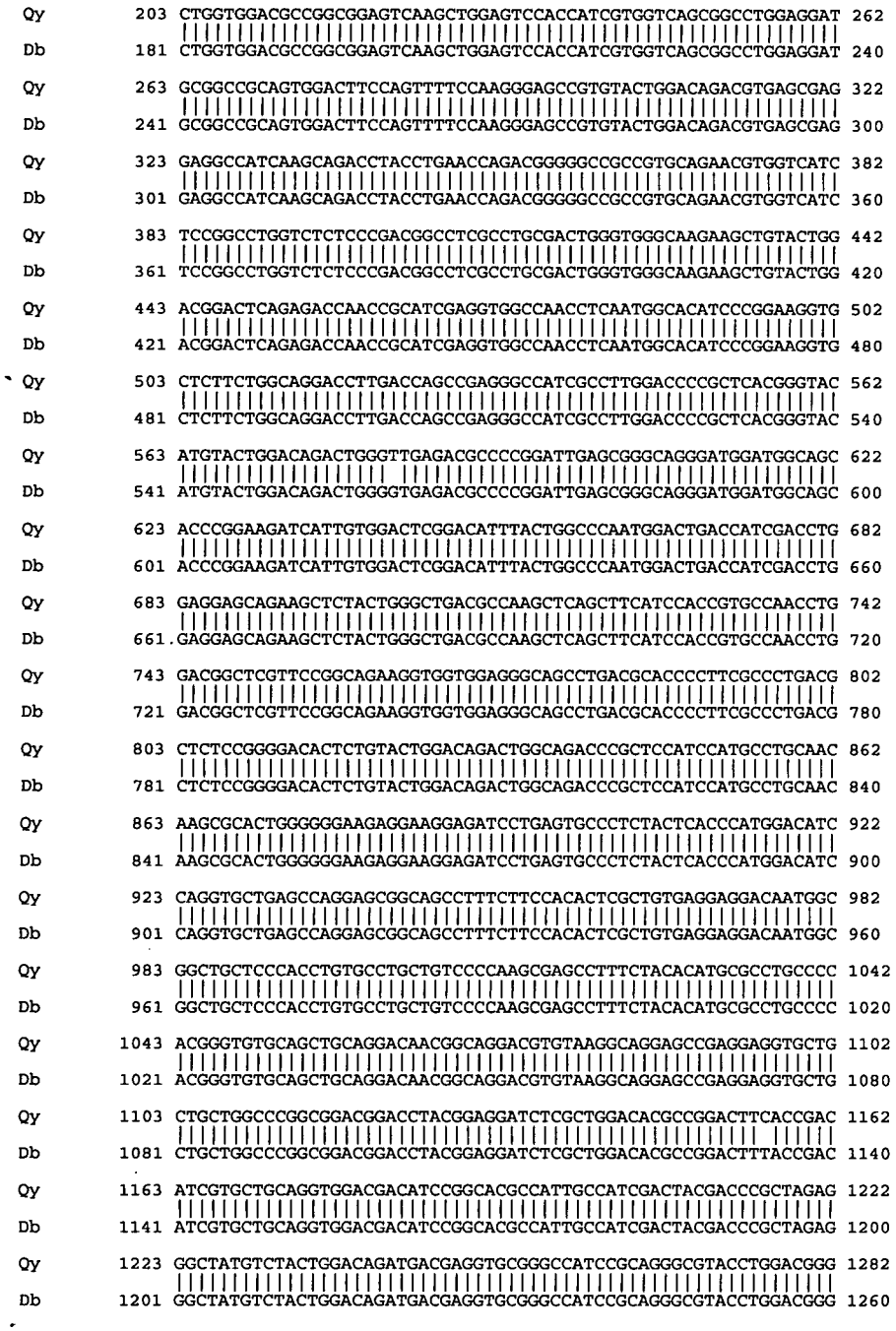
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Db      4381 CATGGCCCCTTCACAGGCATCGCATGCGGAAAGTCCATGATGAGCTCCGTGAGCCTGATG 4440
Qy      4463 GGGGGCCGGGGCGGGGTGCCCCTCTACGACCGGAACCACGTCACAGGGGCCTCGTCCAGC 4522
Db      4441 GGGGGCCGGGGCGGGGTGCCCCTCTACGACCGGAACCACGTCACAGGGGCCTCGTCCAGC 4500
Qy      4523 AGCTCGTCCAGCACGAAGGCCACGCTGTACCCGCCGATCCTGAACCCGCCGCCCTCCCCG 4582
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Qy       4643 GCGAGACCGTACAGGCCCTACATCATTCGAGGAATGGCGCCCCCGACGACGCCCTGCAGC 4702
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Qy       4703 ACCGACGTGTGTGACAGCGACTACAGCGCCAGCCGCTGGAAGGCCAGCAAGTACTACCTG 4762
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RESULT 12
AR305075
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DEFINITION  Sequence 1 from patent US 6545137.
ACCESSION   AR305075
VERSION     AR305075.1  GI:31694385
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 5098)
  AUTHORS   Todd,J.A., Hess,J.W., Caskey,C.T., Cox,R.D., Gerhold,D.,
            Hammond,H., Hey,P., Kawaguchi,Y., Merriman,T.R., Metzker,M.L.,
            Nakagawa,Y., Phillips,M.S. and Twells,R.C.J.
  TITLE     Receptor
  JOURNAL   Patent: US 6545137-A 1 08-APR-2003;
FEATURES             Location/Qualifiers
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                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             98.7%;  Score 5053.4;  DB 6;  Length 5098;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 5090;  Conservative    0;  Mismatches    6;  Indels    3;  Gaps    3;

Qy         23 ATGGAGCCCGAGTGAGCGCGGCGCGGGCCCGTCCGGCCGCCGGACAACATGGAGGCAGCG 82
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Db          1 ATGGAGCCCGAGTGAGCGCGGCGCGGGCCCGTCCGGCCGCCGGACAACATGGAGGCAGCG 60

Qy         83 CCGCCCGGGCCGCCGTGGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGGCGCTGTGCGGC 142
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CCGCCCGGGCCGCCGTGGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGGCGCTGTGCGGC 120

Qy        143 TGCCCGGCCCCCGCCGCGGCCTCGCCGCTCCTGCTATTTGCCAACCGCCGGGACGTACGG 202
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Db        121 TGCCCGGCCCCCGCCGCGGCCTCGCCGCTCCTGCTATTTGCCAACCGCCGGGACGTACGG 180

Qy        203 CTGGTGGACGCCGGCGGAGTCAAGCTGGAGTCCACCATCGTGGTCAGCGGCCTGGAGGAT 262
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Qy        263 GCGGCCGCAGTGGACTTCCAGTTTTCCAAGGGAGCCGTGTACTGGACAGACGTGAGCGAG 322
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Db        241 GCGGCCGCAGTGGACTTCCAGTTTTCCAAGGGAGCCGTGTACTGGACAGACGTGAGCGAG 300

Qy        323 GAGGCCATCAAGCAGACCTACCTGAACCAGACGGGGGCCGCCGTGCAGAACGTGGTCATC 382
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Db        301 GAGGCCATCAAGCAGACCTACCTGAACCAGACGGGGGCCGCCGTGCAGAACGTGGTCATC 360

Qy        383 TCCGGCCTGGTCTCTCCCGACGGCCTCGCCTGCGACTGGGTGGGCAAGAAGCTGTACTGG 442
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Qy       1403 CTCAACGGCACCTCCCGCAAGATCCTGGTGTCGGAGGACCTGGACGAGCCCCGAGCCATC 1462
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Db       3540 AAGCATCTCTACTGGATCGACCGCCAGCAGCAGATGATCGAGCGTGTGGAGAAGACCACC 3599

Qy       3623 GGGGACAAGCGGACTCGCATCCAGGGCCGTGTCGCCCACCTCACTGGCATCCATGCAGTG 3682
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Qy       3683 GAGGAAGTCAGCCTGGAGGAGTTCTCAGCCCACCCATGTGCCCGTGACAATGGTGGCTGC 3742
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Db       3960 TGCGCGCGGGGTCAGTGTGTGGACCTGCGCCTGCGCTGCGACGGCGAGGCAGACTGTCAG 4019

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Qy       4403 CATGGCCCCTTCACAGGCATCGCATGCGGAAAGTCCATGATGAGCTCCGTGAGCCTGATG 4462
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RESULT 13
AR309179
LOCUS       AR309179                5098 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 1 from patent US 6555654.
ACCESSION   AR309179
VERSION     AR309179.1  GI:31701184
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 5098)
  AUTHORS   Todd,J.A., Hess,J.W., Caskey,C.T., Cox,R.D., Gerhold,D.,
            Hammond,H., Hey,P., Kawaguchi,Y., Merriman,T.R., Metzker,M.L.,
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  TITLE     LDL-receptor
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ORIGIN
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  Query Match             98.7%;  Score 5053.4;  DB 6;  Length 5098;
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  Matches 5090;  Conservative    0;  Mismatches    6;  Indels    3;  Gaps    3;

Qy         23 ATGGAGCCCGAGTGAGCGCGGCGCGGGCCCGTCCGGCCGCCGGACAACATGGAGGCAGCG 82
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Db          1 ATGGAGCCCGAGTGAGCGCGGCGCGGGCCCGTCCGGCCGCCGGACAACATGGAGGCAGCG 60

Qy         83 CCGCCCGGGCCGCCGTGGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGGCGCTGTGCGGC 142
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy      143 TGCCCGGCCCCCGCCGCGGCCTCGCCGCTCCTGCTATTTGCCAACCGCCGGGACGTACGG 202
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Qy      203 CTGGTGGACGCCGGCGGAGTCAAGCTGGAGTCCACCATCGTGGTCAGCGGCCTGGAGGAT 262
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Qy      263 GCGGCCGCAGTGGACTTCCAGTTTTCCAAGGGAGCCGTGTACTGGACAGACGTGAGCGAG 322
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Qy      623 ACCCGGAAGATCATTGTGGACTCGGACATTTACTGGCCCAATGGACTGACCATCGACCTG 682
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Qy      683 GAGGAGCAGAAGCTCTACTGGGCTGACGCCAAGCTCAGCTTCATCCACCGTGCCAACCTG 742
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Qy      743 GACGGCTCGTTCCGGCAGAAGGTGGTGGAGGGCAGCCTGACGCACCCCTTCGCCCTGACG 802
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Qy      923 CAGGTGCTGAGCCAGGAGCGGCAGCCTTTCTTCCACACTCGCTGTGAGGAGGACAATGGC 982
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Qy      983 GGCTGCTCCCACCTGTGCCTGCTGTCCCCAAGCGAGCCTTTCTACACATGCGCCTGCCCC 1042
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Qy     1043 ACGGGTGTGCAGCTGCAGGACAACGGCAGGACGTGTAAGGCAGGAGCCGAGGAGGTGCTG 1102
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Db      3000 GACCCACTGGACAAGTTCATCTACTGGGTGGATGGGCGCCAGAACATCAAGCGAGCCAAG 3059
Qy      3083 GACGACGGGACCCAGCCCTTTGTTTTGACCTCTCTGAGCCAAGGCCAAAACCCAGACAGG 3142
Db      3060 GACGACGGGACCCAGCCCTTTGTTTTGACCTCTCTGAGCCAAGGCCAAAACCCAGACAGG 3119
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Qy      3803 GTGCTCCTGCAGAACCTGCTGACCTGTGGAGAGCCGCCCACCTGCTCCCCGGACCAGTTT 3862
Db      3780 GTGCTCCTGCAGAACCTGCTGACCTGTGGAGAGCCGCCCACCTGCTCCCCGGACCAGTTT 3839
Qy      3863 GCATGTGCCACAGGGGAGATCGACTGTATCCCCGGGGCCTGGCGCTGTGACGGCTTTCCC 3922
Db      3840 GCATGTGCCACAGGGGAGATCGACTGTATCCCCGGGGCCTGGCGCTGTGACGGCTTTCCC 3899
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Db      3900 GAGTGCGATGACCAGAGCGACGAGGAGGGCTGCCCCGTGTGCTCCGCCGCCCAGTTCCCC 3959
Qy      3983 TGCGCGCGGGGGTCAGTGTGTGGACCTGCGCCTGCGCTGCGACGGCGAGGCAGACTGTCAG 4042
Db      3960 TGCGCGCGGGGTCAGTGTGTGGACCTGCGCCTGCGCTGCGACGGCGAGGCAGACTGTCAG 4019
Qy      4043 GACCGCTCAGACGAGGTGGACTGTGACGCCATCTGCCTGCCCAACCAGTTCCGGTGTGCG 4102
Db      4020 GACCGCTCAGACGAGGCGGACTGTGACGCCATCTGCCTGCCCAACCAGTTCCGGTGTGCG 4079
Qy      4103 AGCGGCCAGTGTGTCCTCATCAAACAGCAGTGCGACTCCTTCCCCGACTGTATCGACGGC 4162
Db      4080 AGCGGCCAGTGTGTCCT-ATCAAACAGCAGTGCGACTCCTTCCCCGACTGTATCGACGGC 4138
Qy      4163 TCCGACGAGCTCATGTGTGAAATCACCAAGCCGCCCTCAGACGACAGCCCGGCCCACAGC 4222
Db      4139 TCCGACGAGCTCATGTGTGAAATCACCAAGCCGCCCTCAGACGACAGCCCGGCCCACAGC 4198
Qy      4223 AGTGCCATCGGGCCCGTCATTGGCATCATCCTCTCTCTCTTCGTCATGGGTGGTGTCTAT 4282
Db      4199 AGTGCCATCGGGCCCGTCATTGGCATCATCCTCTCTCTCTTCGTCATGGGTGGTGTCTAT 4258
Qy      4283 TTTGTGTGCCAGCGCGTGGTGTGCCAGCGCTATGCGGGGGCCAACGGGCCCTTCCCGCAC 4342
Db      4259 TTTGTGTGCCAGCGCGTGGTGTGCCAGCGCTATGCGGGGGCCAACGGGCCCTTCCCGCAC 4318
Qy      4343 GAGTATGTCAGCGGGACCCCGCACGTGCCCCTCAATTTCATAGCCCCGGGCGGTTCCCAG 4402
Db      4319 GAGTATGTCAGCGGGACCCCGCACGTGCCCCTCAATTTCATAGCCCCGGGCGGTTCCCAG 4378
Qy      4403 CATGGCCCCTTCACAGGCATCGCATGCGGAAAGTCCATGATGAGCTCCGTGAGCCTGATG 4462
Db      4379 CATGGCCCCTTCACAGGCATCGCATGCGGAAAGTCCATGATGAGCTCCGTGAGCCTGATG 4438
Qy      4463 GGGGGCCGGGGCGGGGTGCCCCTCTACGACCGGAACCACGTCACAGGGGCCTCGTCCAGC 4522
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Qy       4523 AGCTCGTCCAGCACGAAGGCCACGCTGTACCCGCCGATCCTGAACCCGCCGCCCTCCCCG 4582
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Db       4499 AGCTCGTCCAGCACGAAGGCCACGCTGTACCCGCCGATCCTGAACCCGCCGCCCTCCCCG 4558

Qy       4583 GCCACGGACCCCTCCCTGTACAACATGGACATGTTCTACTCTTCAAACATTCCGGCCACT 4642
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Qy       4643 GCGAGACCGTACAGGCCCTACATCATTCGAGGAATGGCGCCCCCGACGACGCCCTGCAGC 4702
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Db       4619 GTGAGACCGTACAGGCCCTACATCATTCGAGGAATGGCGCCCCCGACGACGCCCTGCAGC 4678

Qy       4703 ACCGACGTGTGTGACAGCGACTACAGCGCCAGCCGCTGGAAGGCCAGCAAGTACTACCTG 4762
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Qy       4763 GATTTGAACTCGGACTCAGACCCCTATCCACCCCCACCCACGCCCCACAGCCAGTACCTG 4822
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Qy       4823 TCGGCGGAGGACAGCTGCCCGCCCTCGCCCGCCACCGAGAGGAGCTACTTCCATCTCTTC 4882
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Qy       4883 CCGCCCCCTCCGTCCCCCTGCACGGACTCATCCTGACCTCGGCCGGGCCACTCTGGCTTC 4942
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Qy       5003 AAAAATAAATATAATTGGGATTTTAAAAACATGAGAAATGTGAACTGTGATGGGGTGGGC 5062
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Db       4979 AAAAATAAATATAATTGGGATTTTAAAAACATGAGAAATGTGAACTGTGATGGGGTGGGC 5038

Qy       5063 AGGGCTGGGAGAACTTTGTACAGTGG-AGAAATATTTATAAACTTAATTTTGTAAAACA 5120
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Db       5039 AGGGCTGGGAGAACTTTGTACAGTGGAACAAATATTTATAAACTTAATTTTGTAAAACA 5097
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RESULT 14
BD105986

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LOCUS       BD105986               5098 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Novel LDL-receptor.
ACCESSION   BD105986
VERSION     BD105986.1  GI:23200804
KEYWORDS    JP 2002501376-A/1.
SOURCE      Chlamydia sp.
  ORGANISM  Chlamydia sp.
            Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
REFERENCE   1  (bases 1 to 5098)
  AUTHORS   Todd,J.A., Hess,J.W., Caskey,C.T., Cox,R.D., Gerhold,D., Hammond,H.
            and Hey,P.
  TITLE     Novel LDL-receptor
  JOURNAL   Patent: JP 2002501376-A 1 15-JAN-2002;
            THE WELLCOME TRUST LTD AS TRUSTEE TO THE WELLCOME TRUST, MERCK & CO
            INC
COMMENT     PN   JP 2002501376-A/1
            PD   15-JAN-2002
            PF   15-APR-1998 JP 1998543635
            PR   15-APR-1997 US    60/043553,05-JUN-1997 US    60/048740 PI
            JOHN ANDREW TODD,JOHN WILFRED HESS,CHARLES
            THOMAS CASKEY,ROGER
            PI   DAVID COX,
            PI   DAVID GERHOLD,HOLLY HAMMOND,PATRICIA HEY
            PC   C12N15/12,C12N15/11,C12Q1/68,C07K14/705,C07K16/28,A61K38/17,
            PC   A61K39/395,
            PC   A61K48/00
            CC   Strandedness: Single;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
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                     /organism="Chlamydia sp."
                     /mol_type="genomic DNA"
                     /db_xref="taxon:35827"
ORIGIN

  Query Match             98.7%;  Score 5053.4;  DB 6;  Length 5098;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 5090;  Conservative    0;  Mismatches    6;  Indels    3;  Gaps    3;

Qy         23 ATGGAGCCCGAGTGAGCGCGGCGCGGGCCCGTCCGGCCGCCGGACAACATGGAGGCAGCG 82
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGAGCCCGAGTGAGCGCGGCGCGGGCCCGTCCGGCCGCCGGACAACATGGAGGCAGCG 60

Qy         83 CCGCCCGGGCCGCCGTGGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGGCGCTGTGCGGC 142
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CCGCCCGGGCCGCCGTGGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGGCGCTGTGCGGC 120

Qy        143 TGCCCGGCCCCCGCCGCGGCCTCGCCGCTCCTGCTATTTGCCAACCGCCGGGACGTACGG 202
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Db        121 TGCCCGGCCCCCGCCGCGGCCTCGCCGCTCCTGCTATTTGCCAACCGCCGGGACGTACGG 180

Qy        203 CTGGTGGACGCCGGCGGAGTCAAGCTGGAGTCCACCATCGTGGTCAGCGGCCTGGAGGAT 262
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Db        181 CTGGTGGACGCCGGCGGAGTCAAGCTGGAGTCCACCATCGTGGTCAGCGGCCTGGAGGAT 240

Qy        263 GCGGCCGCAGTGGACTTCCAGTTTTCCAAGGGAGCCGTGTACTGGACAGACGTGAGCGAG 322
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Db        241 GCGGCCGCAGTGGACTTCCAGTTTTCCAAGGGAGCCGTGTACTGGACAGACGTGAGCGAG 300

Qy        323 GAGGCCATCAAGCAGACCTACCTGAACCAGACGGGGGCCGCCGTGCAGAACGTGGTCATC 382
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GAGGCCATCAAGCAGACCTACCTGAACCAGACGGGGGCCGCCGTGCAGAACGTGGTCATC 360

Qy        383 TCCGGCCTGGTCTCTCCCGACGGCCTCGCCTGCGACTGGGTGGGCAAGAAGCTGTACTGG 442
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Db        361 TCCGGCCTGGTCTCTCCCGACGGCCTCGCCTGCGACTGGGTGGGCAAGAAGCTGTACTGG 420

Qy        443 ACGGACTCAGAGACCAACCGCATCGAGGTGGCCAACCTCAATGGCACATCCCGGAAGGTG 502
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Db        421 ACGGACTCAGAGACCAACCGCATCGAGGTGGCCAACCTCAATGGCACATCCCGGAAGGTG 480

Qy        503 CTCTTCTGGCAGGACCTTGACCAGCCGAGGGCCATCGCCTTGGACCCCGCTCACGGGTAC 562
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Db        481 CTCTTCTGGCAGGACCTTGACCAGCCGAGGGCCATCGCCTTGGACCCCGCTCACGGGTAC 540

Qy        563 ATGTACTGGACAGACTGGGTTGAGACGCCCCGGATTGAGCGGGCAGGGATGGATGGCAGC 622
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Db        541 ATGTACTGGACAGACTGGGGTGAGACGCCCCGGATTGAGCGGGCAGGGATGGATGGCAGC 600

Qy        623 ACCCGGAAGATCATTGTGGACTCGGACATTTACTGGCCCAATGGACTGACCATCGACCTG 682
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Db        601 ACCCGGAAGATCATTGTGGACTCGGACATTTACTGGCCCAATGGACTGACCATCGACCTG 660

Qy        683 GAGGAGCAGAAGCTCTACTGGGCTGACGCCAAGCTCAGCTTCATCCACCGTGCCAACCTG 742
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Db        661 GAGGAGCAGAAGCTCTACTGGGCTGACGCCAAGCTCAGCTTCATCCACCGTGCCAACCTG 720

Qy        743 GACGGCTCGTTCCGGCAGAAGGTGGTGGAGGGCAGCCTGACGCACCCCTTCGCCCTGACG 802
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GACGGCTCGTTCCGGCAGAAGGTGGTGGAGGGCAGCCTGACGCACCCCTTCGCCCTGACG 780

Qy        803 CTCTCCGGGGACACTCTGTACTGGACAGACTGGCAGACCCGCTCCATCCATGCCTGCAAC 862
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Db        781 CTCTCCGGGGACACTCTGTACTGGACAGACTGGCAGACCCGCTCCATCCATGCCTGCAAC 840

Qy        863 AAGCGCACTGGGGGGAAGAGGAAGGAGATCCTGAGTGCCCTCTACTCACCCATGGACATC 922
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGCGCACTGGGGGGAAGAGGAAGGAGATCCTGAGTGCCCTCTACTCACCCATGGACATC 900

Qy        923 CAGGTGCTGAGCCAGGAGCGGCAGCCTTTCTTCCACACTCGCTGTGAGGAGGACAATGGC 982
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        901 CAGGTGCTGAGCCAGGAGCGGCAGCCTTTCTTCCACACTCGCTGTGAGGAGGACAATGGC 960

Qy        983 GGCTGCTCCCACCTGTGCCTGCTGTCCCCAAGCGAGCCTTTCTACACATGCGCCTGCCCC 1042
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Db        961 GGCTGCTCCCACCTGTGCCTGCTGTCCCCAAGCGAGCCTTTCTACACATGCGCCTGCCCC 1020

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Qy       1103 CTGCTGGCCCGGCGGACGGACCTACGGAGGATCTCGCTGGACACGCCGGACTTCACCGAC 1162
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Db       1081 CTGCTGGCCCGGCGGACGGACCTACGGAGGATCTCGCTGGACACGCCGGACTTTACCGAC 1140

Qy       1163 ATCGTGCTGCAGGTGGACGACATCCGGCACGCCATTGCCATCGACTACGACCCGCTAGAG 1222
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Db       1141 ATCGTGCTGCAGGTGGACGACATCCGGCACGCCATTGCCATCGACTACGACCCGCTAGAG 1200

Qy       1223 GGCTATGTCTACTGGACAGATGACGAGGTGCGGGCCATCCGCAGGGCGTACCTGGACGGG 1282
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Db       1201 GGCTATGTCTACTGGACAGATGACGAGGTGCGGGCCATCCGCAGGGCGTACCTGGACGGG 1260

Qy       1283 TCTGGGGCGCAGACGCTGGTCAACACCGAGATCAACGACCCCGATGGCATCGCGGTCGAC 1342
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Db       1261 TCTGGGGCGCAGACGCTGGTCAACACCGAGATCAACGACCCCGATGGCATCGCGGTCGAC 1320

Qy       1343 TGGGTGGCCCGAAACCTCTACTGGACCGACACGGGCACGGACCGCATCGAGGTGACGCGC 1402
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Db       1321 TGGGTGGCCCGAAACCTCTACTGGACCGACACGGGCACGGACCGCATCGAGGTGACGCGC 1380

Qy       1403 CTCAACGGCACCTCCCGCAAGATCCTGGTGTCGGAGGACCTGGACGAGCCCCGAGCCATC 1462
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Db       1381 CTCAACGGCACCTCCCGCAAGATCCTGGTGTCGGAGGACCTGGACGAGCCCCGAGCCATC 1440

Qy       1463 GCACTGCACCCCGTGATGGGCCTCATGTACTGGACAGACTGGGGAGAGAACCCTAAAATC 1522
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Db       1441 GCACTGCACCCCGTGATGGGCCTCATGTACTGGACAGACTGGGGAGAGAACCCTAAAATC 1500

Qy       1523 GAGTGTGCCAACTTGGATGGGCAGGAGCGGCGTGTGCTGGTCAATGCCTCCCTCGGGTGG 1582
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Db       1501 GAGTGTGCCAACTTGGATGGGCAGGAGCGGCGTGTGCTGGTCAATGCCTCCCTCGGGTGG 1560

Qy       1583 CCCAACGGCCTGGCCCTGGACCTGCAGGAGGGGAAGCTCTACTGGGGAGACGCCAAGACA 1642
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Db       1561 CCCAACGGCCTGGCCCTGGACCTGCAGGAGGGGAAGCTCTACTGGGGAGACGCCAAGACA 1620

Qy       1643 GACAAGATCGAGGTGATCAATGTTGATGGGACGAAGAGGCGGACCCTCCTGGAGGACAAG 1702
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Db       1621 GACAAGATCGAGGTGATCAATGTTGATGGGACGAAGAGGCGGACCCTCCTGGAGGACAAG 1680

Qy       1703 CTCCCGCACATTTTCGGGTTCACGCTGCTGGGGGACTTCATCTACTGGACTGACTGGCAG 1762
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Qy       1763 CGCCGCAGCATCGAGCGGGTGCACAAGGTCAAGGCCAGCCGGGACGTCATCATTGACCAG 1822
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Qy       1823 CTGCCCGACCTGATGGGGCTCAAAGCTGTGAATGTGGCCAAGGTCGTCGGAACCAACCCG 1882
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Qy       1883 TGTGCGGACAGGAACGGGGGGTGCAGCCACCTGTGCTTCTTCACACCCCACGCAACCCGG 1942
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Qy       1943 TGTGGCTGCCCCATCGGCCTGGAGCTGCTGAGTGACATGAAGACCTGCATCGTGCCTGAG 2002
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Qy       2123 TCCAACAACCACATCTACTGGACAGACGTCAGCCTGAAGACCATCAGCCGCGCCTTCATG 2182
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Qy       2183 AACGGGAGCTCGGTGGAGCACGTGGTGGAGTTTGGCCTTGACTACCCCGAGGGCATGGCC 2242
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Db       2160 AACGGGAGCTCGGTGGAGCACGTGGTGGAGTTTGGCCTTGACTACCCCGAGGGCATGGCC 2219

Qy       2243 GTTGACTGGATGGGCAAGAACCTCTACTGGGCCGACACTGGGACCAACAGAATCGAAGTG 2302
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Db       2220 GTTGACTGGATGGGCAAGAACCTCTACTGGGCCGACACTGGGACCAACAGAATCGAAGTG 2279

Qy       2303 GCGCGGCTGGACGGGCAGTTCCGGCAAGTCCTCGTGTGGAGGGACTTGGACAACCCGAGG 2362
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Qy       2423 AGGATCGTGCGGGCCTTCATGGACGGGACCAACTGCATGACGCTGGTGGACAAGGTGGGC 2482
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Qy       2483 CGGGCCAACGACCTCACCATTGACTACGCTGACCAGCGCCTCTACTGGACCGACCTGGAC 2542
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Qy       2663 CTGCACAGCATTGAGCGGGCCGACAAGACTAGCGGCCGGAACCGCACCCTCATCCAGGGC 2722
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Db       2640 CTGCACAGCATTGAGCGGGCCGACAAGACTAGCGGCCGGAACCGCACCCTCATCCAGGGC 2699

Qy       2723 CACCTGGACTTCGTGATGGACATCCTGGTGTTCCACTCCTCCCGCCAGGATGGCCTCAAT 2782
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Qy       2783 GACTGTATGCACAACAACGGGCAGTGTGGGCAGCTGTGCCTTGCCATCCCCGGCGGCCAC 2842
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Db       2760 GACTGTATGCACAACAACGGGCAGTGTGGGCAGCTGTGCCTTGCCATCCCCGGCGGCCAC 2819

Qy       2843 CGCTGCGGCTGCGCCTCACACTACACCCTGGACCCCAGCAGCCGCAACTGCAGCCCGCCC 2902
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Db       2820 CGCTGCGGCTGCGCCTCACACTACACCCTGGACCCCAGCAGCCGCAACTGCAGCCCGCCC 2879

Qy       2903 ACCACCTTCTTGCTGTTCAGCCAGAAATCTGCCATCAGTCGGATGATCCCGGACGACCAG 2962
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Db       2880 ACCACCTTCTTGCTGTTCAGCCAGAAATCTGCCATCAGTCGGATGATCCCGGACGACCAG 2939

Qy       2963 CACAGCCCGGATCTCATCCTGCCCCTGCATGGACTGAGGAACGTCAAAGCCATCGACTAT 3022
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Db       3060 GACGACGGGACCCAGCCCTTTGTTTTGACCTCTCTGAGCCAAGGCCAAAACCCAGACAGG 3119
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Qy       3143 CAGCCCCACGACCTCAGCATCGACATCTACAGCCGGACACTGTTCTGGACGTGCGAGGCC 3202
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Qy       3203 ACCAATACCATCAACGTCCACAGGCTGAGCGGGGAAGCCATGGGGGTGGTGCTGCGTGGG 3262
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Qy       3443 AAGCTGTTCTGGGTGGACGCGGACCTGAAGCGCATTGAGAGCTGTGACCTGTCAGGGGCC 3502
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Qy       3563 AAGCATCTCTACTGGATCGACCGCCAGCAGCAGATGATCGAGCGTGTGGAGAAGACCACC 3622
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Qy       3623 GGGGACAAGCGGACTCGCATCCAGGGCCGTGTCGCCCACCTCACTGGCATCCATGCAGTG 3682
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Qy       3683 GAGGAAGTCAGCCTGGAGGAGTTCTCAGCCCACCCATGTGCCCGTGACAATGGTGGCTGC 3742
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Qy       3803 GTGCTCCTGCAGAACCTGCTGACCTGTGGAGAGCCGCCCACCTGCTCCCCGGACCAGTTT 3862
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Qy       3863 GCATGTGCCACAGGGGAGATCGACTGTATCCCCGGGGCCTGGCGCTGTGACGGCTTTCCC 3922
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Qy       4163 TCCGACGAGCTCATGTGTGAAATCACCAAGCCGCCCTCAGACGACAGCCCGGCCCACAGC 4222
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Qy       4283 TTTGTGTGCCAGCGCGTGGTGTGCCAGCGCTATGCGGGGGCCAACGGGCCCTTCCCGCAC 4342
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Qy       4523 AGCTCGTCCAGCACGAAGGCCACGCTGTACCCGCCGATCCTGAACCCGCCGCCCTCCCCG 4582
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Qy       4583 GCCACGGACCCCTCCCTGTACAACATGGACATGTTCTACTCTTCAAACATTCCGGCCACT 4642
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Qy       4643 GCGAGACCGTACAGGCCCTACATCATTCGAGGAATGGCGCCCCCGACGACGCCCTGCAGC 4702
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Qy       4883 CCGCCCCCTCCGTCCCCCTGCACGGACTCATCCTGACCTCGGCCGGGCCACTCTGGCTTC 4942
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Qy       5063 AGGGCTGGGAGAACTTTGTACAGTGG-AGAAATATTTATAAACTTAATTTTGTAAAACA 5120
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RESULT 15
CQ870242
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DEFINITION Sequence 663 from Patent WO2004074320.
ACCESSION CQ870242
VERSION CQ870242.1 GI:51999860
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Morris,D.W., Morris,D.W. and Malandro,M.S.

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  TITLE     Novel therapeutic targets in cancer
  JOURNAL   Patent: WO 2004074320-A 663 02-SEP-2004;
            Sagres Discovery, Inc. (US)
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match             98.6%;  Score 5048.8;  DB 6;  Length 5135;
  Best Local Similarity   99.3%;  Pred. No. 0;
  Matches 5096;  Conservative    0;  Mismatches    2;  Indels   36;  Gaps    1;

Qy         23 ATGGAGCCCGAGTGAGCGCGGCGCGGGCCCGTCCGGCCGCCGGACAACATGGAGGCAGCG 82
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Db          1 ATGGAGCCCGAGTGAGCGCGGCGCGGGCCCGTCCGGCCGCCGGACAACATGGAGGCAGCG 60

Qy         83 CCGCCCGGGCCGCCGTGGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGGCGCTGTGCGGC 142
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Qy        143 TGCCCGGCCCCCGCCGCGGCCTCGCCGCTCCTGCTATTTGCCAACCGCCGGGACGTACGG 202
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Qy        263 GCGGCCGCAGTGGACTTCCAGTTTTCCAAGGGAGCCGTGTACTGGACAGACGTGAGCGAG 322
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Qy        383 TCCGGCCTGGTCTCTCCCGACGGCCTCGCCTGCGACTGGGTGGGCAAGAAGCTGTACTGG 442
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Qy        563 ATGTACTGGACAGACTGGGTTGAGACGCCCCGGATTGAGCGGGCAGGGATGGATGGCAGC 622
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Db        541 ATGTACTGGACAGACTGGGGTGAGACGCCCCGGATTGAGCGGGCAGGGATGGATGGCAGC 600

Qy        623 ACCCGGAAGATCATTGTGGACTCGGACATTTACTGGCCCAATGGACTGACCATCGACCTG 682
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Qy        683 GAGGAGCAGAAGCTCTACTGGGCTGACGCCAAGCTCAGCTTCATCCACCGTGCCAACCTG 742
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Qy        803 CTCTCCGGGGACACTCTGTACTGGACAGACTGGCAGACCCGCTCCATCCATGCCTGCAAC 862
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Qy        923 CAGGTGCTGAGCCAGGAGCGGCAGCCTTTCTTCCACACTCGCTGTGAGGAGGACAATGGC 982
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Qy       1043 ACGGGTGTGCAGCTGCAGGACAACGGCAGGACGTGTAAGGCAGGAGCCGAGGAGGTGCTG 1102
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Qy       1223 GGCTATGTCTACTGGACAGATGACGAGGTGCGGGCCATCCGCAGGGCGTACCTGGACGGG 1282
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Qy       2543 ACCAACATGATCGAGTCGTCCAACATGCTGGGTCAGGAGCGGGTCGTGATTGCCGACGAT 2602
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Search completed: May 19, 2005, 09:34:12
Job time : 21165 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 18, 2005, 14:57:53 ; Search time 2706 Seconds
(without alignments)
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Title: US-10-680-287A-2
Perfect score: 5120
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5695437 seqs, 3066160638 residues

Total number of hits satisfying chosen parameters: 11390874

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

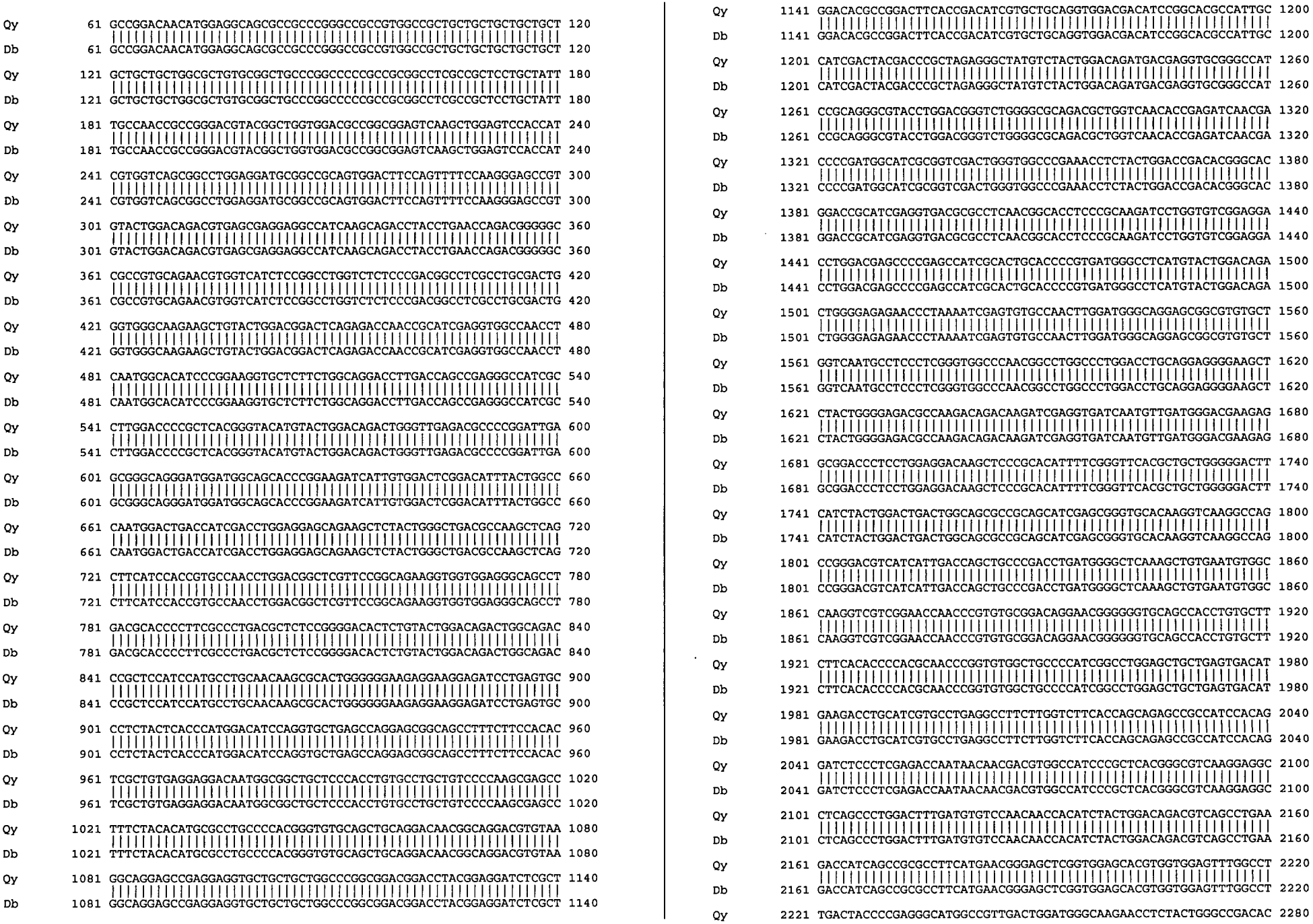
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3	5120	100.0	5120	18	US-10-731-739-2	Sequence 2, Appli
4	5120	100.0	5120	18	US-10-477-238A-2	Sequence 2, Appli
5	5120	100.0	5120	18	US-10-680-287A-2	Sequence 2, Appli
6	5120	100.0	5120	19	US-10-477-173-2	Sequence 2, Appli
7	5118.4	100.0	5120	17	US-10-374-979-1	Sequence 1, Appli
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21	5056.6	98.8	5063	10	US-09-931-375A-1	Sequence 1, Appli
22	5053.4	98.7	5098	16	US-10-331-907-1	Sequence 1, Appli
23	5048.8	98.6	5135	13	US-10-087-192-1409	Sequence 1409, Ap
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26	4927.4	96.2	5022	16	US-10-331-907-32	Sequence 32, Appl
27	4919.8	96.1	5263	16	US-10-331-907-31	Sequence 31, Appl
28	4916	96.0	5125	16	US-10-331-907-26	Sequence 26, Appl
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ALIGNMENTS

RESULT 1
US-10-374-979-2
; Sequence 2, Application US/10374979
; Publication No. US20030219793A1
; GENERAL INFORMATION:
; APPLICANT: John P. Carulli et al.
; TITLE OF INVENTION: THE HIGH BONE MASS GENE OF 11q13.3
; FILE REFERENCE: 032796-021
; CURRENT APPLICATION NUMBER: US/10/374,979
; CURRENT FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: US 09/544,398
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 09/543,771
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 09/229,319
; PRIOR FILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: US 60/071,449
; PRIOR FILING DATE: 1998-01-13
; PRIOR APPLICATION NUMBER: US 60/105,511
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 109
; SEQ ID NO 2
; LENGTH: 5120
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-374-979-2

Query Match 100.0%; Score 5120; DB 17; Length 5120;
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Matches 5120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 361 CGCCGTGCAGAACGTGGTCATCTCCGGCCTGGTCTCTCCCGACGGCCTCGCCTGCGACTG 420
Db 361 CGCCGTGCAGAACGTGGTCATCTCCGGCCTGGTCTCTCCCGACGGCCTCGCCTGCGACTG 420
Qy 421 GGTGGGCAAGAAGCTGTACTGGACGGACTCAGAGACCAACCGCATCGAGGTGGCCAACCT 480
Db 421 GGTGGGCAAGAAGCTGTACTGGACGGACTCAGAGACCAACCGCATCGAGGTGGCCAACCT 480
Qy 481 CAATGGCACATCCCGGAAGGTGCTCTTCTGGCAGGACCTTGACCAGCCGAGGGCCATCGC 540
Db 481 CAATGGCACATCCCGGAAGGTGCTCTTCTGGCAGGACCTTGACCAGCCGAGGGCCATCGC 540
Qy 541 CTTGGACCCCGCTCACGGGTACATGTACTGGACAGACTGGGTTGAGACGCCCCGGATTGA 600
Db 541 CTTGGACCCCGCTCACGGGTACATGTACTGGACAGACTGGGTTGAGACGCCCCGGATTGA 600
Qy 601 GCGGGCAGGGATGGATGGCAGCACCCGGAAGATCATTGTGGACTCGGACATTTACTGGCC 660
Db 601 GCGGGCAGGGATGGATGGCAGCACCCGGAAGATCATTGTGGACTCGGACATTTACTGGCC 660
Qy 661 CAATGGACTGACCATCGACCTGGAGGAGCAGAAGCTCTACTGGGCTGACGCCAAGCTCAG 720
Db 661 CAATGGACTGACCATCGACCTGGAGGAGCAGAAGCTCTACTGGGCTGACGCCAAGCTCAG 720
Qy 721 CTTCATCCACCGTGCCAACCTGGACGGCTCGTTCCGGCAGAAGGTGGTGGAGGGCAGCCT 780
Db 721 CTTCATCCACCGTGCCAACCTGGACGGCTCGTTCCGGCAGAAGGTGGTGGAGGGCAGCCT 780
Qy 781 GACGCACCCCTTCGCCCTGACGCTCTCCGGGGACACTCTGTACTGGACAGACTGGCAGAC 840
Db 781 GACGCACCCCTTCGCCCTGACGCTCTCCGGGGACACTCTGTACTGGACAGACTGGCAGAC 840
Qy 841 CCGCTCCATCCATGCCTGCAACAAGCGCACTGGGGGGAAGAGGAAGGAGATCCTGAGTGC 900
Db 841 CCGCTCCATCCATGCCTGCAACAAGCGCACTGGGGGGAAGAGGAAGGAGATCCTGAGTGC 900
Qy 901 CCTCTACTCACCCATGGACATCCAGGTGCTGAGCCAGGAGCGGCAGCCTTTCTTCCACAC 960
Db 901 CCTCTACTCACCCATGGACATCCAGGTGCTGAGCCAGGAGCGGCAGCCTTTCTTCCACAC 960
Qy 961 TCGCTGTGAGGAGGACAATGGCGGCTGCTCCCACCTGTGCCTGCTGTCCCCAAGCGAGCC 1020
Db 961 TCGCTGTGAGGAGGACAATGGCGGCTGCTCCCACCTGTGCCTGCTGTCCCCAAGCGAGCC 1020
Qy 1021 TTTCTACACATGCGCCTGCCCCACGGGTGTGCAGCTGCAGGACAACGGCAGGACGTGTAA 1080
Db 1021 TTTCTACACATGCGCCTGCCCCACGGGTGTGCAGCTGCAGGACAACGGCAGGACGTGTAA 1080
Qy 1081 GGCAGGAGCCGAGGAGGTGCTGCTGCTGGCCCGGCGGACGGACCTACGGAGGATCTCGCT 1140
Db 1081 GGCAGGAGCCGAGGAGGTGCTGCTGCTGGCCCGGCGGACGGACCTACGGAGGATCTCGCT 1140
Qy 1141 GGACACGCCGGACTTCACCGACATCGTGCTGCAGGTGGACGACATCCGGCACGCCATTGC 1200
Db 1141 GGACACGCCGGACTTCACCGACATCGTGCTGCAGGTGGACGACATCCGGCACGCCATTGC 1200
Qy 1201 CATCGACTACGACCCGCTAGAGGGCTATGTCTACTGGACAGATGACGAGGTGCGGGCCAT 1260
Db 1201 CATCGACTACGACCCGCTAGAGGGCTATGTCTACTGGACAGATGACGAGGTGCGGGCCAT 1260
Qy 1261 CCGCAGGGCGTACCTGGACGGGTCTGGGGCGCAGACGCTGGTCAACACCGAGATCAACGA 1320
Db 1261 CCGCAGGGCGTACCTGGACGGGTCTGGGGCGCAGACGCTGGTCAACACCGAGATCAACGA 1320
Qy 1321 CCCCGATGGCATCGCGGTCGACTGGGTGGCCCGAAACCTCTACTGGACCGACACGGGCAC 1380
Db 1321 CCCCGATGGCATCGCGGTCGACTGGGTGGCCCGAAACCTCTACTGGACCGACACGGGCAC 1380
Qy 1381 GGACCGCATCGAGGTGACGCGCCTCAACGGCACCTCCCGCAAGATCCTGGTGTCGGAGGA 1440
Db 1381 GGACCGCATCGAGGTGACGCGCCTCAACGGCACCTCCCGCAAGATCCTGGTGTCGGAGGA 1440
Qy 1441 CCTGGACGAGCCCCGAGCCATCGCACTGCACCCCGTGATGGGCCTCATGTACTGGACAGA 1500
Db 1441 CCTGGACGAGCCCCGAGCCATCGCACTGCACCCCGTGATGGGCCTCATGTACTGGACAGA 1500
Qy 1501 CTGGGGAGAGAACCCTAAAATCGAGTGTGCCAACTTGGATGGGCAGGAGCGGCGTGTGCT 1560
Db 1501 CTGGGGAGAGAACCCTAAAATCGAGTGTGCCAACTTGGATGGGCAGGAGCGGCGTGTGCT 1560
Qy 1561 GGTCAATGCCTCCCTCGGGTGGCCCAACGGCCTGGCCCTGGACCTGCAGGAGGGGAAGCT 1620
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Qy 1741 CATCTACTGGACTGACTGGCAGCGCCGCAGCATCGAGCGGGTGCACAAGGTCAAGGCCAG 1800
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Qy 1801 CCGGGACGTCATCATTGACCAGCTGCCCGACCTGATGGGGCTCAAAGCTGTGAATGTGGC 1860
Db 1801 CCGGGACGTCATCATTGACCAGCTGCCCGACCTGATGGGGCTCAAAGCTGTGAATGTGGC 1860
Qy 1861 CAAGGTCGTCGGAACCAACCCGTGTGCGGACAGGAACGGGGGGTGCAGCCACCTGTGCTT 1920
Db 1861 CAAGGTCGTCGGAACCAACCCGTGTGCGGACAGGAACGGGGGGTGCAGCCACCTGTGCTT 1920
Qy 1921 CTTCACACCCCACGCAACCCGGTGTGGCTGCCCCATCGGCCTGGAGCTGCTGAGTGACAT 1980
Db 1921 CTTCACACCCCACGCAACCCGGTGTGGCTGCCCCATCGGCCTGGAGCTGCTGAGTGACAT 1980
Qy 1981 GAAGACCTGCATCGTGCCTGAGGCCTTCTTGGTCTTCACCAGCAGAGCCGCCATCCACAG 2040
Db 1981 GAAGACCTGCATCGTGCCTGAGGCCTTCTTGGTCTTCACCAGCAGAGCCGCCATCCACAG 2040
Qy 2041 GATCTCCCTCGAGACCAATAACAACGACGTGGCCATCCCGCTCACGGGCGTCAAGGAGGC 2100
Db 2041 GATCTCCCTCGAGACCAATAACAACGACGTGGCCATCCCGCTCACGGGCGTCAAGGAGGC 2100
Qy 2101 CTCAGCCCTGGACTTTGATGTGTCCAACAACCACATCTACTGGACAGACGTCAGCCTGAA 2160
Db 2101 CTCAGCCCTGGACTTTGATGTGTCCAACAACCACATCTACTGGACAGACGTCAGCCTGAA 2160
Qy 2161 GACCATCAGCCGCGCCTTCATGAACGGGAGCTCGGTGGAGCACGTGGTGGAGTTTGGCCT 2220
Db 2161 GACCATCAGCCGCGCCTTCATGAACGGGAGCTCGGTGGAGCACGTGGTGGAGTTTGGCCT 2220
Qy 2221 TGACTACCCCGAGGGCATGGCCGTTGACTGGATGGGCAAGAACCTCTACTGGGCCGACAC 2280

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Db      2221 TGACTACCCCGAGGGCATGGCCGTTGACTGGATGGGCAAGAACCTCTACTGGGCCGACAC 2280
Qy      2281 TGGGACCAACAGAATCGAAGTGGCGCGGCTGGACGGGCAGTTCCGGCAAGTCCTCGTGTG 2340
Db      2281 TGGGACCAACAGAATCGAAGTGGCGCGGCTGGACGGGCAGTTCCGGCAAGTCCTCGTGTG 2340
Qy      2341 GAGGGACTTGGACAACCCGAGGTCGCTGGCCCTGGATCCCACCAAGGGCTACATCTACTG 2400
Db      2341 GAGGGACTTGGACAACCCGAGGTCGCTGGCCCTGGATCCCACCAAGGGCTACATCTACTG 2400
Qy      2401 GACCGAGTGGGGCGGCAAGCCGAGGATCGTGCGGGCCTTCATGGACGGGACCAACTGCAT 2460
Db      2401 GACCGAGTGGGGCGGCAAGCCGAGGATCGTGCGGGCCTTCATGGACGGGACCAACTGCAT 2460
Qy      2461 GACGCTGGTGGACAAGGTGGGCCGGGCCAACGACCTCACCATTGACTACGCTGACCAGCG 2520
Db      2461 GACGCTGGTGGACAAGGTGGGCCGGGCCAACGACCTCACCATTGACTACGCTGACCAGCG 2520
Qy      2521 CCTCTACTGGACCGACCTGGACACCAACATGATCGAGTCGTCCAACATGCTGGGTCAGGA 2580
Db      2521 CCTCTACTGGACCGACCTGGACACCAACATGATCGAGTCGTCCAACATGCTGGGTCAGGA 2580
Qy      2581 GCGGGTCGTGATTGCCGACGATCTCCCGCACCCGTTCGGTCTGACGCAGTACAGCGATTA 2640
Db      2581 GCGGGTCGTGATTGCCGACGATCTCCCGCACCCGTTCGGTCTGACGCAGTACAGCGATTA 2640
Qy      2641 TATCTACTGGACAGACTGGAATCTGCACAGCATTGAGCGGGCCGACAAGACTAGCGGCCG 2700
Db      2641 TATCTACTGGACAGACTGGAATCTGCACAGCATTGAGCGGGCCGACAAGACTAGCGGCCG 2700
Qy      2701 GAACCGCACCCTCATCCAGGGCCACCTGGACTTCGTGATGGACATCCTGGTGTTCCACTC 2760
Db      2701 GAACCGCACCCTCATCCAGGGCCACCTGGACTTCGTGATGGACATCCTGGTGTTCCACTC 2760
Qy      2761 CTCCCGCCAGGATGGCCTCAATGACTGTATGCACAACAACGGGCAGTGTGGGCAGCTGTG 2820
Db      2761 CTCCCGCCAGGATGGCCTCAATGACTGTATGCACAACAACGGGCAGTGTGGGCAGCTGTG 2820
Qy      2821 CCTTGCCATCCCCGGCGGCCACCGCTGCGGCTGCGCCTCACACTACACCCTGGACCCCAG 2880
Db      2821 CCTTGCCATCCCCGGCGGCCACCGCTGCGGCTGCGCCTCACACTACACCCTGGACCCCAG 2880
Qy      2881 CAGCCGCAACTGCAGCCCGCCCACCACCTTCTTGCTGTTCAGCCAGAAATCTGCCATCAG 2940
Db      2881 CAGCCGCAACTGCAGCCCGCCCACCACCTTCTTGCTGTTCAGCCAGAAATCTGCCATCAG 2940
Qy      2941 TCGGATGATCCCGGACGACCAGCACAGCCCGGATCTCATCCTGCCCCTGCATGGACTGAG 3000
Db      2941 TCGGATGATCCCGGACGACCAGCACAGCCCGGATCTCATCCTGCCCCTGCATGGACTGAG 3000
Qy      3001 GAACGTCAAAGCCATCGACTATGACCCACTGGACAAGTTCATCTACTGGGTGGATGGGCG 3060
Db      3001 GAACGTCAAAGCCATCGACTATGACCCACTGGACAAGTTCATCTACTGGGTGGATGGGCG 3060
Qy      3061 CCAGAACATCAAGCGAGCCAAGGACGACGGGACCCAGCCCTTTGTTTTGACCTCTCTGAG 3120
Db      3061 CCAGAACATCAAGCGAGCCAAGGACGACGGGACCCAGCCCTTTGTTTTGACCTCTCTGAG 3120
Qy      3121 CCAAGGCCAAAACCCAGACAGGCAGCCCCACGACCTCAGCATCGACATCTACAGCCGGAC 3180
Db      3121 CCAAGGCCAAAACCCAGACAGGCAGCCCCACGACCTCAGCATCGACATCTACAGCCGGAC 3180
Qy      3181 ACTGTTCTGGACGTGCGAGGCCACCAATACCATCAACGTCCACAGGCTGAGCGGGGAAGC 3240
Db      3181 ACTGTTCTGGACGTGCGAGGCCACCAATACCATCAACGTCCACAGGCTGAGCGGGGAAGC 3240
Qy      3241 CATGGGGGTGGTGCTGCGTGGGGACCGCGACAAGCCCAGGGCCATCGTCGTCAACGCGGA 3300
Db      3241 CATGGGGGTGGTGCTGCGTGGGGACCGCGACAAGCCCAGGGCCATCGTCGTCAACGCGGA 3300
Qy      3301 GCGAGGGTACCTGTACTTCACCAACATGCAGGACCGGGCAGCCAAGATCGAACGCGCAGC 3360
Db      3301 GCGAGGGTACCTGTACTTCACCAACATGCAGGACCGGGCAGCCAAGATCGAACGCGCAGC 3360
Qy      3361 CCTGGACGGCACCGAGCGCGAGGTCCTCTTCACCACCGGCCTCATCCGCCCTGTGGCCCT 3420
Db      3361 CCTGGACGGCACCGAGCGCGAGGTCCTCTTCACCACCGGCCTCATCCGCCCTGTGGCCCT 3420
Qy      3421 GGTGGTGGACAACACACTGGGCAAGCTGTTCTGGGTGGACGCGGACCTGAAGCGCATTGA 3480
Db      3421 GGTGGTGGACAACACACTGGGCAAGCTGTTCTGGGTGGACGCGGACCTGAAGCGCATTGA 3480
Qy      3481 GAGCTGTGACCTGTCAGGGGCCAACCGCCTGACCCTGGAGGACGCCAACATCGTGCAGCC 3540
Db      3481 GAGCTGTGACCTGTCAGGGGCCAACCGCCTGACCCTGGAGGACGCCAACATCGTGCAGCC 3540
Qy      3541 TCTGGGCCTGACCATCCTTGGCAAGCATCTCTACTGGATCGACCGCCAGCAGCAGATGAT 3600
Db      3541 TCTGGGCCTGACCATCCTTGGCAAGCATCTCTACTGGATCGACCGCCAGCAGCAGATGAT 3600
Qy      3601 CGAGCGTGTGGAGAAGACCACCGGGGACAAGCGGACTCGCATCCAGGGCCGTGTCGCCCA 3660
Db      3601 CGAGCGTGTGGAGAAGACCACCGGGGACAAGCGGACTCGCATCCAGGGCCGTGTCGCCCA 3660
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Qy      3721 TGCCCGTGACAATGGTGGCTGCTCCCACATCTGTATTGCCAAGGGTGATGGGACACCACG 3780
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Qy      3781 GTGCTCATGCCCAGTCCACCTCGTGCTCCTGCAGAACCTGCTGACCTGTGGAGAGCCGCC 3840
Db      3781 GTGCTCATGCCCAGTCCACCTCGTGCTCCTGCAGAACCTGCTGACCTGTGGAGAGCCGCC 3840
Qy      3841 CACCTGCTCCCCGGACCAGTTTGCATGTGCCACAGGGGAGATCGACTGTATCCCCGGGGC 3900
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Qy      3901 CTGGCGCTGTGACGGCTTTCCCGAGTGCGATGACCAGAGCGACGAGGAGGGCTGCCCCGT 3960
Db      3901 CTGGCGCTGTGACGGCTTTCCCGAGTGCGATGACCAGAGCGACGAGGAGGGCTGCCCCGT 3960
Qy      3961 GTGCTCCGCCGCCCAGTTCCCCTGCGCGCGGGGTCAGTGTGTGGACCTGCGCCTGCGCTG 4020
Db      3961 GTGCTCCGCCGCCCAGTTCCCCTGCGCGCGGGGTCAGTGTGTGGACCTGCGCCTGCGCTG 4020
Qy      4021 CGACGGCGAGGCAGACTGTCAGGACCGCTCAGACGAGGTGGACTGTGACGCCATCTGCCT 4080
Db      4021 CGACGGCGAGGCAGACTGTCAGGACCGCTCAGACGAGGTGGACTGTGACGCCATCTGCCT 4080
Qy      4081 GCCCAACCAGTTCCGGTGTGCGAGCGGCCAGTGTGTCCTCATCAAACAGCAGTGCGACTC 4140
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Qy      4141 CTTCCCCGACTGTATCGACGGCTCCGACGAGCTCATGTGTGAAATCACCAAGCCGCCCTC 4200
Db      4141 CTTCCCCGACTGTATCGACGGCTCCGACGAGCTCATGTGTGAAATCACCAAGCCGCCCTC 4200
Qy      4201 AGACGACAGCCCGGCCCACAGCAGTGCCATCGGGCCCGTCATTGGCATCATCCTCTCTCT 4260
Db      4201 AGACGACAGCCCGGCCCACAGCAGTGCCATCGGGCCCGTCATTGGCATCATCCTCTCTCT 4260
Qy      4261 CTTCGTCATGGGTGGTGTCTATTTTGTGTGCCAGCGCGTGGTGTGCCAGCGCTATGCGGG 4320
Db      4261 CTTCGTCATGGGTGGTGTCTATTTTGTGTGCCAGCGCGTGGTGTGCCAGCGCTATGCGGG 4320
Qy      4321 GGCCAACGGGCCCTTCCCGCACGAGTATGTCAGCGGGACCCCGCACGTGCCCCTCAATTT 4380
Db      4321 GGCCAACGGGCCCTTCCCGCACGAGTATGTCAGCGGGACCCCGCACGTGCCCCTCAATTT 4380
Qy      4381 CATAGCCCCGGGCGGTTCCCAGCATGGCCCCTTCACAGGCATCGCATGCGGAAAGTCCAT 4440
Db      4381 CATAGCCCCGGGCGGTTCCCAGCATGGCCCCTTCACAGGCATCGCATGCGGAAAGTCCAT 4440
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Qy       4441 GATGAGCTCCGTGAGCCTGATGGGGGGCCGGGGCGGGGTGCCCCTCTACGACCGGAACCA 4500
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Db       4441 GATGAGCTCCGTGAGCCTGATGGGGGGCCGGGGCGGGGTGCCCCTCTACGACCGGAACCA 4500

Qy       4501 CGTCACAGGGGCCTCGTCCAGCAGCTCGTCCAGCACGAAGGCCACGCTGTACCCGCCGAT 4560
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Qy       4561 CCTGAACCCGCCGCCCTCCCCGGCCACGGACCCCTCCCTGTACAACATGGACATGTTCTA 4620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4561 CCTGAACCCGCCGCCCTCCCCGGCCACGGACCCCTCCCTGTACAACATGGACATGTTCTA 4620

Qy       4621 CTCTTCAAACATTCCGGCCACTGCGAGACCGTACAGGCCCTACATCATTCGAGGAATGGC 4680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4621 CTCTTCAAACATTCCGGCCACTGCGAGACCGTACAGGCCCTACATCATTCGAGGAATGGC 4680

Qy       4681 GCCCCCGACGACGCCCTGCAGCACCGACGTGTGTGACAGCGACTACAGCGCCAGCCGCTG 4740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4681 GCCCCCGACGACGCCCTGCAGCACCGACGTGTGTGACAGCGACTACAGCGCCAGCCGCTG 4740

Qy       4741 GAAGGCCAGCAAGTACTACCTGGATTTGAACTCGGACTCAGACCCCTATCCACCCCCACC 4800
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4741 GAAGGCCAGCAAGTACTACCTGGATTTGAACTCGGACTCAGACCCCTATCCACCCCCACC 4800

Qy       4801 CACGCCCCACAGCCAGTACCTGTCGGCGGAGGACAGCTGCCCGCCCTCGCCCGCCACCGA 4860
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4801 CACGCCCCACAGCCAGTACCTGTCGGCGGAGGACAGCTGCCCGCCCTCGCCCGCCACCGA 4860

Qy       4861 GAGGAGCTACTTCCATCTCTTCCCGCCCCCTCCGTCCCCCTGCACGGACTCATCCTGACC 4920
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Db       4861 GAGGAGCTACTTCCATCTCTTCCCGCCCCCTCCGTCCCCCTGCACGGACTCATCCTGACC 4920

Qy       4921 TCGGCCGGGCCACTCTGGCTTCTCTGTGCCCCTGTAAATAGTTTTAAATATGAACAAAGA 4980
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Db       4921 TCGGCCGGGCCACTCTGGCTTCTCTGTGCCCCTGTAAATAGTTTTAAATATGAACAAAGA 4980

Qy       4981 AAAAAATATATTTTATGATTTAAAAAATAAATATAATTGGGATTTTAAAAACATGAGAAA 5040
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4981 AAAAAATATATTTTATGATTTAAAAAATAAATATAATTGGGATTTTAAAAACATGAGAAA 5040

Qy       5041 TGTGAACTGTGATGGGGTGGGCAGGGCTGGGAGAACTTTGTACAGTGGAGAAATATTTAT 5100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5041 TGTGAACTGTGATGGGGTGGGCAGGGCTGGGAGAACTTTGTACAGTGGAGAAATATTTAT 5100

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Db       5101 AAACTTAATTTTGTAAAACA 5120
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RESULT 2
US-10-182-936A-2
; Sequence 2, Application US/10182936A
; Publication No. US20040038860A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Kristina M.
; APPLICANT: Anisowicz, Anthony
; APPLICANT: Bhat, Bheem
; APPLICANT: Damagnez, Veronique
; APPLICANT: Robinson, John
; APPLICANT: Yaworsky, Paul
; TITLE OF INVENTION: Reagents and Method for Modulating DKK-Mediated Interactions
; FILE REFERENCE: 032796-143
; CURRENT APPLICATION NUMBER: US/10/182,936A
; CURRENT FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: PCT/US02/15982
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: US 60/291,311
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: US 60/353,058
; PRIOR FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: US 60/361,293
; PRIOR FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 216
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 5120
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-182-936A-2

Query Match 100.0%; Score 5120; DB 17; Length 5120;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ACTAAAGCGCCGCCGCCGCGCCATGGAGCCCGAGTGAGCGCGGCGCGGGCCCGTCCGGCC 60
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Db          1 ACTAAAGCGCCGCCGCCGCGCCATGGAGCCCGAGTGAGCGCGGCGCGGGCCCGTCCGGCC 60

Qy         61 GCCGGACAACATGGAGGCAGCGCCGCCCGGGCCGCCGTGGCCGCTGCTGCTGCTGCTGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCCGGACAACATGGAGGCAGCGCCGCCCGGGCCGCCGTGGCCGCTGCTGCTGCTGCTGCT 120

Qy        121 GCTGCTGCTGGCGCTGTGCGGCTGCCCGGCCCCCGCCGCGGCCTCGCCGCTCCTGCTATT 180
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Db        121 GCTGCTGCTGGCGCTGTGCGGCTGCCCGGCCCCCGCCGCGGCCTCGCCGCTCCTGCTATT 180

Qy        181 TGCCAACCGCCGGGACGTACGGCTGGTGGACGCCGGCGGAGTCAAGCTGGAGTCCACCAT 240
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Db        181 TGCCAACCGCCGGGACGTACGGCTGGTGGACGCCGGCGGAGTCAAGCTGGAGTCCACCAT 240

Qy        241 CGTGGTCAGCGGCCTGGAGGATGCGGCCGCAGTGGACTTCCAGTTTTCCAAGGGAGCCGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CGTGGTCAGCGGCCTGGAGGATGCGGCCGCAGTGGACTTCCAGTTTTCCAAGGGAGCCGT 300

Qy        301 GTACTGGACAGACGTGAGCGAGGAGGCCATCAAGCAGACCTACCTGAACCAGACGGGGGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GTACTGGACAGACGTGAGCGAGGAGGCCATCAAGCAGACCTACCTGAACCAGACGGGGGC 360

Qy        361 CGCCGTGCAGAACGTGGTCATCTCCGGCCTGGTCTCTCCCGACGGCCTCGCCTGCGACTG 420
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Db        361 CGCCGTGCAGAACGTGGTCATCTCCGGCCTGGTCTCTCCCGACGGCCTCGCCTGCGACTG 420

Qy        421 GGTGGGCAAGAAGCTGTACTGGACGGACTCAGAGACCAACCGCATCGAGGTGGCCAACCT 480
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Qy        481 CAATGGCACATCCCGGAAGGTGCTCTTCTGGCAGGACCTTGACCAGCCGAGGGCCATCGC 540
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Qy        541 CTTGGACCCCGCTCACGGGTACATGTACTGGACAGACTGGGTTGAGACGCCCCGGATTGA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CTTGGACCCCGCTCACGGGTACATGTACTGGACAGACTGGGTTGAGACGCCCCGGATTGA 600

Qy        601 GCGGGCAGGGATGGATGGCAGCACCCGGAAGATCATTGTGGACTCGGACATTTACTGGCC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GCGGGCAGGGATGGATGGCAGCACCCGGAAGATCATTGTGGACTCGGACATTTACTGGCC 660

Qy        661 CAATGGACTGACCATCGACCTGGAGGAGCAGAAGCTCTACTGGGCTGACGCCAAGCTCAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAATGGACTGACCATCGACCTGGAGGAGCAGAAGCTCTACTGGGCTGACGCCAAGCTCAG 720

Qy        721 CTTCATCCACCGTGCCAACCTGGACGGCTCGTTCCGGCAGAAGGTGGTGGAGGGCAGCCT 780
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Db        721 CTTCATCCACCGTGCCAACCTGGACGGCTCGTTCCGGCAGAAGGTGGTGGAGGGCAGCCT 780

Qy        781 GACGCACCCCTTCGCCCTGACGCTCTCCGGGGACACTCTGTACTGGACAGACTGGCAGAC 840
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Db        781 GACGCACCCCTTCGCCCTGACGCTCTCCGGGGACACTCTGTACTGGACAGACTGGCAGAC 840

Qy        841 CCGCTCCATCCATGCCTGCAACAAGCGCACTGGGGGGAAGAGGAAGGAGATCCTGAGTGC 900
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Db        841 CCGCTCCATCCATGCCTGCAACAAGCGCACTGGGGGGAAGAGGAAGGAGATCCTGAGTGC 900

Qy        901 CCTCTACTCACCCATGGACATCCAGGTGCTGAGCCAGGAGCGGCAGCCTTTCTTCCACAC 960
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Db        901 CCTCTACTCACCCATGGACATCCAGGTGCTGAGCCAGGAGCGGCAGCCTTTCTTCCACAC 960
Qy        961 TCGCTGTGAGGAGGACAATGGCGGCTGCTCCCACCTGTGCCTGCTGTCCCCAAGCGAGCC 1020
Db        961 TCGCTGTGAGGAGGACAATGGCGGCTGCTCCCACCTGTGCCTGCTGTCCCCAAGCGAGCC 1020
Qy       1021 TTTCTACACATGCGCCTGCCCCACGGGTGTGCAGCTGCAGGACAACGGCAGGACGTGTAA 1080
Db       1021 TTTCTACACATGCGCCTGCCCCACGGGTGTGCAGCTGCAGGACAACGGCAGGACGTGTAA 1080
Qy       1081 GGCAGGAGCCGAGGAGGTGCTGCTGCTGGCCCGGCGGACGGACCTACGGAGGATCTCGCT 1140
Db       1081 GGCAGGAGCCGAGGAGGTGCTGCTGCTGGCCCGGCGGACGGACCTACGGAGGATCTCGCT 1140
Qy       1141 GGACACGCCGGACTTCACCGACATCGTGCTGCAGGTGGACGACATCCGGCACGCCATTGC 1200
Db       1141 GGACACGCCGGACTTCACCGACATCGTGCTGCAGGTGGACGACATCCGGCACGCCATTGC 1200
Qy       1201 CATCGACTACGACCCGCTAGAGGGCTATGTCTACTGGACAGATGACGAGGTGCGGGCCAT 1260
Db       1201 CATCGACTACGACCCGCTAGAGGGCTATGTCTACTGGACAGATGACGAGGTGCGGGCCAT 1260
Qy       1261 CCGCAGGGCGTACCTGGACGGGTCTGGGGCGCAGACGCTGGTCAACACCGAGATCAACGA 1320
Db       1261 CCGCAGGGCGTACCTGGACGGGTCTGGGGCGCAGACGCTGGTCAACACCGAGATCAACGA 1320
Qy       1321 CCCCGATGGCATCGCGGTCGACTGGGTGGCCCGAAACCTCTACTGGACCGACACGGGCAC 1380
Db       1321 CCCCGATGGCATCGCGGTCGACTGGGTGGCCCGAAACCTCTACTGGACCGACACGGGCAC 1380
Qy       1381 GGACCGCATCGAGGTGACGCGCCTCAACGGCACCTCCCGCAAGATCCTGGTGTCGGAGGA 1440
Db       1381 GGACCGCATCGAGGTGACGCGCCTCAACGGCACCTCCCGCAAGATCCTGGTGTCGGAGGA 1440
Qy       1441 CCTGGACGAGCCCCGAGCCATCGCACTGCACCCCGTGATGGGCCTCATGTACTGGACAGA 1500
Db       1441 CCTGGACGAGCCCCGAGCCATCGCACTGCACCCCGTGATGGGCCTCATGTACTGGACAGA 1500
Qy       1501 CTGGGGAGAGAACCCTAAAATCGAGTGTGCCAACTTGGATGGGCAGGAGCGGCGTGTGCT 1560
Db       1501 CTGGGGAGAGAACCCTAAAATCGAGTGTGCCAACTTGGATGGGCAGGAGCGGCGTGTGCT 1560
Qy       1561 GGTCAATGCCTCCCTCGGGTGGCCCAACGGCCTGGCCCTGGACCTGCAGGAGGGGAAGCT 1620
Db       1561 GGTCAATGCCTCCCTCGGGTGGCCCAACGGCCTGGCCCTGGACCTGCAGGAGGGGAAGCT 1620
Qy       1621 CTACTGGGGAGACGCCAAGACAGACAAGATCGAGGTGATCAATGTTGATGGGACGAAGAG 1680
Db       1621 CTACTGGGGAGACGCCAAGACAGACAAGATCGAGGTGATCAATGTTGATGGGACGAAGAG 1680
Qy       1681 GCGGACCCTCCTGGAGGACAAGCTCCCGCACATTTTCGGGTTCACGCTGCTGGGGGACTT 1740
Db       1681 GCGGACCCTCCTGGAGGACAAGCTCCCGCACATTTTCGGGTTCACGCTGCTGGGGGACTT 1740
Qy       1741 CATCTACTGGACTGACTGGCAGCGCCGCAGCATCGAGCGGGTGCACAAGGTCAAGGCCAG 1800
Db       1741 CATCTACTGGACTGACTGGCAGCGCCGCAGCATCGAGCGGGTGCACAAGGTCAAGGCCAG 1800
Qy       1801 CCGGGACGTCATCATTGACCAGCTGCCCGACCTGATGGGGCTCAAAGCTGTGAATGTGGC 1860
Db       1801 CCGGGACGTCATCATTGACCAGCTGCCCGACCTGATGGGGCTCAAAGCTGTGAATGTGGC 1860
Qy       1861 CAAGGTCGTCGGAACCAACCCGTGTGCGGACAGGAACGGGGGGTGCAGCCACCTGTGCTT 1920
Db       1861 CAAGGTCGTCGGAACCAACCCGTGTGCGGACAGGAACGGGGGGTGCAGCCACCTGTGCTT 1920
Qy       1921 CTTCACACCCCACGCAACCCGGTGTGGCTGCCCCATCGGCCTGGAGCTGCTGAGTGACAT 1980
Db       1921 CTTCACACCCCACGCAACCCGGTGTGGCTGCCCCATCGGCCTGGAGCTGCTGAGTGACAT 1980
Qy       1981 GAAGACCTGCATCGTGCCTGAGGCCTTCTTGGTCTTCACCAGCAGAGCCGCCATCCACAG 2040
Db       1981 GAAGACCTGCATCGTGCCTGAGGCCTTCTTGGTCTTCACCAGCAGAGCCGCCATCCACAG 2040
Qy       2041 GATCTCCCTCGAGACCAATAACAACGACGTGGCCATCCCGCTCACGGGCGTCAAGGAGGC 2100
Db       2041 GATCTCCCTCGAGACCAATAACAACGACGTGGCCATCCCGCTCACGGGCGTCAAGGAGGC 2100
Qy       2101 CTCAGCCCTGGACTTTGATGTGTCCAACAACCACATCTACTGGACAGACGTCAGCCTGAA 2160
Db       2101 CTCAGCCCTGGACTTTGATGTGTCCAACAACCACATCTACTGGACAGACGTCAGCCTGAA 2160
Qy       2161 GACCATCAGCCGCGCCTTCATGAACGGGAGCTCGGTGGAGCACGTGGTGGAGTTTGGCCT 2220
Db       2161 GACCATCAGCCGCGCCTTCATGAACGGGAGCTCGGTGGAGCACGTGGTGGAGTTTGGCCT 2220
Qy       2221 TGACTACCCCGAGGGCATGGCCGTTGACTGGATGGGCAAGAACCTCTACTGGGCCGACAC 2280
Db       2221 TGACTACCCCGAGGGCATGGCCGTTGACTGGATGGGCAAGAACCTCTACTGGGCCGACAC 2280
Qy       2281 TGGGACCAACAGAATCGAAGTGGCGCGGCTGGACGGGCAGTTCCGGCAAGTCCTCGTGTG 2340
Db       2281 TGGGACCAACAGAATCGAAGTGGCGCGGCTGGACGGGCAGTTCCGGCAAGTCCTCGTGTG 2340
Qy       2341 GAGGGACTTGGACAACCCGAGGTCGCTGGCCCTGGATCCCACCAAGGGCTACATCTACTG 2400
Db       2341 GAGGGACTTGGACAACCCGAGGTCGCTGGCCCTGGATCCCACCAAGGGCTACATCTACTG 2400
Qy       2401 GACCGAGTGGGGCGGCAAGCCGAGGATCGTGCGGGCCTTCATGGACGGGACCAACTGCAT 2460
Db       2401 GACCGAGTGGGGCGGCAAGCCGAGGATCGTGCGGGCCTTCATGGACGGGACCAACTGCAT 2460
Qy       2461 GACGCTGGTGGACAAGGTGGGCCGGGCCAACGACCTCACCATTGACTACGCTGACCAGCG 2520
Db       2461 GACGCTGGTGGACAAGGTGGGCCGGGCCAACGACCTCACCATTGACTACGCTGACCAGCG 2520
Qy       2521 CCTCTACTGGACCGACCTGGACACCAACATGATCGAGTCGTCCAACATGCTGGGTCAGGA 2580
Db       2521 CCTCTACTGGACCGACCTGGACACCAACATGATCGAGTCGTCCAACATGCTGGGTCAGGA 2580
Qy       2581 GCGGGTCGTGATTGCCGACGATCTCCCGCACCCGTTCGGTCTGACGCAGTACAGCGATTA 2640
Db       2581 GCGGGTCGTGATTGCCGACGATCTCCCGCACCCGTTCGGTCTGACGCAGTACAGCGATTA 2640
Qy       2641 TATCTACTGGACAGACTGGAATCTGCACAGCATTGAGCGGGCCGACAAGACTAGCGGCCG 2700
Db       2641 TATCTACTGGACAGACTGGAATCTGCACAGCATTGAGCGGGCCGACAAGACTAGCGGCCG 2700
Qy       2701 GAACCGCACCCTCATCCAGGGCCACCTGGACTTCGTGATGGACATCCTGGTGTTCCACTC 2760
Db       2701 GAACCGCACCCTCATCCAGGGCCACCTGGACTTCGTGATGGACATCCTGGTGTTCCACTC 2760
Qy       2761 CTCCCGCCAGGATGGCCTCAATGACTGTATGCACAACAACGGGCAGTGTGGGCAGCTGTG 2820
Db       2761 CTCCCGCCAGGATGGCCTCAATGACTGTATGCACAACAACGGGCAGTGTGGGCAGCTGTG 2820
Qy       2821 CCTTGCCATCCCCGGCGGCCACCGCTGCGGCTGCGCCTCACACTACACCCTGGACCCCAG 2880
Db       2821 CCTTGCCATCCCCGGCGGCCACCGCTGCGGCTGCGCCTCACACTACACCCTGGACCCCAG 2880
Qy       2881 CAGCCGCAACTGCAGCCCGCCCACCACCTTCTTGCTGTTCAGCCAGAAATCTGCCATCAG 2940
Db       2881 CAGCCGCAACTGCAGCCCGCCCACCACCTTCTTGCTGTTCAGCCAGAAATCTGCCATCAG 2940
Qy       2941 TCGGATGATCCCGGACGACCAGCACAGCCCGGATCTCATCCTGCCCCTGCATGGACTGAG 3000
Db       2941 TCGGATGATCCCGGACGACCAGCACAGCCCGGATCTCATCCTGCCCCTGCATGGACTGAG 3000
Qy       3001 GAACGTCAAAGCCATCGACTATGACCCACTGGACAAGTTCATCTACTGGGTGGATGGGCG 3060
Db       3001 GAACGTCAAAGCCATCGACTATGACCCACTGGACAAGTTCATCTACTGGGTGGATGGGCG 3060
Qy       3061 CCAGAACATCAAGCGAGCCAAGGACGACGGGACCCAGCCCTTTGTTTTGACCTCTCTGAG 3120
Db       3061 CCAGAACATCAAGCGAGCCAAGGACGACGGGACCCAGCCCTTTGTTTTGACCTCTCTGAG 3120
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Qy       3121 CCAAGGCCAAAACCCAGACAGGCAGCCCCACGACCTCAGCATCGACATCTACAGCCGGAC 3180
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Db       3121 CCAAGGCCAAAACCCAGACAGGCAGCCCCACGACCTCAGCATCGACATCTACAGCCGGAC 3180

Qy       3181 ACTGTTCTGGACGTGCGAGGCCACCAATACCATCAACGTCCACAGGCTGAGCGGGGAAGC 3240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3181 ACTGTTCTGGACGTGCGAGGCCACCAATACCATCAACGTCCACAGGCTGAGCGGGGAAGC 3240

Qy       3241 CATGGGGGTGGTGCTGCGTGGGGACCGCGACAAGCCCAGGGCCATCGTCGTCAACGCGGA 3300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3241 CATGGGGGTGGTGCTGCGTGGGGACCGCGACAAGCCCAGGGCCATCGTCGTCAACGCGGA 3300

Qy       3301 GCGAGGGTACCTGTACTTCACCAACATGCAGGACCGGGCAGCCAAGATCGAACGCGCAGC 3360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3301 GCGAGGGTACCTGTACTTCACCAACATGCAGGACCGGGCAGCCAAGATCGAACGCGCAGC 3360

Qy       3361 CCTGGACGGCACCGAGCGCGAGGTCCTCTTCACCACCGGCCTCATCCGCCCTGTGGCCCT 3420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3361 CCTGGACGGCACCGAGCGCGAGGTCCTCTTCACCACCGGCCTCATCCGCCCTGTGGCCCT 3420

Qy       3421 GGTGGTGGACAACACACTGGGCAAGCTGTTCTGGGTGGACGCGGACCTGAAGCGCATTGA 3480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3421 GGTGGTGGACAACACACTGGGCAAGCTGTTCTGGGTGGACGCGGACCTGAAGCGCATTGA 3480

Qy       3481 GAGCTGTGACCTGTCAGGGGCCAACCGCCTGACCCTGGAGGACGCCAACATCGTGCAGCC 3540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3481 GAGCTGTGACCTGTCAGGGGCCAACCGCCTGACCCTGGAGGACGCCAACATCGTGCAGCC 3540

Qy       3541 TCTGGGCCTGACCATCCTTGGCAAGCATCTCTACTGGATCGACCGCCAGCAGCAGATGAT 3600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3541 TCTGGGCCTGACCATCCTTGGCAAGCATCTCTACTGGATCGACCGCCAGCAGCAGATGAT 3600

Qy       3601 CGAGCGTGTGGAGAAGACCACCGGGGACAAGCGGACTCGCATCCAGGGCCGTGTCGCCCA 3660
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Db       3601 CGAGCGTGTGGAGAAGACCACCGGGGACAAGCGGACTCGCATCCAGGGCCGTGTCGCCCA 3660

Qy       3661 CCTCACTGGCATCCATGCAGTGGAGGAAGTCAGCCTGGAGGAGTTCTCAGCCCACCCATG 3720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3661 CCTCACTGGCATCCATGCAGTGGAGGAAGTCAGCCTGGAGGAGTTCTCAGCCCACCCATG 3720

Qy       3721 TGCCCGTGACAATGGTGGCTGCTCCCACATCTGTATTGCCAAGGGTGATGGGACACCACG 3780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3721 TGCCCGTGACAATGGTGGCTGCTCCCACATCTGTATTGCCAAGGGTGATGGGACACCACG 3780

Qy       3781 GTGCTCATGCCCAGTCCACCTCGTGCTCCTGCAGAACCTGCTGACCTGTGGAGAGCCGCC 3840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3781 GTGCTCATGCCCAGTCCACCTCGTGCTCCTGCAGAACCTGCTGACCTGTGGAGAGCCGCC 3840

Qy       3841 CACCTGCTCCCCGGACCAGTTTGCATGTGCCACAGGGGAGATCGACTGTATCCCCGGGGC 3900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3841 CACCTGCTCCCCGGACCAGTTTGCATGTGCCACAGGGGAGATCGACTGTATCCCCGGGGC 3900

Qy       3901 CTGGCGCTGTGACGGCTTTCCCGAGTGCGATGACCAGAGCGACGAGGAGGGCTGCCCCGT 3960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3901 CTGGCGCTGTGACGGCTTTCCCGAGTGCGATGACCAGAGCGACGAGGAGGGCTGCCCCGT 3960

Qy       3961 GTGCTCCGCCGCCCAGTTCCCCTGCGCGCGGGGTCAGTGTGTGGACCTGCGCCTGCGCTG 4020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3961 GTGCTCCGCCGCCCAGTTCCCCTGCGCGCGGGGTCAGTGTGTGGACCTGCGCCTGCGCTG 4020

Qy       4021 CGACGGCGAGGCAGACTGTCAGGACCGCTCAGACGAGGTGGACTGTGACGCCATCTGCCT 4080
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Db       4021 CGACGGCGAGGCAGACTGTCAGGACCGCTCAGACGAGGTGGACTGTGACGCCATCTGCCT 4080

Qy       4081 GCCCAACCAGTTCCGGTGTGCGAGCGGCCAGTGTGTCCTCATCAAACAGCAGTGCGACTC 4140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4081 GCCCAACCAGTTCCGGTGTGCGAGCGGCCAGTGTGTCCTCATCAAACAGCAGTGCGACTC 4140

Qy       4141 CTTCCCCGACTGTATCGACGGCTCCGACGAGCTCATGTGTGAAATCACCAAGCCGCCCTC 4200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4141 CTTCCCCGACTGTATCGACGGCTCCGACGAGCTCATGTGTGAAATCACCAAGCCGCCCTC 4200

Qy       4201 AGACGACAGCCCGGCCCACAGCAGTGCCATCGGGCCCGTCATTGGCATCATCCTCTCTCT 4260
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Db       4201 AGACGACAGCCCGGCCCACAGCAGTGCCATCGGGCCCGTCATTGGCATCATCCTCTCTCT 4260

Qy       4261 CTTCGTCATGGGTGGTGTCTATTTTGTGTGCCAGCGCGTGGTGTGCCAGCGCTATGCGGG 4320
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Db       4261 CTTCGTCATGGGTGGTGTCTATTTTGTGTGCCAGCGCGTGGTGTGCCAGCGCTATGCGGG 4320

Qy       4321 GGCCAACGGGCCCTTCCCGCACGAGTATGTCAGCGGGACCCCGCACGTGCCCCTCAATTT 4380
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Db       4321 GGCCAACGGGCCCTTCCCGCACGAGTATGTCAGCGGGACCCCGCACGTGCCCCTCAATTT 4380

Qy       4381 CATAGCCCCGGGCGGTTCCCAGCATGGCCCCTTCACAGGCATCGCATGCGGAAAGTCCAT 4440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4381 CATAGCCCCGGGCGGTTCCCAGCATGGCCCCTTCACAGGCATCGCATGCGGAAAGTCCAT 4440

Qy       4441 GATGAGCTCCGTGAGCCTGATGGGGGGCCGGGGCGGGGTGCCCCCTCTACGACCGGAACCA 4500
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Db       4441 GATGAGCTCCGTGAGCCTGATGGGGGGCCGGGGCGGGGTGCCCCCTCTACGACCGGAACCA 4500

Qy       4501 CGTCACAGGGGCCTCGTCCAGCAGCTCGTCCAGCACGAAGGCCACGCTGTACCCGCCGAT 4560
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Db       4501 CGTCACAGGGGCCTCGTCCAGCAGCTCGTCCAGCACGAAGGCCACGCTGTACCCGCCGAT 4560

Qy       4561 CCTGAACCCGCCGCCCTCCCCGGCCACGGACCCCTCCCTGTACAACATGGACATGTTCTA 4620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4561 CCTGAACCCGCCGCCCTCCCCGGCCACGGACCCCTCCCTGTACAACATGGACATGTTCTA 4620

Qy       4621 CTCTTCAAACATTCCGGCCACTGCGAGACCGTACAGGCCCTACATCATTCGAGGAATGGC 4680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4621 CTCTTCAAACATTCCGGCCACTGCGAGACCGTACAGGCCCTACATCATTCGAGGAATGGC 4680

Qy       4681 GCCCCCGACGACGCCCTGCAGCACCGACGTGTGTGACAGCGACTACAGCGCCAGCCGCTG 4740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4681 GCCCCCGACGACGCCCTGCAGCACCGACGTGTGTGACAGCGACTACAGCGCCAGCCGCTG 4740

Qy       4741 GAAGGCCAGCAAGTACTACCTGGATTTGAACTCGGACTCAGACCCCTATCCACCCCCACC 4800
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4741 GAAGGCCAGCAAGTACTACCTGGATTTGAACTCGGACTCAGACCCCTATCCACCCCCACC 4800

Qy       4801 CACGCCCCACAGCCAGTACCTGTCGGCGGAGGACAGCTGCCCGCCCTCGCCCGCCACCGA 4860
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4801 CACGCCCCACAGCCAGTACCTGTCGGCGGAGGACAGCTGCCCGCCCTCGCCCGCCACCGA 4860

Qy       4861 GAGGAGCTACTTCCATCTCTTCCCGCCCCCTCCGTCCCCCTGCACGGACTCATCCTGACC 4920
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4861 GAGGAGCTACTTCCATCTCTTCCCGCCCCCTCCGTCCCCCTGCACGGACTCATCCTGACC 4920

Qy       4921 TCGGCCGGGCCACTCTGGCTTCTCTGTGCCCCTGTAAATAGTTTTAAATATGAACAAAGA 4980
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Qy       4981 AAAAAATATATTTTATGATTTAAAAAATAAATATAATTGGGATTTTAAAAACATGAGAAA 5040
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Qy       5041 TGTGAACTGTGATGGGGTGGGCAGGGCTGGGAGAACTTTGTACAGTGGAGAAATATTTAT 5100
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Db       5041 TGTGAACTGTGATGGGGTGGGCAGGGCTGGGAGAACTTTGTACAGTGGAGAAATATTTAT 5100

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Db       5101 AAACTTAATTTTGTAAAACA 5120
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RESULT 3
US-10-731-739-2
; Sequence 2, Application US/10731739
; Publication No. US20040176582A1
; GENERAL INFORMATION:
; APPLICANT: Carulli, John P.
; APPLICANT: Little, Randall D.
; APPLICANT: Recker, Robert R.

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;  APPLICANT:  Johnson, Mark L.
;  TITLE OF INVENTION: High bone mass gene of 11q13.3
;  FILE REFERENCE: 032796-013
;  CURRENT APPLICATION NUMBER: US/10/731,739
;  CURRENT FILING DATE:  2003-12-10
;  PRIOR APPLICATION NUMBER: US/09/544,398B
;  PRIOR FILING DATE: 2002-06-10
;  PRIOR APPLICATION NUMBER: US 09/229,319
;  PRIOR FILING DATE: 1999-01-13
;  PRIOR APPLICATION NUMBER: US 60/071,449
;  PRIOR FILING DATE: 1998-01-13
;  PRIOR APPLICATION NUMBER: US 60/105,511
;  PRIOR FILING DATE: 1998-10-23
;  NUMBER OF SEQ ID NOS: 641
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 5120
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-731-739-2

  Query Match           100.0%;  Score 5120;  DB 18;  Length 5120;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 5120;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ACTAAAGCGCCGCCGCCGCGCCATGGAGCCCGAGTGAGCGCGGCGCGGGCCCGTCCGGCC 60
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Qy        121 GCTGCTGCTGGCGCTGTGCGGCTGCCCGGCCCCCGCCGCGGCCTCGCCGCTCCTGCTATT 180
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Db        121 GCTGCTGCTGGCGCTGTGCGGCTGCCCGGCCCCCGCCGCGGCCTCGCCGCTCCTGCTATT 180

Qy        181 TGCCAACCGCCGGGACGTACGGCTGGTGGACGCCGGCGGAGTCAAGCTGGAGTCCACCAT 240
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Db        181 TGCCAACCGCCGGGACGTACGGCTGGTGGACGCCGGCGGAGTCAAGCTGGAGTCCACCAT 240

Qy        241 CGTGGTCAGCGGCCTGGAGGATGCGGCCGCAGTGGACTTCCAGTTTTCCAAGGGAGCCGT 300
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Db        421 GGTGGGCAAGAAGCTGTACTGGACGGACTCAGAGACCAACCGCATCGAGGTGGCCAACCT 480

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Qy        541 CTTGGACCCCGCTCACGGGTACATGTACTGGACAGACTGGGTTGAGACGCCCCGGATTGA 600
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Db        541 CTTGGACCCCGCTCACGGGTACATGTACTGGACAGACTGGGTTGAGACGCCCCGGATTGA 600

Qy        601 GCGGGCAGGGATGGATGGCAGCACCCGGAAGATCATTGTGGACTCGGACATTTACTGGCC 660
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Db        601 GCGGGCAGGGATGGATGGCAGCACCCGGAAGATCATTGTGGACTCGGACATTTACTGGCC 660

Qy        661 CAATGGACTGACCATCGACCTGGAGGAGCAGAAGCTCTACTGGGCTGACGCCAAGCTCAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAATGGACTGACCATCGACCTGGAGGAGCAGAAGCTCTACTGGGCTGACGCCAAGCTCAG 720

Qy        721 CTTCATCCACCGTGCCAACCTGGACGGCTCGTTCCGGCAGAAGGTGGTGGAGGGCAGCCT 780
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Qy        781 GACGCACCCCTTCGCCCTGACGCTCTCCGGGGACACTCTGTACTGGACAGACTGGCAGAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACGCACCCCTTCGCCCTGACGCTCTCCGGGGACACTCTGTACTGGACAGACTGGCAGAC 840

Qy        841 CCGCTCCATCCATGCCTGCAACAAGCGCACTGGGGGGAAGAGGAAGGAGATCCTGAGTGC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CCGCTCCATCCATGCCTGCAACAAGCGCACTGGGGGGAAGAGGAAGGAGATCCTGAGTGC 900

Qy        901 CCTCTACTCACCCATGGACATCCAGGTGCTGAGCCAGGAGCGGCAGCCTTTCTTCCACAC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CCTCTACTCACCCATGGACATCCAGGTGCTGAGCCAGGAGCGGCAGCCTTTCTTCCACAC 960

Qy        961 TCGCTGTGAGGAGGACAATGGCGGCTGCTCCCACCTGTGCCTGCTGTCCCCAAGCGAGCC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TCGCTGTGAGGAGGACAATGGCGGCTGCTCCCACCTGTGCCTGCTGTCCCCAAGCGAGCC 1020

Qy       1021 TTTCTACACATGCGCCTGCCCCACGGGTGTGCAGCTGCAGGACAACGGCAGGACGTGTAA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 TTTCTACACATGCGCCTGCCCCACGGGTGTGCAGCTGCAGGACAACGGCAGGACGTGTAA 1080

Qy       1081 GGCAGGAGCCGAGGAGGTGCTGCTGCTGGCCCGGCGGACGGACCTACGGAGGATCTCGCT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 GGCAGGAGCCGAGGAGGTGCTGCTGCTGGCCCGGCGGACGGACCTACGGAGGATCTCGCT 1140

Qy       1141 GGACACGCCGGACTTCACCGACATCGTGCTGCAGGTGGACGACATCCGGCACGCCATTGC 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GGACACGCCGGACTTCACCGACATCGTGCTGCAGGTGGACGACATCCGGCACGCCATTGC 1200

Qy       1201 CATCGACTACGACCCGCTAGAGGGCTATGTCTACTGGACAGATGACGAGGTGCGGGCCAT 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 CATCGACTACGACCCGCTAGAGGGCTATGTCTACTGGACAGATGACGAGGTGCGGGCCAT 1260

Qy       1261 CCGCAGGGCGTACCTGGACGGGTCTGGGGCGCAGACGCTGGTCAACACCGAGATCAACGA 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 CCGCAGGGCGTACCTGGACGGGTCTGGGGCGCAGACGCTGGTCAACACCGAGATCAACGA 1320

Qy       1321 CCCCGATGGCATCGCGGTCGACTGGGTGGCCCGAAACCTCTACTGGACCGACACGGGCAC 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 CCCCGATGGCATCGCGGTCGACTGGGTGGCCCGAAACCTCTACTGGACCGACACGGGCAC 1380

Qy       1381 GGACCGCATCGAGGTGACGCGCCTCAACGGCACCTCCCGCAAGATCCTGGTGTCGGAGGA 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 GGACCGCATCGAGGTGACGCGCCTCAACGGCACCTCCCGCAAGATCCTGGTGTCGGAGGA 1440

Qy       1441 CCTGGACGAGCCCCGAGCCATCGCACTGCACCCCGTGATGGGCCTCATGTACTGGACAGA 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 CCTGGACGAGCCCCGAGCCATCGCACTGCACCCCGTGATGGGCCTCATGTACTGGACAGA 1500

Qy       1501 CTGGGGAGAGAACCCTAAAATCGAGTGTGCCAACTTGGATGGGCAGGAGCGGCGTGTGCT 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 CTGGGGAGAGAACCCTAAAATCGAGTGTGCCAACTTGGATGGGCAGGAGCGGCGTGTGCT 1560

Qy       1561 GGTCAATGCCTCCCTCGGGTGGCCCAACGGCCTGGCCCTGGACCTGCAGGAGGGGAAGCT 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 GGTCAATGCCTCCCTCGGGTGGCCCAACGGCCTGGCCCTGGACCTGCAGGAGGGGAAGCT 1620

Qy       1621 CTACTGGGGAGACGCCAAGACAGACAAGATCGAGGTGATCAATGTTGATGGGACGAAGAG 1680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 CTACTGGGGAGACGCCAAGACAGACAAGATCGAGGTGATCAATGTTGATGGGACGAAGAG 1680

Qy       1681 GCGGACCCTCCTGGAGGACAAGCTCCCGCACATTTTCGGGTTCACGCTGCTGGGGGACTT 1740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 GCGGACCCTCCTGGAGGACAAGCTCCCGCACATTTTCGGGTTCACGCTGCTGGGGGACTT 1740

Qy       1741 CATCTACTGGACTGACTGGCAGCGCCGCAGCATCGAGCGGGTGCACAAGGTCAAGGCCAG 1800
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 CATCTACTGGACTGACTGGCAGCGCCGCAGCATCGAGCGGGTGCACAAGGTCAAGGCCAG 1800

Qy       1801 CCGGGACGTCATCATTGACCAGCTGCCCGACCTGATGGGGCTCAAAGCTGTGAATGTGGC 1860
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Db      1801 CCGGGACGTCATCATTGACCAGCTGCCCGACCTGATGGGGCTCAAAGCTGTGAATGTGGC 1860
Qy      1861 CAAGGTCGTCGGAACCAACCCGTGTGCGGACAGGAACGGGGGGTGCAGCCACCTGTGCTT 1920
Db      1861 CAAGGTCGTCGGAACCAACCCGTGTGCGGACAGGAACGGGGGGTGCAGCCACCTGTGCTT 1920
Qy      1921 CTTCACACCCCACGCAACCCGGTGTGGCTGCCCCATCGGCCTGGAGCTGCTGAGTGACAT 1980
Db      1921 CTTCACACCCCACGCAACCCGGTGTGGCTGCCCCATCGGCCTGGAGCTGCTGAGTGACAT 1980
Qy      1981 GAAGACCTGCATCGTGCCTGAGGCCTTCTTGGTCTTCACCAGCAGAGCCGCCATCCACAG 2040
Db      1981 GAAGACCTGCATCGTGCCTGAGGCCTTCTTGGTCTTCACCAGCAGAGCCGCCATCCACAG 2040
Qy      2041 GATCTCCCTCGAGACCAATAACAACGACGTGGCCATCCCGCTCACGGGCGTCAAGGAGGC 2100
Db      2041 GATCTCCCTCGAGACCAATAACAACGACGTGGCCATCCCGCTCACGGGCGTCAAGGAGGC 2100
Qy      2101 CTCAGCCCTGGACTTTGATGTGTCCAACAACCACATCTACTGGACAGACGTCAGCCTGAA 2160
Db      2101 CTCAGCCCTGGACTTTGATGTGTCCAACAACCACATCTACTGGACAGACGTCAGCCTGAA 2160
Qy      2161 GACCATCAGCCGCGCCTTCATGAACGGGAGCTCGGTGGAGCACGTGGTGGAGTTTGGCCT 2220
Db      2161 GACCATCAGCCGCGCCTTCATGAACGGGAGCTCGGTGGAGCACGTGGTGGAGTTTGGCCT 2220
Qy      2221 TGACTACCCCGAGGGCATGGCCGTTGACTGGATGGGCAAGAACCTCTACTGGGCCGACAC 2280
Db      2221 TGACTACCCCGAGGGCATGGCCGTTGACTGGATGGGCAAGAACCTCTACTGGGCCGACAC 2280
Qy      2281 TGGGACCAACAGAATCGAAGTGGCGCGGCTGGACGGGCAGTTCCGGCAAGTCCTCGTGTG 2340
Db      2281 TGGGACCAACAGAATCGAAGTGGCGCGGCTGGACGGGCAGTTCCGGCAAGTCCTCGTGTG 2340
Qy      2341 GAGGGACTTGGACAACCCGAGGTCGCTGGCCCTGGATCCCACCAAGGGCTACATCTACTG 2400
Db      2341 GAGGGACTTGGACAACCCGAGGTCGCTGGCCCTGGATCCCACCAAGGGCTACATCTACTG 2400
Qy      2401 GACCGAGTGGGGCGGCAAGCCGAGGATCGTGCGGGCCTTCATGGACGGGACCAACTGCAT 2460
Db      2401 GACCGAGTGGGGCGGCAAGCCGAGGATCGTGCGGGCCTTCATGGACGGGACCAACTGCAT 2460
Qy      2461 GACGCTGGTGGACAAGGTGGGCCGGGCCAACGACCTCACCATTGACTACGCTGACCAGCG 2520
Db      2461 GACGCTGGTGGACAAGGTGGGCCGGGCCAACGACCTCACCATTGACTACGCTGACCAGCG 2520
Qy      2521 CCTCTACTGGACCGACCTGGACACCAACATGATCGAGTCGTCCAACATGCTGGGTCAGGA 2580
Db      2521 CCTCTACTGGACCGACCTGGACACCAACATGATCGAGTCGTCCAACATGCTGGGTCAGGA 2580
Qy      2581 GCGGGTCGTGATTGCCGACGATCTCCCGCACCCGTTCGGTCTGACGCAGTACAGCGATTA 2640
Db      2581 GCGGGTCGTGATTGCCGACGATCTCCCGCACCCGTTCGGTCTGACGCAGTACAGCGATTA 2640
Qy      2641 TATCTACTGGACAGACTGGAATCTGCACAGCATTGAGCGGGCCGACAAGACTAGCGGCCG 2700
Db      2641 TATCTACTGGACAGACTGGAATCTGCACAGCATTGAGCGGGCCGACAAGACTAGCGGCCG 2700
Qy      2701 GAACCGCACCCTCATCCAGGGCCACCTGGACTTCGTGATGGACATCCTGGTGTTCCACTC 2760
Db      2701 GAACCGCACCCTCATCCAGGGCCACCTGGACTTCGTGATGGACATCCTGGTGTTCCACTC 2760
Qy      2761 CTCCCGCCAGGATGGCCTCAATGACTGTATGCACAACAACGGGCAGTGTGGGCAGCTGTG 2820
Db      2761 CTCCCGCCAGGATGGCCTCAATGACTGTATGCACAACAACGGGCAGTGTGGGCAGCTGTG 2820
Qy      2821 CCTTGCCATCCCCGGCGGCCACCGCTGCGGCTGCGCCTCACACTACACCCTGGACCCCAG 2880
Db      2821 CCTTGCCATCCCCGGCGGCCACCGCTGCGGCTGCGCCTCACACTACACCCTGGACCCCAG 2880
Qy      2881 CAGCCGCAACTGCAGCCCGCCCACCACCTTCTTGCTGTTCAGCCAGAAATCTGCCATCAG 2940
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Db      2881 CAGCCGCAACTGCAGCCCGCCCACCACCTTCTTGCTGTTCAGCCAGAAATCTGCCATCAG 2940
Qy      2941 TCGGATGATCCCCGGACGACCAGCACAGCCCGGATCTCATCCTGCCCCTGCATGGACTGAG 3000
Db      2941 TCGGATGATCCCCGGACGACCAGCACAGCCCGGATCTCATCCTGCCCCTGCATGGACTGAG 3000
Qy      3001 GAACGTCAAAGCCATCGACTATGACCCACTGGACAAGTTCATCTACTGGGTGGATGGGCG 3060
Db      3001 GAACGTCAAAGCCATCGACTATGACCCACTGGACAAGTTCATCTACTGGGTGGATGGGCG 3060
Qy      3061 CCAGAACATCAAGCGAGCCAAGGACGACGGGACCCAGCCCTTTGTTTTGACCTCTCTGAG 3120
Db      3061 CCAGAACATCAAGCGAGCCAAGGACGACGGGACCCAGCCCTTTGTTTTGACCTCTCTGAG 3120
Qy      3121 CCAAGGCCAAAACCCAGACAGGCAGCCCCACGACCTCAGCATCGACATCTACAGCCGGAC 3180
Db      3121 CCAAGGCCAAAACCCAGACAGGCAGCCCCACGACCTCAGCATCGACATCTACAGCCGGAC 3180
Qy      3181 ACTGTTCTGGACGTGCGAGGCCACCAATACCATCAACGTCCACAGGCTGAGCGGGGAAGC 3240
Db      3181 ACTGTTCTGGACGTGCGAGGCCACCAATACCATCAACGTCCACAGGCTGAGCGGGGAAGC 3240
Qy      3241 CATGGGGGTGGTGCTGCGTGGGGACCGCGACAAGCCCAGGGCCATCGTCGTCAACGCGGA 3300
Db      3241 CATGGGGGTGGTGCTGCGTGGGGACCGCGACAAGCCCAGGGCCATCGTCGTCAACGCGGA 3300
Qy      3301 GCGAGGGTACCTGTACTTCACCAACATGCAGGACCGGGCAGCCAAGATCGAACGCGCAGC 3360
Db      3301 GCGAGGGTACCTGTACTTCACCAACATGCAGGACCGGGCAGCCAAGATCGAACGCGCAGC 3360
Qy      3361 CCTGGACGGCACCGAGCGCGAGGTCCTCTTCACCACCGGCCTCATCCGCCCTGTGGCCCT 3420
Db      3361 CCTGGACGGCACCGAGCGCGAGGTCCTCTTCACCACCGGCCTCATCCGCCCTGTGGCCCT 3420
Qy      3421 GGTGGTGGACAACACACTGGGCAAGCTGTTCTGGGTGGACGCGGACCTGAAGCGCATTGA 3480
Db      3421 GGTGGTGGACAACACACTGGGCAAGCTGTTCTGGGTGGACGCGGACCTGAAGCGCATTGA 3480
Qy      3481 GAGCTGTGACCTGTCAGGGGCCAACCGCCTGACCCTGGAGGACGCCAACATCGTGCAGCC 3540
Db      3481 GAGCTGTGACCTGTCAGGGGCCAACCGCCTGACCCTGGAGGACGCCAACATCGTGCAGCC 3540
Qy      3541 TCTGGGCCTGACCATCCTTGGCAAGCATCTCTACTGGATCGACCGCCAGCAGCAGATGAT 3600
Db      3541 TCTGGGCCTGACCATCCTTGGCAAGCATCTCTACTGGATCGACCGCCAGCAGCAGATGAT 3600
Qy      3601 CGAGCGTGTGGAGAAGACCACCGGGGACAAGCGGACTCGCATCCAGGGCCGTGTCGCCCA 3660
Db      3601 CGAGCGTGTGGAGAAGACCACCGGGGACAAGCGGACTCGCATCCAGGGCCGTGTCGCCCA 3660
Qy      3661 CCTCACTGGCATCCATGCAGTGGAGGAAGTCAGCCTGGAGGAGTTCTCAGCCCACCCATG 3720
Db      3661 CCTCACTGGCATCCATGCAGTGGAGGAAGTCAGCCTGGAGGAGTTCTCAGCCCACCCATG 3720
Qy      3721 TGCCCGTGACAATGGTGGCTGCTCCCACATCTGTATTGCCAAGGGTGATGGGACACCACG 3780
Db      3721 TGCCCGTGACAATGGTGGCTGCTCCCACATCTGTATTGCCAAGGGTGATGGGACACCACG 3780
Qy      3781 GTGCTCATGCCCAGTCCACCTCGTGCTCCTGCAGAACCTGCTGACCTGTGGAGAGCCGCC 3840
Db      3781 GTGCTCATGCCCAGTCCACCTCGTGCTCCTGCAGAACCTGCTGACCTGTGGAGAGCCGCC 3840
Qy      3841 CACCTGCTCCCCGGACCAGTTTGCATGTGCCACAGGGGAGATCGACTGTATCCCCGGGGC 3900
Db      3841 CACCTGCTCCCCGGACCAGTTTGCATGTGCCACAGGGGAGATCGACTGTATCCCCGGGGC 3900
Qy      3901 CTGGCGCTGTGACGGCTTTCCCGAGTGCGATGACCAGAGCGACGAGGAGGGCTGCCCCGT 3960
Db      3901 CTGGCGCTGTGACGGCTTTCCCGAGTGCGATGACCAGAGCGACGAGGAGGGCTGCCCCGT 3960
Qy      3961 GTGCTCCGCCGCCCAGTTCCCCTGCGCGCGGGGTCAGTGTGTGGACCTGCGCCTGCGCTG 4020
Db      3961 GTGCTCCGCCGCCCAGTTCCCCTGCGCGCGGGGTCAGTGTGTGGACCTGCGCCTGCGCTG 4020
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Qy       4021 CGACGGCGAGGCAGACTGTCAGGACCGCTCAGACGAGGTGGACTGTGACGCCATCTGCCT 4080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4021 CGACGGCGAGGCAGACTGTCAGGACCGCTCAGACGAGGTGGACTGTGACGCCATCTGCCT 4080

Qy       4081 GCCCAACCAGTTCCGGTGTGCGAGCGGCCAGTGTGTCCTCATCAAACAGCAGTGCGACTC 4140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4081 GCCCAACCAGTTCCGGTGTGCGAGCGGCCAGTGTGTCCTCATCAAACAGCAGTGCGACTC 4140

Qy       4141 CTTCCCCGACTGTATCGACGGCTCCGACGAGCTCATGTGTGAAATCACCAAGCCGCCCTC 4200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4141 CTTCCCCGACTGTATCGACGGCTCCGACGAGCTCATGTGTGAAATCACCAAGCCGCCCTC 4200

Qy       4201 AGACGACAGCCCGGCCCACAGCAGTGCCATCGGGCCCGTCATTGGCATCATCCTCTCTCT 4260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4201 AGACGACAGCCCGGCCCACAGCAGTGCCATCGGGCCCGTCATTGGCATCATCCTCTCTCT 4260

Qy       4261 CTTCGTCATGGGTGGTGTCTATTTTGTGTGCCAGCGCGTGGTGTGCCAGCGCTATGCGGG 4320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4261 CTTCGTCATGGGTGGTGTCTATTTTGTGTGCCAGCGCGTGGTGTGCCAGCGCTATGCGGG 4320

Qy       4321 GGCCAACGGGCCCTTCCCGCACGAGTATGTCAGCGGGACCCCGCACGTGCCCCTCAATTT 4380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4321 GGCCAACGGGCCCTTCCCGCACGAGTATGTCAGCGGGACCCCGCACGTGCCCCTCAATTT 4380

Qy       4381 CATAGCCCCGGGCGGTTCCCAGCATGGCCCCTTCACAGGCATCGCATGCGGAAAGTCCAT 4440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4381 CATAGCCCCGGGCGGTTCCCAGCATGGCCCCTTCACAGGCATCGCATGCGGAAAGTCCAT 4440

Qy       4441 GATGAGCTCCGTGAGCCTGATGGGGGGCCGGGGCGGGGTGCCCCTCTACGACCGGAACCA 4500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4441 GATGAGCTCCGTGAGCCTGATGGGGGGCCGGGGCGGGGTGCCCCTCTACGACCGGAACCA 4500

Qy       4501 CGTCACAGGGGCCTCGTCCAGCAGCTCGTCCAGCACGAAGGCCACGCTGTACCCGCCGAT 4560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4501 CGTCACAGGGGCCTCGTCCAGCAGCTCGTCCAGCACGAAGGCCACGCTGTACCCGCCGAT 4560

Qy       4561 CCTGAACCCGCCGCCCTCCCCGGCCACGGACCCCTCCCTGTACAACATGGACATGTTCTA 4620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4561 CCTGAACCCGCCGCCCTCCCCGGCCACGGACCCCTCCCTGTACAACATGGACATGTTCTA 4620

Qy       4621 CTCTTCAAACATTCCGGCCACTGCGAGACCGTACAGGCCCTACATCATTCGAGGAATGGC 4680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4621 CTCTTCAAACATTCCGGCCACTGCGAGACCGTACAGGCCCTACATCATTCGAGGAATGGC 4680

Qy       4681 GCCCCCGACGACGCCCTGCAGCACCGACGTGTGTGACAGCGACTACAGCGCCAGCCGCTG 4740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4681 GCCCCCGACGACGCCCTGCAGCACCGACGTGTGTGACAGCGACTACAGCGCCAGCCGCTG 4740

Qy       4741 GAAGGCCAGCAAGTACTACCTGGATTTGAACTCGGACTCAGACCCCTATCCACCCCCACC 4800
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4741 GAAGGCCAGCAAGTACTACCTGGATTTGAACTCGGACTCAGACCCCTATCCACCCCCACC 4800

Qy       4801 CACGCCCCACAGCCAGTACCTGTCGGCGGAGGACAGCTGCCCGCCCTCGCCCGCCACCGA 4860
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4801 CACGCCCCACAGCCAGTACCTGTCGGCGGAGGACAGCTGCCCGCCCTCGCCCGCCACCGA 4860

Qy       4861 GAGGAGCTACTTCCATCTCTTCCCGCCCCCTCCGTCCCCCTGCACGGACTCATCCTGACC 4920
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4861 GAGGAGCTACTTCCATCTCTTCCCGCCCCCTCCGTCCCCCTGCACGGACTCATCCTGACC 4920

Qy       4921 TCGGCCGGGCCACTCTGGCTTCTCTGTGCCCCTGTAAATAGTTTTAAATATGAACAAAGA 4980
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4921 TCGGCCGGGCCACTCTGGCTTCTCTGTGCCCCTGTAAATAGTTTTAAATATGAACAAAGA 4980

Qy       4981 AAAAAATATATTTTATGATTTAAAAAATAAATATAATTGGGATTTTAAAAACATGAGAAA 5040
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4981 AAAAAATATATTTTATGATTTAAAAAATAAATATAATTGGGATTTTAAAAACATGAGAAA 5040

Qy       5041 TGTGAACTGTGATGGGGTGGGCAGGGCTGGGAGAACTTTGTACAGTGGAGAAATATTTAT 5100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5041 TGTGAACTGTGATGGGGTGGGCAGGGCTGGGAGAACTTTGTACAGTGGAGAAATATTTAT 5100

Qy       5101 AAACTTAATTTTGTAAAACA 5120
             ||||||||||||||||||||
Db       5101 AAACTTAATTTTGTAAAACA 5120
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RESULT 4
US-10-477-238A-2
; Sequence 2, Application US/10477238A
; Publication No. US20040221326A1
; GENERAL INFORMATION:
; APPLICANT: Babij, Philip
; APPLICANT: Yaworsky, Paul
; APPLICANT: Bex, Frederick J. III
; APPLICANT: Bodine, Peter Van Nest
; TITLE OF INVENTION: Transgenic Animal Model of Bone Mass Modulation
; FILE REFERENCE: 032796-212
; CURRENT APPLICATION NUMBER: US/10/477,238A
; CURRENT FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: US 60/290,071
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US 60/291,311
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: US 60/353,058
; PRIOR FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: US 60/361,293
; PRIOR FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 812
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 5120
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-477-238A-2

Query Match 100.0%; Score 5120; DB 18; Length 5120;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ACTAAAGCGCCGCCGCCGCGCCATGGAGCCCGAGTGAGCGCGGCGCGGGCCCGTCCGGCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ACTAAAGCGCCGCCGCCGCGCCATGGAGCCCGAGTGAGCGCGGCGCGGGCCCGTCCGGCC 60

Qy         61 GCCGGACAACATGGAGGCAGCGCCGCCCGGGCCGCCGTGGCCGCTGCTGCTGCTGCTGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCCGGACAACATGGAGGCAGCGCCGCCCGGGCCGCCGTGGCCGCTGCTGCTGCTGCTGCT 120

Qy        121 GCTGCTGCTGGCGCTGTGCGGCTGCCCGGCCCCCGCCGCGGCCTCGCCGCTCCTGCTATT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCTGCTGCTGGCGCTGTGCGGCTGCCCGGCCCCCGCCGCGGCCTCGCCGCTCCTGCTATT 180

Qy        181 TGCCAACCGCCGGGACGTACGGCTGGTGGACGCCGGCGGAGTCAAGCTGGAGTCCACCAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TGCCAACCGCCGGGACGTACGGCTGGTGGACGCCGGCGGAGTCAAGCTGGAGTCCACCAT 240

Qy        241 CGTGGTCAGCGGCCTGGAGGATGCGGCCGCAGTGGACTTCCAGTTTTCCAAGGGAGCCGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CGTGGTCAGCGGCCTGGAGGATGCGGCCGCAGTGGACTTCCAGTTTTCCAAGGGAGCCGT 300

Qy        301 GTACTGGACAGACGTGAGCGAGGAGGCCATCAAGCAGACCTACCTGAACCAGACGGGGGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GTACTGGACAGACGTGAGCGAGGAGGCCATCAAGCAGACCTACCTGAACCAGACGGGGGC 360

Qy        361 CGCCGTGCAGAACGTGGTCATCTCCGGCCTGGTCTCTCCCGACGGCCTCGCCTGCGACTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CGCCGTGCAGAACGTGGTCATCTCCGGCCTGGTCTCTCCCGACGGCCTCGCCTGCGACTG 420

Qy        421 GGTGGGCAAGAAGCTGTACTGGACGGACTCAGAGACCAACCGCATCGAGGTGGCCAACCT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GGTGGGCAAGAAGCTGTACTGGACGGACTCAGAGACCAACCGCATCGAGGTGGCCAACCT 480

Qy        481 CAATGGCACATCCCGGAAGGTGCTCTTCTGGCAGGACCTTGACCAGCCGAGGGCCATCGC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CAATGGCACATCCCGGAAGGTGCTCTTCTGGCAGGACCTTGACCAGCCGAGGGCCATCGC 540
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Qy       541 CTTGGACCCCGCTCACGGGTACATGTACTGGACAGACTGGGTTGAGACGCCCCGGATTGA 600
Db       541 CTTGGACCCCGCTCACGGGTACATGTACTGGACAGACTGGGTTGAGACGCCCCGGATTGA 600

Qy       601 GCGGGCAGGGATGGATGGCAGCACCCGGAAGATCATTGTGGACTCGGACATTTACTGGCC 660
Db       601 GCGGGCAGGGATGGATGGCAGCACCCGGAAGATCATTGTGGACTCGGACATTTACTGGCC 660

Qy       661 CAATGGACTGACCATCGACCTGGAGGAGCAGAAGCTCTACTGGGCTGACGCCAAGCTCAG 720
Db       661 CAATGGACTGACCATCGACCTGGAGGAGCAGAAGCTCTACTGGGCTGACGCCAAGCTCAG 720

Qy       721 CTTCATCCACCGTGCCAACCTGGACGGCTCGTTCCGGCAGAAGGTGGTGGAGGGCAGCCT 780
Db       721 CTTCATCCACCGTGCCAACCTGGACGGCTCGTTCCGGCAGAAGGTGGTGGAGGGCAGCCT 780

Qy       781 GACGCACCCCTTCGCCCTGACGCTCTCCGGGGACACTCTGTACTGGACAGACTGGCAGAC 840
Db       781 GACGCACCCCTTCGCCCTGACGCTCTCCGGGGACACTCTGTACTGGACAGACTGGCAGAC 840

Qy       841 CCGCTCCATCCATGCCTGCAACAAGCGCACTGGGGGGAAGAGGAAGGAGATCCTGAGTGC 900
Db       841 CCGCTCCATCCATGCCTGCAACAAGCGCACTGGGGGGAAGAGGAAGGAGATCCTGAGTGC 900

Qy       901 CCTCTACTCACCCATGGACATCCAGGTGCTGAGCCAGGAGCGGCAGCCTTTCTTCCACAC 960
Db       901 CCTCTACTCACCCATGGACATCCAGGTGCTGAGCCAGGAGCGGCAGCCTTTCTTCCACAC 960

Qy       961 TCGCTGTGAGGAGGACAATGGCGGCTGCTCCCACCTGTGCCTGCTGTCCCCAAGCGAGCC 1020
Db       961 TCGCTGTGAGGAGGACAATGGCGGCTGCTCCCACCTGTGCCTGCTGTCCCCAAGCGAGCC 1020

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Db      1081 GGCAGGAGCCGAGGAGGTGCTGCTGCTGGCCCGGCGGACGGACCTACGGAGGATCTCGCT 1140

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Db      1741 CATCTACTGGACTGACTGGCAGCGCCGCAGCATCGAGCGGGTGCACAAGGTCAAGGCCAG 1800

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Qy      2221 TGACTACCCCGAGGGCATGGCCGTTGACTGGATGGGCAAGAACCTCTACTGGGCCGACAC 2280
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Qy      2341 GAGGGACTTGGACAACCCGAGGTCGCTGGCCCTGGATCCCACCAAGGGCTACATCTACTG 2400
Db      2341 GAGGGACTTGGACAACCCGAGGTCGCTGGCCCTGGATCCCACCAAGGGCTACATCTACTG 2400

Qy      2401 GACCGAGTGGGGCGGCAAGCCGAGGATCGTGCGGGCCTTCATGGACGGGACCAACTGCAT 2460
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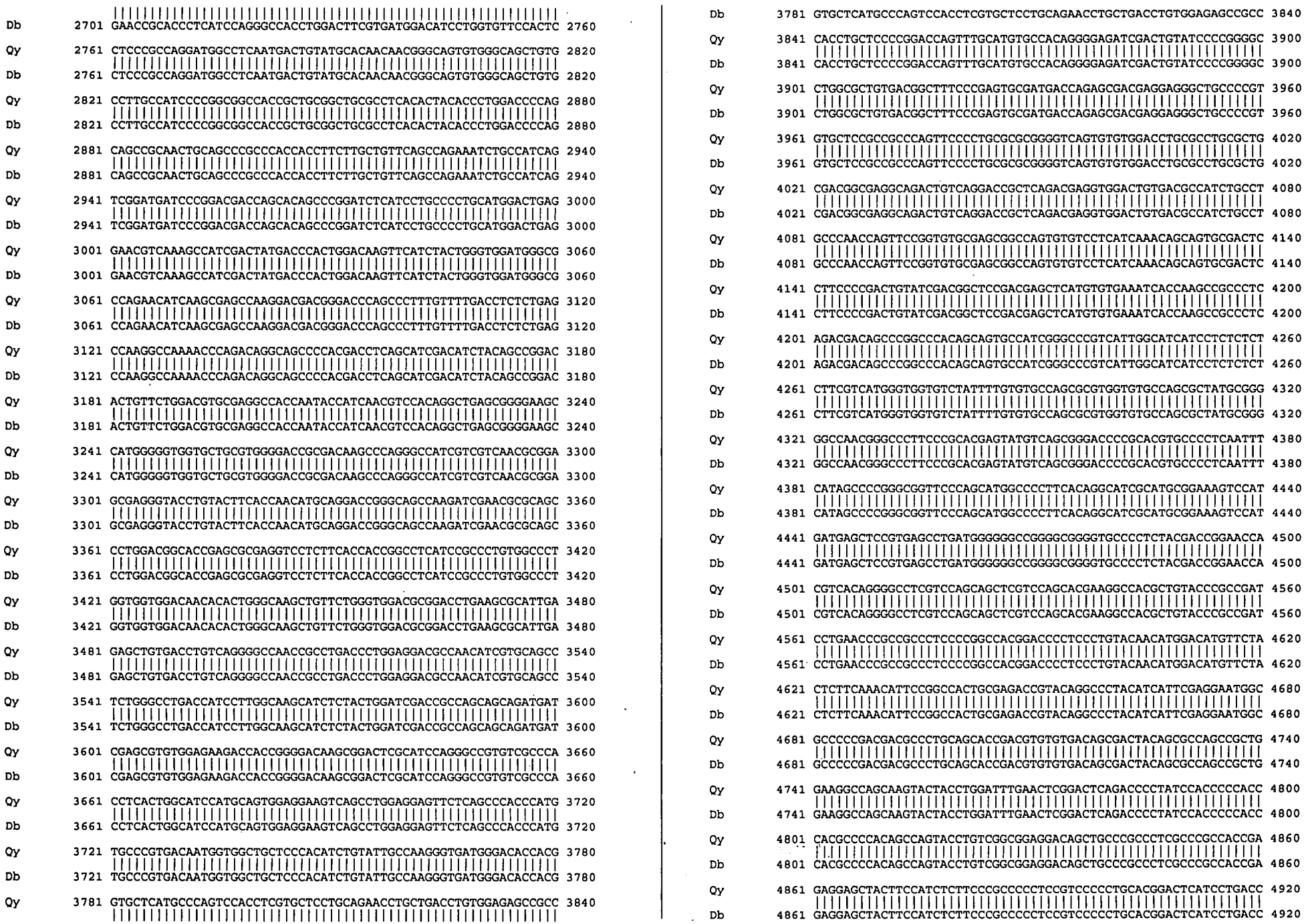
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Qy      2521 CCTCTACTGGACCGACCTGGACACCAACATGATCGAGTCGTCCAACATGCTGGGTCAGGA 2580
Db      2521 CCTCTACTGGACCGACCTGGACACCAACATGATCGAGTCGTCCAACATGCTGGGTCAGGA 2580

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Db      2581 GCGGGTCGTGATTGCCGACGATCTCCCGCACCCGTTCGGTCTGACGCAGTACAGCGATTA 2640

Qy      2641 TATCTACTGGACAGACTGGAATCTGCACAGCATTGAGCGGGCCGACAAGACTAGCGGCCG 2700
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Qy      2701 GAACCGCACCCTCATCCAGGGCCACCTGGACTTCGTGATGGACATCCTGGTGTTCCACTC 2760
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RESULT 5
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; Sequence 2, Application US/10680287A
; Publication No. US20040244069A1
; GENERAL INFORMATION:
; APPLICANT: Babij, Philip
; APPLICANT: Yaworsky, Paul
; APPLICANT: Bex, Frederick J. III
; APPLICANT: Bodine, Peter Van Nest
; TITLE OF INVENTION: Transgenic Animal Model of Bone Mass Modulation
; FILE REFERENCE: 032796-179
; CURRENT APPLICATION NUMBER: US/10/680,287A
; CURRENT FILING DATE: 2003-10-08
; PRIOR APPLICATION NUMBER: PCT/US02/14876
; PRIOR FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: US 60/290,071
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US 60/291,311
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: US 60/353,058
; PRIOR FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: US 60/361,293
; PRIOR FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 812
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 5120
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-680-287A-2

Query Match 100.0%; Score 5120; DB 18; Length 5120;
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Db        721 CTTCATCCACCGTGCCAACCTGGACGGCTCGTTCCGGCAGAAGGTGGTGGAGGGCAGCCT 780

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Qy      1441 CCTGGACGAGCCCCGAGCCATCGCACTGCACCCCGTGATGGGCCTCATGTACTGGACAGA 1500
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Qy      1501 CTGGGGAGAGAACCCTAAAATCGAGTGTGCCAACTTGGATGGGCAGGAGCGGCGTGTGCT 1560
Db      1501 CTGGGGAGAGAACCCTAAAATCGAGTGTGCCAACTTGGATGGGCAGGAGCGGCGTGTGCT 1560
Qy      1561 GGTCAATGCCTCCCTCGGGTGGCCCAACGGCCTGGCCCTGGACCTGCAGGAGGGGAAGCT 1620
Db      1561 GGTCAATGCCTCCCTCGGGTGGCCCAACGGCCTGGCCCTGGACCTGCAGGAGGGGAAGCT 1620
Qy      1621 CTACTGGGGAGACGCCAAGACAGACAAGATCGAGGTGATCAATGTTGATGGGACGAAGAG 1680
Db      1621 CTACTGGGGAGACGCCAAGACAGACAAGATCGAGGTGATCAATGTTGATGGGACGAAGAG 1680
Qy      1681 GCGGACCCTCCTGGAGGACAAGCTCCCGCACATTTTCGGGTTCACGCTGCTGGGGGACTT 1740
Db      1681 GCGGACCCTCCTGGAGGACAAGCTCCCGCACATTTTCGGGTTCACGCTGCTGGGGGACTT 1740
Qy      1741 CATCTACTGGACTGACTGGCAGCGCCGCAGCATCGAGCGGGTGCACAAGGTCAAGGCCAG 1800
Db      1741 CATCTACTGGACTGACTGGCAGCGCCGCAGCATCGAGCGGGTGCACAAGGTCAAGGCCAG 1800
Qy      1801 CCGGGACGTCATCATTGACCAGCTGCCCGACCTGATGGGGCTCAAAGCTGTGAATGTGGC 1860
Db      1801 CCGGGACGTCATCATTGACCAGCTGCCCGACCTGATGGGGCTCAAAGCTGTGAATGTGGC 1860
Qy      1861 CAAGGTCGTCGGAACCAACCCGTGTGCGGACAGGAACGGGGGGGTGCAGCCACCTGTGCTT 1920
Db      1861 CAAGGTCGTCGGAACCAACCCGTGTGCGGACAGGAACGGGGGGGTGCAGCCACCTGTGCTT 1920
Qy      1921 CTTCACACCCCACGCAACCCGGTGTGGCTGCCCCATCGGCCTGGAGCTGCTGAGTGACAT 1980
Db      1921 CTTCACACCCCACGCAACCCGGTGTGGCTGCCCCATCGGCCTGGAGCTGCTGAGTGACAT 1980
Qy      1981 GAAGACCTGCATCGTGCCTGAGGCCTTCTTGGTCTTCACCAGCAGAGCCGCCATCCACAG 2040
Db      1981 GAAGACCTGCATCGTGCCTGAGGCCTTCTTGGTCTTCACCAGCAGAGCCGCCATCCACAG 2040
Qy      2041 GATCTCCCTCGAGACCAATAACAACGACGTGGCCATCCCGCTCACGGGCGTCAAGGAGGC 2100
Db      2041 GATCTCCCTCGAGACCAATAACAACGACGTGGCCATCCCGCTCACGGGCGTCAAGGAGGC 2100
Qy      2101 CTCAGCCCTGGACTTTGATGTGTCCAACAACCACATCTACTGGACAGACGTCAGCCTGAA 2160
Db      2101 CTCAGCCCTGGACTTTGATGTGTCCAACAACCACATCTACTGGACAGACGTCAGCCTGAA 2160
Qy      2161 GACCATCAGCCGCGCCTTCATGAACGGGAGCTCGGTGGAGCACGTGGTGGAGTTTGGCCT 2220
Db      2161 GACCATCAGCCGCGCCTTCATGAACGGGAGCTCGGTGGAGCACGTGGTGGAGTTTGGCCT 2220
Qy      2221 TGACTACCCCGAGGGCATGGCCGTTGACTGGATGGGCAAGAACCTCTACTGGGCCGACAC 2280
Db      2221 TGACTACCCCGAGGGCATGGCCGTTGACTGGATGGGCAAGAACCTCTACTGGGCCGACAC 2280
Qy      2281 TGGGACCAACAGAATCGAAGTGGCGCGGCTGGACGGGCAGTTCCGGCAAGTCCTCGTGTG 2340
Db      2281 TGGGACCAACAGAATCGAAGTGGCGCGGCTGGACGGGCAGTTCCGGCAAGTCCTCGTGTG 2340
Qy      2341 GAGGGACTTGGACAACCCGAGGTCGCTGGCCCTGGATCCCACCAAGGGCTACATCTACTG 2400
Db      2341 GAGGGACTTGGACAACCCGAGGTCGCTGGCCCTGGATCCCACCAAGGGCTACATCTACTG 2400
Qy      2401 GACCGAGTGGGGCGGCAAGCCGAGGATCGTGCGGGCCTTCATGGACGGGACCAACTGCAT 2460
Db      2401 GACCGAGTGGGGCGGCAAGCCGAGGATCGTGCGGGCCTTCATGGACGGGACCAACTGCAT 2460
Qy      2461 GACGCTGGTGGACAAGGTGGGCCGGGCCAACGACCTCACCATTGACTACGCTGACCAGCG 2520
Db      2461 GACGCTGGTGGACAAGGTGGGCCGGGCCAACGACCTCACCATTGACTACGCTGACCAGCG 2520
Qy      2521 CCTCTACTGGACCGACCTGGACACCAACATGATCGAGTCGTCCAACATGCTGGGTCAGGA 2580
Db      2521 CCTCTACTGGACCGACCTGGACACCAACATGATCGAGTCGTCCAACATGCTGGGTCAGGA 2580
Qy      2581 GCGGGTCGTGATTGCCGACGATCTCCCGCACCCGTTCGGTCTGACGCAGTACAGCGATTA 2640
Db      2581 GCGGGTCGTGATTGCCGACGATCTCCCGCACCCGTTCGGTCTGACGCAGTACAGCGATTA 2640
Qy      2641 TATCTACTGGACAGACTGGAATCTGCACAGCATTGAGCGGGCCGACAAGACTAGCGGCCG 2700
Db      2641 TATCTACTGGACAGACTGGAATCTGCACAGCATTGAGCGGGCCGACAAGACTAGCGGCCG 2700
Qy      2701 GAACCGCACCCTCATCCAGGGCCACCTGGACTTCGTGATGGACATCCTGGTGTTCCACTC 2760
Db      2701 GAACCGCACCCTCATCCAGGGCCACCTGGACTTCGTGATGGACATCCTGGTGTTCCACTC 2760
Qy      2761 CTCCCGCCAGGATGGCCTCAATGACTGTATGCACAACAACGGGCAGTGTGGGCAGCTGTG 2820
Db      2761 CTCCCGCCAGGATGGCCTCAATGACTGTATGCACAACAACGGGCAGTGTGGGCAGCTGTG 2820
Qy      2821 CCTTGCCATCCCCGGCGGCCACCGCTGCGGCTGCGCCTCACACTACACCCTGGACCCCAG 2880
Db      2821 CCTTGCCATCCCCGGCGGCCACCGCTGCGGCTGCGCCTCACACTACACCCTGGACCCCAG 2880
Qy      2881 CAGCCGCAACTGCAGCCCGCCCACCACCTTCTTGCTGTTCAGCCAGAAATCTGCCATCAG 2940
Db      2881 CAGCCGCAACTGCAGCCCGCCCACCACCTTCTTGCTGTTCAGCCAGAAATCTGCCATCAG 2940
Qy      2941 TCGGATGATCCCGGACGACCAGCACAGCCCGGATCTCATCCTGCCCCTGCATGGACTGAG 3000
Db      2941 TCGGATGATCCCGGACGACCAGCACAGCCCGGATCTCATCCTGCCCCTGCATGGACTGAG 3000
Qy      3001 GAACGTCAAAGCCATCGACTATGACCCACTGGACAAGTTCATCTACTGGGTGGATGGGCG 3060
Db      3001 GAACGTCAAAGCCATCGACTATGACCCACTGGACAAGTTCATCTACTGGGTGGATGGGCG 3060
Qy      3061 CCAGAACATCAAGCGAGCCAAGGACGACGGGACCCAGCCCTTTGTTTTGACCTCTCTGAG 3120
Db      3061 CCAGAACATCAAGCGAGCCAAGGACGACGGGACCCAGCCCTTTGTTTTGACCTCTCTGAG 3120
Qy      3121 CCAAGGCCAAAACCCAGACAGGCAGCCCCACGACCTCAGCATCGACATCTACAGCCGGAC 3180
Db      3121 CCAAGGCCAAAACCCAGACAGGCAGCCCCACGACCTCAGCATCGACATCTACAGCCGGAC 3180
Qy      3181 ACTGTTCTGGACGTGCGAGGCCACCAATACCATCAACGTCCACAGGCTGAGCGGGGAAGC 3240
Db      3181 ACTGTTCTGGACGTGCGAGGCCACCAATACCATCAACGTCCACAGGCTGAGCGGGGAAGC 3240
Qy      3241 CATGGGGGTGGTGCTGCGTGGGGACCGCGACAAGCCCAGGGCCATCGTCGTCAACGCGGA 3300
Db      3241 CATGGGGGTGGTGCTGCGTGGGGACCGCGACAAGCCCAGGGCCATCGTCGTCAACGCGGA 3300
Qy      3301 GCGAGGGTACCTGTACTTCACCAACATGCAGGACCGGGCAGCCAAGATCGAACGCGCAGC 3360
Db      3301 GCGAGGGTACCTGTACTTCACCAACATGCAGGACCGGGCAGCCAAGATCGAACGCGCAGC 3360
Qy      3361 CCTGGACGGCACCGAGCGCGAGGTCCTCTTCACCACCGGCCTCATCCGCCCTGTGGCCCT 3420
Db      3361 CCTGGACGGCACCGAGCGCGAGGTCCTCTTCACCACCGGCCTCATCCGCCCTGTGGCCCT 3420
Qy      3421 GGTGGTGGACAACACACTGGGCAAGCTGTTCTGGGTGGACGCGGACCTGAAGCGCATTGA 3480
Db      3421 GGTGGTGGACAACACACTGGGCAAGCTGTTCTGGGTGGACGCGGACCTGAAGCGCATTGA 3480
Qy      3481 GAGCTGTGACCTGTCAGGGGCCAACCGCCTGACCCTGGAGGACGCCAACATCGTGCAGCC 3540
Db      3481 GAGCTGTGACCTGTCAGGGGCCAACCGCCTGACCCTGGAGGACGCCAACATCGTGCAGCC 3540
Qy      3541 TCTGGGCCTGACCATCCTTGGCAAGCATCTCTACTGGATCGACCGCCAGCAGCAGATGAT 3600
Db      3541 TCTGGGCCTGACCATCCTTGGCAAGCATCTCTACTGGATCGACCGCCAGCAGCAGATGAT 3600
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Qy       3601 CGAGCGTGTGGAGAAGACCACCGGGGACAAGCGGACTCGCATCCAGGGCCGTGTCGCCCA 3660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3601 CGAGCGTGTGGAGAAGACCACCGGGGACAAGCGGACTCGCATCCAGGGCCGTGTCGCCCA 3660

Qy       3661 CCTCACTGGCATCCATGCAGTGGAGGAAGTCAGCCTGGAGGAGTTCTCAGCCCACCCATG 3720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3661 CCTCACTGGCATCCATGCAGTGGAGGAAGTCAGCCTGGAGGAGTTCTCAGCCCACCCATG 3720

Qy       3721 TGCCCGTGACAATGGTGGCTGCTCCCACATCTGTATTGCCAAGGGTGATGGGACACCACG 3780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3721 TGCCCGTGACAATGGTGGCTGCTCCCACATCTGTATTGCCAAGGGTGATGGGACACCACG 3780

Qy       3781 GTGCTCATGCCCAGTCCACCTCGTGCTCCTGCAGAACCTGCTGACCTGTGGAGAGCCGCC 3840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3781 GTGCTCATGCCCAGTCCACCTCGTGCTCCTGCAGAACCTGCTGACCTGTGGAGAGCCGCC 3840

Qy       3841 CACCTGCTCCCCGGACCAGTTTGCATGTGCCACAGGGGAGATCGACTGTATCCCCGGGGC 3900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3841 CACCTGCTCCCCGGACCAGTTTGCATGTGCCACAGGGGAGATCGACTGTATCCCCGGGGC 3900

Qy       3901 CTGGCGCTGTGACGGCTTTCCCGAGTGCGATGACCAGAGCGACGAGGAGGGCTGCCCCGT 3960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3901 CTGGCGCTGTGACGGCTTTCCCGAGTGCGATGACCAGAGCGACGAGGAGGGCTGCCCCGT 3960

Qy       3961 GTGCTCCGCCGCCCAGTTCCCCTGCGCGCGGGGTCAGTGTGTGGACCTGCGCCTGCGCTG 4020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3961 GTGCTCCGCCGCCCAGTTCCCCTGCGCGCGGGGTCAGTGTGTGGACCTGCGCCTGCGCTG 4020

Qy       4021 CGACGGCGAGGCAGACTGTCAGGACCGCTCAGACGAGGTGGACTGTGACGCCATCTGCCT 4080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4021 CGACGGCGAGGCAGACTGTCAGGACCGCTCAGACGAGGTGGACTGTGACGCCATCTGCCT 4080

Qy       4081 GCCCAACCAGTTCCGGTGTGCGAGCGGCCAGTGTGTCCTCATCAAACAGCAGTGCGACTC 4140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4081 GCCCAACCAGTTCCGGTGTGCGAGCGGCCAGTGTGTCCTCATCAAACAGCAGTGCGACTC 4140

Qy       4141 CTTCCCCGACTGTATCGACGGCTCCGACGAGCTCATGTGTGAAATCACCAAGCCGCCCTC 4200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4141 CTTCCCCGACTGTATCGACGGCTCCGACGAGCTCATGTGTGAAATCACCAAGCCGCCCTC 4200

Qy       4201 AGACGACAGCCCGGCCCACAGCAGTGCCATCGGGCCCGTCATTGGCATCATCCTCTCTCT 4260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4201 AGACGACAGCCCGGCCCACAGCAGTGCCATCGGGCCCGTCATTGGCATCATCCTCTCTCT 4260

Qy       4261 CTTCGTCATGGGTGGTGTCTATTTTGTGTGCCAGCGCGTGGTGTGCCAGCGCTATGCGGG 4320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4261 CTTCGTCATGGGTGGTGTCTATTTTGTGTGCCAGCGCGTGGTGTGCCAGCGCTATGCGGG 4320

Qy       4321 GGCCAACGGGCCCTTCCCGCACGAGTATGTCAGCGGGACCCCGCACGTGCCCCTCAATTT 4380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4321 GGCCAACGGGCCCTTCCCGCACGAGTATGTCAGCGGGACCCCGCACGTGCCCCTCAATTT 4380

Qy       4381 CATAGCCCCGGGCGGTTCCCAGCATGGCCCCTTCACAGGCATCGCATGCGGAAAGTCCAT 4440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4381 CATAGCCCCGGGCGGTTCCCAGCATGGCCCCTTCACAGGCATCGCATGCGGAAAGTCCAT 4440

Qy       4441 GATGAGCTCCGTGAGCCTGATGGGGGGCCGGGGCGGGGTGCCCCTCTACGACCGGAACCA 4500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4441 GATGAGCTCCGTGAGCCTGATGGGGGGCCGGGGCGGGGTGCCCCTCTACGACCGGAACCA 4500

Qy       4501 CGTCACAGGGGCCTCGTCCAGCAGCTCGTCCAGCACGAAGGCCACGCTGTACCCGCCGAT 4560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4501 CGTCACAGGGGCCTCGTCCAGCAGCTCGTCCAGCACGAAGGCCACGCTGTACCCGCCGAT 4560

Qy       4561 CCTGAACCCGCCGCCCTCCCCGGCCACGGACCCCTCCCTGTACAACATGGACATGTTCTA 4620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4561 CCTGAACCCGCCGCCCTCCCCGGCCACGGACCCCTCCCTGTACAACATGGACATGTTCTA 4620

Qy       4621 CTCTTCAAACATTCCGGCCACTGCGAGACCGTACAGGCCCTACATCATTCGAGGAATGGC 4680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4621 CTCTTCAAACATTCCGGCCACTGCGAGACCGTACAGGCCCTACATCATTCGAGGAATGGC 4680

Qy       4681 GCCCCCGACGACGCCCTGCAGCACCGACGTGTGTGACAGCGACTACAGCGCCAGCCGCTG 4740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4681 GCCCCCGACGACGCCCTGCAGCACCGACGTGTGTGACAGCGACTACAGCGCCAGCCGCTG 4740

Qy       4741 GAAGGCCAGCAAGTACTACCTGGATTTGAACTCGGACTCAGACCCCTATCCACCCCCACC 4800
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4741 GAAGGCCAGCAAGTACTACCTGGATTTGAACTCGGACTCAGACCCCTATCCACCCCCACC 4800

Qy       4801 CACGCCCCACAGCCAGTACCTGTCGGCGGAGGACAGCTGCCCGCCCTCGCCCGCCACCGA 4860
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4801 CACGCCCCACAGCCAGTACCTGTCGGCGGAGGACAGCTGCCCGCCCTCGCCCGCCACCGA 4860

Qy       4861 GAGGAGCTACTTCCATCTCTTCCCGCCCCCTCCGTCCCCCTGCACGGACTCATCCTGACC 4920
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4861 GAGGAGCTACTTCCATCTCTTCCCGCCCCCTCCGTCCCCCTGCACGGACTCATCCTGACC 4920

Qy       4921 TCGGCCGGGCCACTCTGGCTTCTCTGTGCCCCTGTAAATAGTTTTAAATATGAACAAAGA 4980
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4921 TCGGCCGGGCCACTCTGGCTTCTCTGTGCCCCTGTAAATAGTTTTAAATATGAACAAAGA 4980

Qy       4981 AAAAAATATATTTTATGATTTAAAAAATAAATATAATTGGGATTTTAAAAACATGAGAAA 5040
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4981 AAAAAATATATTTTATGATTTAAAAAATAAATATAATTGGGATTTTAAAAACATGAGAAA 5040

Qy       5041 TGTGAACTGTGATGGGGTGGGCAGGGCTGGGAGAACTTTGTACAGTGGAGAAATATTTAT 5100
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Db       5041 TGTGAACTGTGATGGGGTGGGCAGGGCTGGGAGAACTTTGTACAGTGGAGAAATATTTAT 5100

Qy       5101 AAACTTAATTTTGTAAAACA 5120
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Db       5101 AAACTTAATTTTGTAAAACA 5120
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RESULT 6
US-10-477-173-2
; Sequence 2, Application US/10477173
; Publication No. US20050070699A1
; GENERAL INFORMATION:
; APPLICANT: Genome Therapeutics Corporation and
; APPLICANT: Allen, Kristina M.
; APPLICANT: Yaworsky, Paul
; APPLICANT: Morales, Arturo J.
; APPLICANT: Graham, James R.
; APPLICANT: Anisowicz, Anthony
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: HBM Variants that Modulate Bone Mass and Lipid Levels
; FILE REFERENCE: 032796-135
; CURRENT APPLICATION NUMBER: US/10/477,173
; CURRENT FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: US 60/290,071
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US 60/291,311
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: US 60/353,058
; PRIOR FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: US 60/361,293
; PRIOR FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 1086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 5120
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-477-173-2

Query Match 100.0%; Score 5120; DB 19; Length 5120;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ACTAAAGCGCCGCCGCCGCGCCATGGAGCCCGAGTGAGCGCGGCGCGGGCCCGTCCGGCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ACTAAAGCGCCGCCGCCGCGCCATGGAGCCCGAGTGAGCGCGGCGCGGGCCCGTCCGGCC 60
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Qy        61 GCCGGACAACATGGAGGCAGCGCCGCCCGGGCCGCCGTGGCCGCTGCTGCTGCTGCTGCT 120
Db        61 GCCGGACAACATGGAGGCAGCGCCGCCCGGGCCGCCGTGGCCGCTGCTGCTGCTGCTGCT 120

Qy       121 GCTGCTGCTGGCGCTGTGCGGCTGCCCGGCCCCCGCCGCGGCCTCGCCGCTCCTGCTATT 180
Db       121 GCTGCTGCTGGCGCTGTGCGGCTGCCCGGCCCCCGCCGCGGCCTCGCCGCTCCTGCTATT 180

Qy       181 TGCCAACCGCCGGGACGTACGGCTGGTGGACGCCGGCGGAGTCAAGCTGGAGTCCACCAT 240
Db       181 TGCCAACCGCCGGGACGTACGGCTGGTGGACGCCGGCGGAGTCAAGCTGGAGTCCACCAT 240

Qy       241 CGTGGTCAGCGGCCTGGAGGATGCGGCCGCAGTGGACTTCCAGTTTTCCAAGGGAGCCGT 300
Db       241 CGTGGTCAGCGGCCTGGAGGATGCGGCCGCAGTGGACTTCCAGTTTTCCAAGGGAGCCGT 300

Qy       301 GTACTGGACAGACGTGAGCGAGGAGGCCATCAAGCAGACCTACCTGAACCAGACGGGGGC 360
Db       301 GTACTGGACAGACGTGAGCGAGGAGGCCATCAAGCAGACCTACCTGAACCAGACGGGGGC 360

Qy       361 CGCCGTGCAGAACGTGGTCATCTCCGGCCTGGTCTCTCCCGACGGCCTCGCCTGCGACTG 420
Db       361 CGCCGTGCAGAACGTGGTCATCTCCGGCCTGGTCTCTCCCGACGGCCTCGCCTGCGACTG 420

Qy       421 GGTGGGCAAGAAGCTGTACTGGACGGACTCAGAGACCAACCGCATCGAGGTGGCCAACCT 480
Db       421 GGTGGGCAAGAAGCTGTACTGGACGGACTCAGAGACCAACCGCATCGAGGTGGCCAACCT 480

Qy       481 CAATGGCACATCCCGGAAGGTGCTCTTCTGGCAGGACCTTGACCAGCCGAGGGCCATCGC 540
Db       481 CAATGGCACATCCCGGAAGGTGCTCTTCTGGCAGGACCTTGACCAGCCGAGGGCCATCGC 540

Qy       541 CTTGGACCCCGCTCACGGGTACATGTACTGGACAGACTGGGTTGAGACGCCCCGGATTGA 600
Db       541 CTTGGACCCCGCTCACGGGTACATGTACTGGACAGACTGGGTTGAGACGCCCCGGATTGA 600

Qy       601 GCGGGCAGGGATGGATGGCAGCACCCGGAAGATCATTGTGGACTCGGACATTTACTGGCC 660
Db       601 GCGGGCAGGGATGGATGGCAGCACCCGGAAGATCATTGTGGACTCGGACATTTACTGGCC 660

Qy       661 CAATGGACTGACCATCGACCTGGAGGAGCAGAAGCTCTACTGGGCTGACGCCAAGCTCAG 720
Db       661 CAATGGACTGACCATCGACCTGGAGGAGCAGAAGCTCTACTGGGCTGACGCCAAGCTCAG 720

Qy       721 CTTCATCCACCGTGCCAACCTGGACGGCTCGTTCCGGCAGAAGGTGGTGGAGGGCAGCCT 780
Db       721 CTTCATCCACCGTGCCAACCTGGACGGCTCGTTCCGGCAGAAGGTGGTGGAGGGCAGCCT 780

Qy       781 GACGCACCCCTTCGCCCTGACGCTCTCCGGGGACACTCTGTACTGGACAGACTGGCAGAC 840
Db       781 GACGCACCCCTTCGCCCTGACGCTCTCCGGGGACACTCTGTACTGGACAGACTGGCAGAC 840

Qy       841 CCGCTCCATCCATGCCTGCAACAAGCGCACTGGGGGGAAGAGGAAGGAGATCCTGAGTGC 900
Db       841 CCGCTCCATCCATGCCTGCAACAAGCGCACTGGGGGGAAGAGGAAGGAGATCCTGAGTGC 900

Qy       901 CCTCTACTCACCCATGGACATCCAGGTGCTGAGCCAGGAGCGGCAGCCTTTCTTCCACAC 960
Db       901 CCTCTACTCACCCATGGACATCCAGGTGCTGAGCCAGGAGCGGCAGCCTTTCTTCCACAC 960

Qy       961 TCGCTGTGAGGAGGACAATGGCGGCTGCTCCCACCTGTGCCTGCTGTCCCCAAGCGAGCC 1020
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Qy      1021 TTTCTACACATGCGCCTGCCCCACGGGTGTGCAGCTGCAGGACAACGGCAGGACGTGTAA 1080
Db      1021 TTTCTACACATGCGCCTGCCCCACGGGTGTGCAGCTGCAGGACAACGGCAGGACGTGTAA 1080

Qy      1081 GGCAGGAGCCGAGGAGGTGCTGCTGCTGGCCCGGCGGACGGACCTACGGAGGATCTCGCT 1140
Db      1081 GGCAGGAGCCGAGGAGGTGCTGCTGCTGGCCCGGCGGACGGACCTACGGAGGATCTCGCT 1140

Qy      1141 GGACACGCCGGACTTCACCGACATCGTGCTGCAGGTGGACGACATCCGGCACGCCATTGC 1200
Db      1141 GGACACGCCGGACTTCACCGACATCGTGCTGCAGGTGGACGACATCCGGCACGCCATTGC 1200

Qy      1201 CATCGACTACGACCCGCTAGAGGGCTATGTCTACTGGACAGATGACGAGGTGCGGGCCAT 1260
Db      1201 CATCGACTACGACCCGCTAGAGGGCTATGTCTACTGGACAGATGACGAGGTGCGGGCCAT 1260

Qy      1261 CCGCAGGGCGTACCTGGACGGGTCTGGGGCGCAGACGCTGGTCAACACCGAGATCAACGA 1320
Db      1261 CCGCAGGGCGTACCTGGACGGGTCTGGGGCGCAGACGCTGGTCAACACCGAGATCAACGA 1320

Qy      1321 CCCCGATGGCATCGCGGTCGACTGGGTGGCCCGAAACCTCTACTGGACCGACACGGGCAC 1380
Db      1321 CCCCGATGGCATCGCGGTCGACTGGGTGGCCCGAAACCTCTACTGGACCGACACGGGCAC 1380

Qy      1381 GGACCGCATCGAGGTGACGCGCCTCAACGGCACCTCCCGCAAGATCCTGGTGTCGGAGGA 1440
Db      1381 GGACCGCATCGAGGTGACGCGCCTCAACGGCACCTCCCGCAAGATCCTGGTGTCGGAGGA 1440

Qy      1441 CCTGGACGAGCCCCGAGCCATCGCACTGCACCCCGTGATGGGCCTCATGTACTGGACAGA 1500
Db      1441 CCTGGACGAGCCCCGAGCCATCGCACTGCACCCCGTGATGGGCCTCATGTACTGGACAGA 1500

Qy      1501 CTGGGGAGAGAACCCTAAAATCGAGTGTGCCAACTTGGATGGGCAGGAGCGGCGTGTGCT 1560
Db      1501 CTGGGGAGAGAACCCTAAAATCGAGTGTGCCAACTTGGATGGGCAGGAGCGGCGTGTGCT 1560

Qy      1561 GGTCAATGCCTCCCTCGGGTGGCCCAACGGCCTGGCCCTGGACCTGCAGGAGGGGAAGCT 1620
Db      1561 GGTCAATGCCTCCCTCGGGTGGCCCAACGGCCTGGCCCTGGACCTGCAGGAGGGGAAGCT 1620

Qy      1621 CTACTGGGGAGACGCCAAGACAGACAAGATCGAGGTGATCAATGTTGATGGGACGAAGAG 1680
Db      1621 CTACTGGGGAGACGCCAAGACAGACAAGATCGAGGTGATCAATGTTGATGGGACGAAGAG 1680

Qy      1681 GCGGACCCTCCTGGAGGACAAGCTCCCGCACATTTTCGGGTTCACGCTGCTGGGGGACTT 1740
Db      1681 GCGGACCCTCCTGGAGGACAAGCTCCCGCACATTTTCGGGTTCACGCTGCTGGGGGACTT 1740

Qy      1741 CATCTACTGGACTGACTGGCAGCGCCGCAGCATCGAGCGGGTGCACAAGGTCAAGGCCAG 1800
Db      1741 CATCTACTGGACTGACTGGCAGCGCCGCAGCATCGAGCGGGTGCACAAGGTCAAGGCCAG 1800

Qy      1801 CCGGGACGTCATCATTGACCAGCTGCCCGACCTGATGGGGCTCAAAGCTGTGAATGTGGC 1860
Db      1801 CCGGGACGTCATCATTGACCAGCTGCCCGACCTGATGGGGCTCAAAGCTGTGAATGTGGC 1860

Qy      1861 CAAGGTCGTCGGAACCAACCCGTGTGCGGACAGGAACGGGGGGGTGCAGCCACCTGTGCTT 1920
Db      1861 CAAGGTCGTCGGAACCAACCCGTGTGCGGACAGGAACGGGGGGGTGCAGCCACCTGTGCTT 1920

Qy      1921 CTTCACACCCCACGCAACCCGGTGTGGCTGCCCCATCGGCCTGGAGCTGCTGAGTGACAT 1980
Db      1921 CTTCACACCCCACGCAACCCGGTGTGGCTGCCCCATCGGCCTGGAGCTGCTGAGTGACAT 1980

Qy      1981 GAAGACCTGCATCGTGCCTGAGGCCTTCTTGGTCTTCACCAGCAGAGCCGCCATCCACAG 2040
Db      1981 GAAGACCTGCATCGTGCCTGAGGCCTTCTTGGTCTTCACCAGCAGAGCCGCCATCCACAG 2040

Qy      2041 GATCTCCCTCGAGACCAATAACAACGACGTGGCCATCCCGCTCACGGGCGTCAAGGAGGC 2100
Db      2041 GATCTCCCTCGAGACCAATAACAACGACGTGGCCATCCCGCTCACGGGCGTCAAGGAGGC 2100

Qy      2101 CTCAGCCCTGGACTTTGATGTGTCCAACAACCACATCTACTGGACAGACGTCAGCCTGAA 2160
Db      2101 CTCAGCCCTGGACTTTGATGTGTCCAACAACCACATCTACTGGACAGACGTCAGCCTGAA 2160

Qy      2161 GACCATCAGCCGCGCCTTCATGAACGGGAGCTCGGTGGAGCACGTGGTGGAGTTTGGCCT 2220
Db      2161 GACCATCAGCCGCGCCTTCATGAACGGGAGCTCGGTGGAGCACGTGGTGGAGTTTGGCCT 2220

Qy      2221 TGACTACCCCGAGGGCATGGCCGTTGACTGGATGGGCAAGAACCTCTACTGGGCCGACAC 2280
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Db      2221 TGACTACCCCGAGGGCATGGCCGTTGACTGGATGGGCAAGAACCTCTACTGGGCCGACAC 2280

Qy      2281 TGGGACCAACAGAATCGAAGTGGCGCGGCTGGACGGGCAGTTCCGGCAAGTCCTCGTGTG 2340
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2281 TGGGACCAACAGAATCGAAGTGGCGCGGCTGGACGGGCAGTTCCGGCAAGTCCTCGTGTG 2340

Qy      2341 GAGGGACTTGGACAACCCGAGGTCGCTGGCCCTGGATCCCACCAAGGGCTACATCTACTG 2400
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2341 GAGGGACTTGGACAACCCGAGGTCGCTGGCCCTGGATCCCACCAAGGGCTACATCTACTG 2400

Qy      2401 GACCGAGTGGGGCGGCAAGCCGAGGATCGTGCGGGCCTTCATGGACGGGACCAACTGCAT 2460
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2401 GACCGAGTGGGGCGGCAAGCCGAGGATCGTGCGGGCCTTCATGGACGGGACCAACTGCAT 2460

Qy      2461 GACGCTGGTGGACAAGGTGGGCCGGGCCAACGACCTCACCATTGACTACGCTGACCAGCG 2520
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Db      2461 GACGCTGGTGGACAAGGTGGGCCGGGCCAACGACCTCACCATTGACTACGCTGACCAGCG 2520

Qy      2521 CCTCTACTGGACCGACCTGGACACCAACATGATCGAGTCGTCCAACATGCTGGGTCAGGA 2580
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Db      2521 CCTCTACTGGACCGACCTGGACACCAACATGATCGAGTCGTCCAACATGCTGGGTCAGGA 2580

Qy      2581 GCGGGTCGTGATTGCCGACGATCTCCCGCACCCGTTCGGTCTGACGCAGTACAGCGATTA 2640
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Db      2581 GCGGGTCGTGATTGCCGACGATCTCCCGCACCCGTTCGGTCTGACGCAGTACAGCGATTA 2640

Qy      2641 TATCTACTGGACAGACTGGAATCTGCACAGCATTGAGCGGGCCGACAAGACTAGCGGCCG 2700
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Db      2641 TATCTACTGGACAGACTGGAATCTGCACAGCATTGAGCGGGCCGACAAGACTAGCGGCCG 2700

Qy      2701 GAACCGCACCCTCATCCAGGGCCACCTGGACTTCGTGATGGACATCCTGGTGTTCCACTC 2760
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Db      2701 GAACCGCACCCTCATCCAGGGCCACCTGGACTTCGTGATGGACATCCTGGTGTTCCACTC 2760

Qy      2761 CTCCCGCCAGGATGGCCTCAATGACTGTATGCACAACAACGGGCAGTGTGGGCAGCTGTG 2820
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Qy      2821 CCTTGCCATCCCCGGCGGCCACCGCTGCGGCTGCGCCTCACACTACACCCTGGACCCCAG 2880
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Db      2821 CCTTGCCATCCCCGGCGGCCACCGCTGCGGCTGCGCCTCACACTACACCCTGGACCCCAG 2880

Qy      2881 CAGCCGCAACTGCAGCCCGCCCACCACCTTCTTGCTGTTCAGCCAGAAATCTGCCATCAG 2940
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Db      2881 CAGCCGCAACTGCAGCCCGCCCACCACCTTCTTGCTGTTCAGCCAGAAATCTGCCATCAG 2940

Qy      2941 TCGGATGATCCCGGACGACCAGCACAGCCCGGATCTCATCCTGCCCCTGCATGGACTGAG 3000
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Db      2941 TCGGATGATCCCGGACGACCAGCACAGCCCGGATCTCATCCTGCCCCTGCATGGACTGAG 3000

Qy      3001 GAACGTCAAAGCCATCGACTATGACCCACTGGACAAGTTCATCTACTGGGTGGATGGGCG 3060
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Db      3001 GAACGTCAAAGCCATCGACTATGACCCACTGGACAAGTTCATCTACTGGGTGGATGGGCG 3060

Qy      3061 CCAGAACATCAAGCGAGCCAAGGACGACGGGACCCAGCCCTTTGTTTTGACCTCTCTGAG 3120
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Db      3061 CCAGAACATCAAGCGAGCCAAGGACGACGGGACCCAGCCCTTTGTTTTGACCTCTCTGAG 3120

Qy      3121 CCAAGGCCAAAACCCAGACAGGCAGCCCCACGACCTCAGCATCGACATCTACAGCCGGAC 3180
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Db      3121 CCAAGGCCAAAACCCAGACAGGCAGCCCCACGACCTCAGCATCGACATCTACAGCCGGAC 3180

Qy      3181 ACTGTTCTGGACGTGCGAGGCCACCAATACCATCAACGTCCACAGGCTGAGCGGGGAAGC 3240
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Db      3181 ACTGTTCTGGACGTGCGAGGCCACCAATACCATCAACGTCCACAGGCTGAGCGGGGAAGC 3240

Qy      3241 CATGGGGGTGGTGCTGCGTGGGGACCGCGACAAGCCCAGGGCCATCGTCGTCAACGCGGA 3300
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Db      3241 CATGGGGGTGGTGCTGCGTGGGGACCGCGACAAGCCCAGGGCCATCGTCGTCAACGCGGA 3300

Qy      3301 GCGAGGGTACCTGTACTTCACCAACATGCAGGACCGGGCAGCCAAGATCGAACGCGCAGC 3360
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Db      3301 GCGAGGGTACCTGTACTTCACCAACATGCAGGACCGGGCAGCCAAGATCGAACGCGCAGC 3360

Qy      3361 CCTGGACGGCACCGAGCGCGAGGTCCTCTTCACCACCGGCCTCATCCGCCCTGTGGCCCT 3420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3361 CCTGGACGGCACCGAGCGCGAGGTCCTCTTCACCACCGGCCTCATCCGCCCTGTGGCCCT 3420

Qy      3421 GGTGGTGGACAACACACTGGGCAAGCTGTTCTGGGTGGACGCGGACCTGAAGCGCATTGA 3480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3421 GGTGGTGGACAACACACTGGGCAAGCTGTTCTGGGTGGACGCGGACCTGAAGCGCATTGA 3480

Qy      3481 GAGCTGTGACCTGTCAGGGGCCAACCGCCTGACCCTGGAGGACGCCAACATCGTGCAGCC 3540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3481 GAGCTGTGACCTGTCAGGGGCCAACCGCCTGACCCTGGAGGACGCCAACATCGTGCAGCC 3540

Qy      3541 TCTGGGCCTGACCATCCTTGGCAAGCATCTCTACTGGATCGACCGCCAGCAGCAGATGAT 3600
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Db      3541 TCTGGGCCTGACCATCCTTGGCAAGCATCTCTACTGGATCGACCGCCAGCAGCAGATGAT 3600

Qy      3601 CGAGCGTGTGGAGAAGACCACCGGGGACAAGCGGACTCGCATCCAGGGCCGTGTCGCCCA 3660
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Db      3601 CGAGCGTGTGGAGAAGACCACCGGGGACAAGCGGACTCGCATCCAGGGCCGTGTCGCCCA 3660

Qy      3661 CCTCACTGGCATCCATGCAGTGGAGGAAGTCAGCCTGGAGGAGTTCTCAGCCCACCCATG 3720
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Db      3661 CCTCACTGGCATCCATGCAGTGGAGGAAGTCAGCCTGGAGGAGTTCTCAGCCCACCCATG 3720

Qy      3721 TGCCCGTGACAATGGTGGCTGCTCCCACATCTGTATTGCCAAGGGTGATGGGACACCACG 3780
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Qy      3781 GTGCTCATGCCCAGTCCACCTCGTGCTCCTGCAGAACCTGCTGACCTGTGGAGAGCCGCC 3840
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Db      3781 GTGCTCATGCCCAGTCCACCTCGTGCTCCTGCAGAACCTGCTGACCTGTGGAGAGCCGCC 3840

Qy      3841 CACCTGCTCCCCGGACCAGTTTGCATGTGCCACAGGGGAGATCGACTGTATCCCCGGGGC 3900
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Qy      3901 CTGGCGCTGTGACGGCTTTCCCGAGTGCGATGACCAGAGCGACGAGGAGGGCTGCCCCGT 3960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3901 CTGGCGCTGTGACGGCTTTCCCGAGTGCGATGACCAGAGCGACGAGGAGGGCTGCCCCGT 3960

Qy      3961 GTGCTCCGCCGCCCAGTTCCCCTGCGCGCGGGGTCAGTGTGTGGACCTGCGCCTGCGCTG 4020
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Qy      4021 CGACGGCGAGGCAGACTGTCAGGACCGCTCAGACGAGGTGGACTGTGACGCCATCTGCCT 4080
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Db      4021 CGACGGCGAGGCAGACTGTCAGGACCGCTCAGACGAGGTGGACTGTGACGCCATCTGCCT 4080

Qy      4081 GCCCAACCAGTTCCGGTGTGCGAGCGGCCAGTGTGTCCTCATCAAACAGCAGTGCGACTC 4140
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Db      4081 GCCCAACCAGTTCCGGTGTGCGAGCGGCCAGTGTGTCCTCATCAAACAGCAGTGCGACTC 4140

Qy      4141 CTTCCCCGACTGTATCGACGGCTCCGACGAGCTCATGTGTGAAATCACCAAGCCGCCCTC 4200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4141 CTTCCCCGACTGTATCGACGGCTCCGACGAGCTCATGTGTGAAATCACCAAGCCGCCCTC 4200

Qy      4201 AGACGACAGCCCGGCCCACAGCAGTGCCATCGGGCCCGTCATTGGCATCATCCTCTCTCT 4260
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Db      4201 AGACGACAGCCCGGCCCACAGCAGTGCCATCGGGCCCGTCATTGGCATCATCCTCTCTCT 4260

Qy      4261 CTTCGTCATGGGTGGTGTCTATTTTGTGTGCCAGCGCGTGGTGTGCCAGCGCTATGCGGG 4320
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Db      4261 CTTCGTCATGGGTGGTGTCTATTTTGTGTGCCAGCGCGTGGTGTGCCAGCGCTATGCGGG 4320

Qy      4321 GGCCAACGGGCCCTTCCCGCACGAGTATGTCAGCGGGACCCCGCACGTGCCCCTCAATTT 4380
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Db      4321 GGCCAACGGGCCCTTCCCGCACGAGTATGTCAGCGGGACCCCGCACGTGCCCCTCAATTT 4380

Qy      4381 CATAGCCCCGGGCGGTTCCCAGCATGGCCCCTTCACAGGCATCGCATGCGGAAAGTCCAT 4440
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Qy       4441 GATGAGCTCCGTGAGCCTGATGGGGGGCCGGGGCGGGGTGCCCCTCTACGACCGGAACCA 4500
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Qy       4561 CCTGAACCCGCCGCCCTCCCCGGCCACGGACCCCTCCCTGTACAACATGGACATGTTCTA 4620
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Db       4561 CCTGAACCCGCCGCCCTCCCCGGCCACGGACCCCTCCCTGTACAACATGGACATGTTCTA 4620

Qy       4621 CTCTTCAAACATTCCGGCCACTGCGAGACCGTACAGGCCCTACATCATTCGAGGAATGGC 4680
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Db       4621 CTCTTCAAACATTCCGGCCACTGCGAGACCGTACAGGCCCTACATCATTCGAGGAATGGC 4680

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Db       4681 GCCCCCGACGACGCCCTGCAGCACCGACGTGTGTGACAGCGACTACAGCGCCAGCCGCTG 4740

Qy       4741 GAAGGCCAGCAAGTACTACCTGGATTTGAACTCGGACTCAGACCCCTATCCACCCCCACC 4800
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Db       4741 GAAGGCCAGCAAGTACTACCTGGATTTGAACTCGGACTCAGACCCCTATCCACCCCCACC 4800

Qy       4801 CACGCCCCACAGCCAGTACCTGTCGGCGGAGGACAGCTGCCCGCCCTCGCCCGCCACCGA 4860
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Qy       4861 GAGGAGCTACTTCCATCTCTTCCCGCCCCCTCCGTCCCCCTGCACGGACTCATCCTGACC 4920
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RESULT 7
US-10-374-979-1
; Sequence 1, Application US/10374979
; Publication No. US20030219793A1
; GENERAL INFORMATION:
;  APPLICANT: John P. Carulli et al.
;  TITLE OF INVENTION: THE HIGH BONE MASS GENE OF 11q13.3
;  FILE REFERENCE: 032796-021
;  CURRENT APPLICATION NUMBER: US/10/374,979
;  CURRENT FILING DATE:  2003-03-04
;  PRIOR APPLICATION NUMBER: US 09/544,398
;  PRIOR FILING DATE: 2000-04-05
;  PRIOR APPLICATION NUMBER: US 09/543,771
;  PRIOR FILING DATE: 2000-04-05
;  PRIOR APPLICATION NUMBER: US 09/229,319
;  PRIOR FILING DATE: 1999-01-13
;  PRIOR APPLICATION NUMBER: US 60/071,449
;  PRIOR FILING DATE: 1998-01-13
;  PRIOR APPLICATION NUMBER: US 60/105,511
;  PRIOR FILING DATE: 1998-10-23
;  NUMBER OF SEQ ID NOS: 109
; SEQ ID NO 1
;   LENGTH: 5120
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-374-979-1

  Query Match           100.0%;  Score 5118.4;  DB 17;  Length 5120;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 5119;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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Qy        121 GCTGCTGCTGGCGCTGTGCGGCTGCCCGGCCCCCGCCGCGGCCTCGCCGCTCCTGCTATT 180
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Qy        181 TGCCAACCGCCGGGACGTACGGCTGGTGGACGCCGGCGGAGTCAAGCTGGAGTCCACCAT 240
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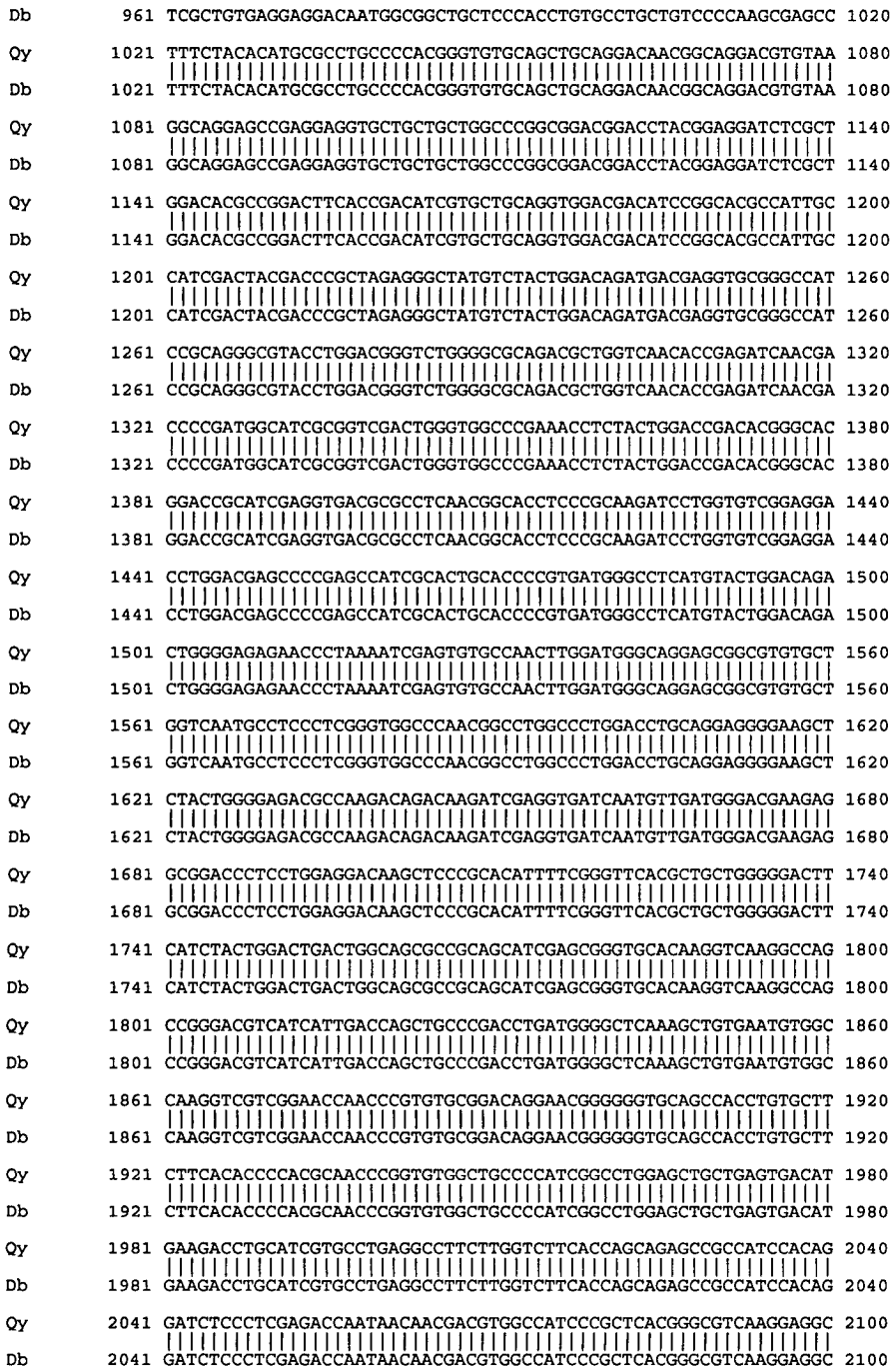
Qy        721 CTTCATCCACCGTGCCAACCTGGACGGCTCGTTCCGGCAGAAGGTGGTGGAGGGCAGCCT 780
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Db        721 CTTCATCCACCGTGCCAACCTGGACGGCTCGTTCCGGCAGAAGGTGGTGGAGGGCAGCCT 780

Qy        781 GACGCACCCCTTCGCCCTGACGCTCTCCGGGGACACTCTGTACTGGACAGACTGGCAGAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACGCACCCCTTCGCCCTGACGCTCTCCGGGGACACTCTGTACTGGACAGACTGGCAGAC 840

Qy        841 CCGCTCCATCCATGCCTGCAACAAGCGCACTGGGGGGAAGAGGAAGGAGATCCTGAGTGC 900
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Db        841 CCGCTCCATCCATGCCTGCAACAAGCGCACTGGGGGGAAGAGGAAGGAGATCCTGAGTGC 900

Qy        901 CCTCTACTCACCCATGGACATCCAGGTGCTGAGCCAGGAGCGGCAGCCTTTCTTCCACAC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CCTCTACTCACCCATGGACATCCAGGTGCTGAGCCAGGAGCGGCAGCCTTTCTTCCACAC 960

Qy        961 TCGCTGTGAGGAGGACAATGGCGGCTGCTCCCACCTGTGCCTGCTGTCCCCAAGCGAGCC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db 961 TCGCTGTGAGGAGGACAATGGCGGCTGCTCCCACCTGTGCCTGCTGTCCCCAAGCGAGCC 1020
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Db 1021 TTTCTACACATGCGCCTGCCCCACGGGTGTGCAGCTGCAGGACAACGGCAGGACGTGTAA 1080
Qy 1081 GGCAGGAGCCGAGGAGGTGCTGCTGCTGGCCCGGCGGACGGACCTACGGAGGATCTCGCT 1140
Db 1081 GGCAGGAGCCGAGGAGGTGCTGCTGCTGGCCCGGCGGACGGACCTACGGAGGATCTCGCT 1140
Qy 1141 GGACACGCCGGACTTCACCGACATCGTGCTGCAGGTGGACGACATCCGGCACGCCATTGC 1200
Db 1141 GGACACGCCGGACTTCACCGACATCGTGCTGCAGGTGGACGACATCCGGCACGCCATTGC 1200
Qy 1201 CATCGACTACGACCCGCTAGAGGGCTATGTCTACTGGACAGATGACGAGGTGCGGGCCAT 1260
Db 1201 CATCGACTACGACCCGCTAGAGGGCTATGTCTACTGGACAGATGACGAGGTGCGGGCCAT 1260
Qy 1261 CCGCAGGGCGTACCTGGACGGGTCTGGGGCGCAGACGCTGGTCAACACCGAGATCAACGA 1320
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Qy 1321 CCCCGATGGCATCGCGGTCGACTGGGTGGCCCGAAACCTCTACTGGACCGACACGGGCAC 1380
Db 1321 CCCCGATGGCATCGCGGTCGACTGGGTGGCCCGAAACCTCTACTGGACCGACACGGGCAC 1380
Qy 1381 GGACCGCATCGAGGTGACGCGCCTCAACGGCACCTCCCGCAAGATCCTGGTGTCGGAGGA 1440
Db 1381 GGACCGCATCGAGGTGACGCGCCTCAACGGCACCTCCCGCAAGATCCTGGTGTCGGAGGA 1440
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Db 1501 CTGGGGAGAGAACCCTAAAATCGAGTGTGCCAACTTGGATGGGCAGGAGCGGCGTGTGCT 1560
Qy 1561 GGTCAATGCCTCCCTCGGGTGGCCCAACGGCCTGGCCCTGGACCTGCAGGAGGGGAAGCT 1620
Db 1561 GGTCAATGCCTCCCTCGGGTGGCCCAACGGCCTGGCCCTGGACCTGCAGGAGGGGAAGCT 1620
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Db 1621 CTACTGGGGAGACGCCAAGACAGACAAGATCGAGGTGATCAATGTTGATGGGACGAAGAG 1680
Qy 1681 GCGGACCCTCCTGGAGGACAAGCTCCCGCACATTTTCGGGTTCACGCTGCTGGGGGACTT 1740
Db 1681 GCGGACCCTCCTGGAGGACAAGCTCCCGCACATTTTCGGGTTCACGCTGCTGGGGGACTT 1740
Qy 1741 CATCTACTGGACTGACTGGCAGCGCCGCAGCATCGAGCGGGTGCACAAGGTCAAGGCCAG 1800
Db 1741 CATCTACTGGACTGACTGGCAGCGCCGCAGCATCGAGCGGGTGCACAAGGTCAAGGCCAG 1800
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Db 1801 CCGGGACGTCATCATTGACCAGCTGCCCGACCTGATGGGGCTCAAAGCTGTGAATGTGGC 1860
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Db 1861 CAAGGTCGTCGGAACCAACCCGTGTGCGGACAGGAACGGGGGGTGCAGCCACCTGTGCTT 1920
Qy 1921 CTTCACACCCCACGCAACCCGGTGTGGCTGCCCCATCGGCCTGGAGCTGCTGAGTGACAT 1980
Db 1921 CTTCACACCCCACGCAACCCGGTGTGGCTGCCCCATCGGCCTGGAGCTGCTGAGTGACAT 1980
Qy 1981 GAAGACCTGCATCGTGCCTGAGGCCTTCTTGGTCTTCACCAGCAGAGCCGCCATCCACAG 2040
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Qy 2041 GATCTCCCTCGAGACCAATAACAACGACGTGGCCATCCCGCTCACGGGCGTCAAGGAGGC 2100
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Db 2101 CTCAGCCCTGGACTTTGATGTGTCCAACAACCACATCTACTGGACAGACGTCAGCCTGAA 2160
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Db 2161 GACCATCAGCCGCGCCTTCATGAACGGGAGCTCGGTGGAGCACGTGGTGGAGTTTGGCCT 2220
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Qy 2341 GAGGGACTTGGACAACCCGAGGTCGCTGGCCCTGGATCCCACCAAGGGCTACATCTACTG 2400
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Db 2401 GACCGAGTGGGGCGGCAAGCCGAGGATCGTGCGGGCCTTCATGGACGGGACCAACTGCAT 2460
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Db 2821 CCTTGCCATCCCCGGCGGCCACCGCTGCGGCTGCGCCTCACACTACACCCTGGACCCCAG 2880
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Qy 3001 GAACGTCAAAGCCATCGACTATGACCCACTGGACAAGTTCATCTACTGGGTGGATGGGCG 3060
Db 3001 GAACGTCAAAGCCATCGACTATGACCCACTGGACAAGTTCATCTACTGGGTGGATGGGCG 3060
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Db 3061 CCAGAACATCAAGCGAGCCAAGGACGACGGGACCCAGCCCTTTGTTTTGACCTCTCTGAG 3120
Qy 3121 CCAAGGCCAAAACCCAGACAGGCAGCCCCACGACCTCAGCATCGACATCTACAGCCGGAC 3180
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Qy       3181 ACTGTTCTGGACGTGCGAGGCCACCAATACCATCAACGTCCACAGGCTGAGCGGGGAAGC 3240
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Db       3181 ACTGTTCTGGACGTGCGAGGCCACCAATACCATCAACGTCCACAGGCTGAGCGGGGAAGC 3240

Qy       3241 CATGGGGGTGGTGCTGCGTGGGGACCGCGACAAGCCCAGGGCCATCGTCGTCAACGCGGA 3300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3241 CATGGGGGTGGTGCTGCGTGGGGACCGCGACAAGCCCAGGGCCATCGTCGTCAACGCGGA 3300

Qy       3301 GCGAGGGTACCTGTACTTCACCAACATGCAGGACCGGGCAGCCAAGATCGAACGCGCAGC 3360
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Qy       3361 CCTGGACGGCACCGAGCGCGAGGTCCTCTTCACCACCGGCCTCATCCGCCCTGTGGCCCT 3420
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Db       3361 CCTGGACGGCACCGAGCGCGAGGTCCTCTTCACCACCGGCCTCATCCGCCCTGTGGCCCT 3420

Qy       3421 GGTGGTGGACAACACACTGGGCAAGCTGTTCTGGGTGGACGCGGACCTGAAGCGCATTGA 3480
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Db       3421 GGTGGTGGACAACACACTGGGCAAGCTGTTCTGGGTGGACGCGGACCTGAAGCGCATTGA 3480

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Qy       3541 TCTGGGCCTGACCATCCTTGGCAAGCATCTCTACTGGATCGACCGCCAGCAGCAGATGAT 3600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3541 TCTGGGCCTGACCATCCTTGGCAAGCATCTCTACTGGATCGACCGCCAGCAGCAGATGAT 3600

Qy       3601 CGAGCGTGTGGAGAAGACCACCGGGGACAAGCGGACTCGCATCCAGGGCCGTGTCGCCCA 3660
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Db       3601 CGAGCGTGTGGAGAAGACCACCGGGGACAAGCGGACTCGCATCCAGGGCCGTGTCGCCCA 3660

Qy       3661 CCTCACTGGCATCCATGCAGTGGAGGAAGTCAGCCTGGAGGAGTTCTCAGCCCACCCATG 3720
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Db       3661 CCTCACTGGCATCCATGCAGTGGAGGAAGTCAGCCTGGAGGAGTTCTCAGCCCACCCATG 3720

Qy       3721 TGCCCGTGACAATGGTGGCTGCTCCCACATCTGTATTGCCAAGGGTGATGGGACACCACG 3780
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Db       3721 TGCCCGTGACAATGGTGGCTGCTCCCACATCTGTATTGCCAAGGGTGATGGGACACCACG 3780

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Db       3781 GTGCTCATGCCCAGTCCACCTCGTGCTCCTGCAGAACCTGCTGACCTGTGGAGAGCCGCC 3840

Qy       3841 CACCTGCTCCCCGGACCAGTTTGCATGTGCCACAGGGGAGATCGACTGTATCCCCGGGGC 3900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3841 CACCTGCTCCCCGGACCAGTTTGCATGTGCCACAGGGGAGATCGACTGTATCCCCGGGGC 3900

Qy       3901 CTGGCGCTGTGACGGCTTTCCCGAGTGCGATGACCAGAGCGACGAGGAGGGCTGCCCCGT 3960
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Qy       3961 GTGCTCCGCCGCCCAGTTCCCCTGCGCGCGGGGTCAGTGTGTGGACCTGCGCCTGCGCTG 4020
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Qy       4021 CGACGGCGAGGCAGACTGTCAGGACCGCTCAGACGAGGTGGACTGTGACGCCATCTGCCT 4080
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Qy       4081 GCCCAACCAGTTCCGGTGTGCGAGCGGCCAGTGTGTCCTCATCAAACAGCAGTGCGACTC 4140
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Qy       4141 CTTCCCCGACTGTATCGACGGCTCCGACGAGCTCATGTGTGAAATCACCAAGCCGCCCTC 4200
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Db       4141 CTTCCCCGACTGTATCGACGGCTCCGACGAGCTCATGTGTGAAATCACCAAGCCGCCCTC 4200

Qy       4201 AGACGACAGCCCGGCCCACAGCAGTGCCATCGGGCCCGTCATTGGCATCATCCTCTCTCT 4260
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Qy       4261 CTTCGTCATGGGTGGTGTCTATTTTGTGTGCCAGCGCGTGGTGTGCCAGCGCTATGCGGG 4320
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Qy       4321 GGCCAACGGGCCCTTCCCGCACGAGTATGTCAGCGGGACCCCGCACGTGCCCCTCAATTT 4380
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Qy       4381 CATAGCCCCGGGCGGTTCCCAGCATGGCCCCTTCACAGGCATCGCATGCGGAAAGTCCAT 4440
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Qy       4441 GATGAGCTCCGTGAGCCTGATGGGGGGCCGGGGCGGGGTGCCCCCTCTACGACCGGAACCA 4500
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Db       4441 GATGAGCTCCGTGAGCCTGATGGGGGGCCGGGGCGGGGTGCCCCCTCTACGACCGGAACCA 4500

Qy       4501 CGTCACAGGGGCCTCGTCCAGCAGCTCGTCCAGCACGAAGGCCACGCTGTACCCGCCGAT 4560
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Qy       4561 CCTGAACCCGCCGCCCTCCCCGGCCACGGACCCCTCCCTGTACAACATGGACATGTTCTA 4620
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Db       4561 CCTGAACCCGCCGCCCTCCCCGGCCACGGACCCCTCCCTGTACAACATGGACATGTTCTA 4620

Qy       4621 CTCTTCAAACATTCCGGCCACTGCGAGACCGTACAGGCCCTACATCATTCGAGGAATGGC 4680
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Db       4621 CTCTTCAAACATTCCGGCCACTGCGAGACCGTACAGGCCCTACATCATTCGAGGAATGGC 4680

Qy       4681 GCCCCCGACGACGCCCTGCAGCACCGACGTGTGTGACAGCGACTACAGCGCCAGCCGCTG 4740
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Db       4681 GCCCCCGACGACGCCCTGCAGCACCGACGTGTGTGACAGCGACTACAGCGCCAGCCGCTG 4740

Qy       4741 GAAGGCCAGCAAGTACTACCTGGATTTGAACTCGGACTCAGACCCCTATCCACCCCCACC 4800
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Db       4741 GAAGGCCAGCAAGTACTACCTGGATTTGAACTCGGACTCAGACCCCTATCCACCCCCACC 4800

Qy       4801 CACGCCCCACAGCCAGTACCTGTCGGCGGAGGACAGCTGCCCGCCCTCGCCCGCCACCGA 4860
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4801 CACGCCCCACAGCCAGTACCTGTCGGCGGAGGACAGCTGCCCGCCCTCGCCCGCCACCGA 4860

Qy       4861 GAGGAGCTACTTCCATCTCTTCCCGCCCCCTCCGTCCCCCTGCACGGACTCATCCTGACC 4920
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Db       4861 GAGGAGCTACTTCCATCTCTTCCCGCCCCCTCCGTCCCCCTGCACGGACTCATCCTGACC 4920

Qy       4921 TCGGCCGGGCCACTCTGGCTTCTCTGTGCCCCTGTAAATAGTTTTAAATATGAACAAAGA 4980
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Db       4981 AAAAAATATATTTTATGATTTAAAAAATAAATATAATTGGGATTTTAAAAACATGAGAAA 5040

Qy       5041 TGTGAACTGTGATGGGGTGGGCAGGGCTGGGAGAACTTTGTACAGTGGAGAAATATTTAT 5100
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RESULT 8
US-10-182-936A-1
; Sequence 1, Application US/10182936A
; Publication No. US20040038860A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Kristina M.
; APPLICANT: Anisowicz, Anthony
; APPLICANT: Bhat, Bheem
; APPLICANT: Damagnez, Veronique
; APPLICANT: Robinson, John
; APPLICANT: Yaworsky, Paul
; TITLE OF INVENTION: Reagents and Method for Modulating DKK-Mediated Interactions
; FILE REFERENCE: 032796-143

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;  CURRENT APPLICATION NUMBER: US/10/182,936A
;  CURRENT FILING DATE:  2002-08-02
;  PRIOR APPLICATION NUMBER: PCT/US02/15982
;  PRIOR FILING DATE: 2002-05-17
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;  PRIOR FILING DATE: 2001-05-17
;  PRIOR APPLICATION NUMBER: US 60/353,058
;  PRIOR FILING DATE: 2002-02-01
;  PRIOR APPLICATION NUMBER: US 60/361,293
;  PRIOR FILING DATE: 2002-03-04
;  NUMBER OF SEQ ID NOS: 216
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 5120
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-182-936A-1

  Query Match            100.0%;  Score 5118.4;  DB 17;  Length 5120;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 5119;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ACTAAAGCGCCGCCGCCGCGCCATGGAGCCCGAGTGAGCGCGGCGCGGGCCCGTCCGGCC 60
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Db         61 GCCGGACAACATGGAGGCAGCGCCGCCCGGGCCGCCGTGGCCGCTGCTGCTGCTGCTGCT 120

Qy        121 GCTGCTGCTGGCGCTGTGCGGCTGCCCGGCCCCCGCCGCGGCCTCGCCGCTCCTGCTATT 180
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Qy        541 CTTGGACCCCGCTCACGGGTACATGTACTGGACAGACTGGGTTGAGACGCCCCGGATTGA 600
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db        541 CTTGGACCCCGCTCACGGGTACATGTACTGGACAGACTGGGGTGAGACGCCCCGGATTGA 600

Qy        601 GCGGGCAGGGATGGATGGCAGCACCCGGAAGATCATTGTGGACTCGGACATTTACTGGCC 660
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Qy        661 CAATGGACTGACCATCGACCTGGAGGAGCAGAAGCTCTACTGGGCTGACGCCAAGCTCAG 720
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Qy        721 CTTCATCCACCGTGCCAACCTGGACGGCTCGTTCCGGCAGAAGGTGGTGGAGGGCAGCCT 780
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Qy        781 GACGCACCCCTTCGCCCTGACGCTCTCCGGGGACACTCTGTACTGGACAGACTGGCAGAC 840
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Db        781 GACGCACCCCTTCGCCCTGACGCTCTCCGGGGACACTCTGTACTGGACAGACTGGCAGAC 840

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Qy        901 CCTCTACTCACCCATGGACATCCAGGTGCTGAGCCAGGAGCGGCAGCCTTTCTTCCACAC 960
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Qy       1021 TTTCTACACATGCGCCTGCCCCACGGGTGTGCAGCTGCAGGACAACGGCAGGACGTGTAA 1080
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Qy       1141 GGACACGCCGGACTTCACCGACATCGTGCTGCAGGTGGACGACATCCGGCACGCCATTGC 1200
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Db       1141 GGACACGCCGGACTTCACCGACATCGTGCTGCAGGTGGACGACATCCGGCACGCCATTGC 1200

Qy       1201 CATCGACTACGACCCGCTAGAGGGCTATGTCTACTGGACAGATGACGAGGTGCGGGCCAT 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 CATCGACTACGACCCGCTAGAGGGCTATGTCTACTGGACAGATGACGAGGTGCGGGCCAT 1260

Qy       1261 CCGCAGGGCGTACCTGGACGGGTCTGGGGCGCAGACGCTGGTCAACACCGAGATCAACGA 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 CCGCAGGGCGTACCTGGACGGGTCTGGGGCGCAGACGCTGGTCAACACCGAGATCAACGA 1320

Qy       1321 CCCCGATGGCATCGCGGTCGACTGGGTGGCCCGAAACCTCTACTGGACCGACACGGGCAC 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 CCCCGATGGCATCGCGGTCGACTGGGTGGCCCGAAACCTCTACTGGACCGACACGGGCAC 1380

Qy       1381 GGACCGCATCGAGGTGACGCGCCTCAACGGCACCTCCCGCAAGATCCTGGTGTCGGAGGA 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 GGACCGCATCGAGGTGACGCGCCTCAACGGCACCTCCCGCAAGATCCTGGTGTCGGAGGA 1440

Qy       1441 CCTGGACGAGCCCCGAGCCATCGCACTGCACCCCGTGATGGGCCTCATGTACTGGACAGA 1500
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Db       1441 CCTGGACGAGCCCCGAGCCATCGCACTGCACCCCGTGATGGGCCTCATGTACTGGACAGA 1500

Qy       1501 CTGGGGAGAGAACCCTAAAATCGAGTGTGCCAACTTGGATGGGCAGGAGCGGCGTGTGCT 1560
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Qy       1561 GGTCAATGCCTCCCTCGGGTGGCCCAACGGCCTGGCCCTGGACCTGCAGGAGGGGAAGCT 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 GGTCAATGCCTCCCTCGGGTGGCCCAACGGCCTGGCCCTGGACCTGCAGGAGGGGAAGCT 1620

Qy       1621 CTACTGGGGAGACGCCAAGACAGACAAGATCGAGGTGATCAATGTTGATGGGACGAAGAG 1680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 CTACTGGGGAGACGCCAAGACAGACAAGATCGAGGTGATCAATGTTGATGGGACGAAGAG 1680

Qy       1681 GCGGACCCTCCTGGAGGACAAGCTCCCGCACATTTTCGGGTTCACGCTGCTGGGGGACTT 1740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 GCGGACCCTCCTGGAGGACAAGCTCCCGCACATTTTCGGGTTCACGCTGCTGGGGGACTT 1740

Qy       1741 CATCTACTGGACTGACTGGCAGCGCCGCAGCATCGAGCGGGTGCACAAGGTCAAGGCCAG 1800
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Db       1741 CATCTACTGGACTGACTGGCAGCGCCGCAGCATCGAGCGGGTGCACAAGGTCAAGGCCAG 1800

Qy       1801 CCGGGACGTCATCATTGACCAGCTGCCCGACCTGATGGGGCTCAAAGCTGTGAATGTGGC 1860
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Qy       1861 CAAGGTCGTCGGAACCAACCCGTGTGCGGACAGGAACGGGGGGGTGCAGCCACCTGTGCTT 1920
Db       1861 CAAGGTCGTCGGAACCAACCCGTGTGCGGACAGGAACGGGGGGGTGCAGCCACCTGTGCTT 1920

Qy       1921 CTTCACACCCCACGCAACCCGGTGTGGCTGCCCCATCGGCCTGGAGCTGCTGAGTGACAT 1980
Db       1921 CTTCACACCCCACGCAACCCGGTGTGGCTGCCCCATCGGCCTGGAGCTGCTGAGTGACAT 1980

Qy       1981 GAAGACCTGCATCGTGCCTGAGGCCTTCTTGGTCTTCACCAGCAGAGCCGCCATCCACAG 2040
Db       1981 GAAGACCTGCATCGTGCCTGAGGCCTTCTTGGTCTTCACCAGCAGAGCCGCCATCCACAG 2040

Qy       2041 GATCTCCCTCGAGACCAATAACAACGACGTGGCCATCCCGCTCACGGGCGTCAAGGAGGC 2100
Db       2041 GATCTCCCTCGAGACCAATAACAACGACGTGGCCATCCCGCTCACGGGCGTCAAGGAGGC 2100

Qy       2101 CTCAGCCCTGGACTTTGATGTGTCCAACAACCACATCTACTGGACAGACGTCAGCCTGAA 2160
Db       2101 CTCAGCCCTGGACTTTGATGTGTCCAACAACCACATCTACTGGACAGACGTCAGCCTGAA 2160

Qy       2161 GACCATCAGCCGCGCCTTCATGAACGGGAGCTCGGTGGAGCACGTGGTGGAGTTTGGCCT 2220
Db       2161 GACCATCAGCCGCGCCTTCATGAACGGGAGCTCGGTGGAGCACGTGGTGGAGTTTGGCCT 2220

Qy       2221 TGACTACCCCGAGGGCATGGCCGTTGACTGGATGGGCAAGAACCTCTACTGGGCCGACAC 2280
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Qy       2281 TGGGACCAACAGAATCGAAGTGGCGCGGCTGGACGGGCAGTTCCGGCAAGTCCTCGTGTG 2340
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Qy       2341 GAGGGACTTGGACAACCCGAGGTCGCTGGCCCTGGATCCCACCAAGGGCTACATCTACTG 2400
Db       2341 GAGGGACTTGGACAACCCGAGGTCGCTGGCCCTGGATCCCACCAAGGGCTACATCTACTG 2400

Qy       2401 GACCGAGTGGGGCGGCAAGCCGAGGATCGTGCGGGCCTTCATGGACGGGACCAACTGCAT 2460
Db       2401 GACCGAGTGGGGCGGCAAGCCGAGGATCGTGCGGGCCTTCATGGACGGGACCAACTGCAT 2460

Qy       2461 GACGCTGGTGGACAAGGTGGGCCGGGCCAACGACCTCACCATTGACTACGCTGACCAGCG 2520
Db       2461 GACGCTGGTGGACAAGGTGGGCCGGGCCAACGACCTCACCATTGACTACGCTGACCAGCG 2520

Qy       2521 CCTCTACTGGACCGACCTGGACACCAACATGATCGAGTCGTCCAACATGCTGGGTCAGGA 2580
Db       2521 CCTCTACTGGACCGACCTGGACACCAACATGATCGAGTCGTCCAACATGCTGGGTCAGGA 2580

Qy       2581 GCGGGTCGTGATTGCCGACGATCTCCCGCACCCGTTCGGTCTGACGCAGTACAGCGATTA 2640
Db       2581 GCGGGTCGTGATTGCCGACGATCTCCCGCACCCGTTCGGTCTGACGCAGTACAGCGATTA 2640

Qy       2641 TATCTACTGGACAGACTGGAATCTGCACAGCATTGAGCGGGCCGACAAGACTAGCGGCCG 2700
Db       2641 TATCTACTGGACAGACTGGAATCTGCACAGCATTGAGCGGGCCGACAAGACTAGCGGCCG 2700

Qy       2701 GAACCGCACCCTCATCCAGGGCCACCTGGACTTCGTGATGGACATCCTGGTGTTCCACTC 2760
Db       2701 GAACCGCACCCTCATCCAGGGCCACCTGGACTTCGTGATGGACATCCTGGTGTTCCACTC 2760

Qy       2761 CTCCCGCCAGGATGGCCTCAATGACTGTATGCACAACAACGGGCAGTGTGGGCAGCTGTG 2820
Db       2761 CTCCCGCCAGGATGGCCTCAATGACTGTATGCACAACAACGGGCAGTGTGGGCAGCTGTG 2820

Qy       2821 CCTTGCCATCCCCGGCGGCCACCGCTGCGGCTGCGCCTCACACTACACCCTGGACCCCAG 2880
Db       2821 CCTTGCCATCCCCGGCGGCCACCGCTGCGGCTGCGCCTCACACTACACCCTGGACCCCAG 2880

Qy       2881 CAGCCGCAACTGCAGCCCGCCCACCACCTTCTTGCTGTTCAGCCAGAAATCTGCCATCAG 2940
Db       2881 CAGCCGCAACTGCAGCCCGCCCACCACCTTCTTGCTGTTCAGCCAGAAATCTGCCATCAG 2940

Qy       2941 TCGGATGATCCCCGGACGACCAGCACAGCCCGGATCTCATCCTGCCCCTGCATGGACTGAG 3000
Db       2941 TCGGATGATCCCCGGACGACCAGCACAGCCCGGATCTCATCCTGCCCCTGCATGGACTGAG 3000

Qy       3001 GAACGTCAAAGCCATCGACTATGACCCACTGGACAAGTTCATCTACTGGGTGGATGGGCG 3060
Db       3001 GAACGTCAAAGCCATCGACTATGACCCACTGGACAAGTTCATCTACTGGGTGGATGGGCG 3060

Qy       3061 CCAGAACATCAAGCGAGCCAAGGACGACGGGACCCAGCCCTTTGTTTTGACCTCTCTGAG 3120
Db       3061 CCAGAACATCAAGCGAGCCAAGGACGACGGGACCCAGCCCTTTGTTTTGACCTCTCTGAG 3120

Qy       3121 CCAAGGCCAAAACCCAGACAGGCAGCCCCACGACCTCAGCATCGACATCTACAGCCGGAC 3180
Db       3121 CCAAGGCCAAAACCCAGACAGGCAGCCCCACGACCTCAGCATCGACATCTACAGCCGGAC 3180

Qy       3181 ACTGTTCTGGACGTGCGAGGCCACCAATACCATCAACGTCCACAGGCTGAGCGGGGAAGC 3240
Db       3181 ACTGTTCTGGACGTGCGAGGCCACCAATACCATCAACGTCCACAGGCTGAGCGGGGAAGC 3240

Qy       3241 CATGGGGGTGGTGCTGCGTGGGGACCGCGACAAGCCCAGGGCCATCGTCGTCAACGCGGA 3300
Db       3241 CATGGGGGTGGTGCTGCGTGGGGACCGCGACAAGCCCAGGGCCATCGTCGTCAACGCGGA 3300

Qy       3301 GCGAGGGTACCTGTACTTCACCAACATGCAGGACCGGGCAGCCAAGATCGAACGCGCAGC 3360
Db       3301 GCGAGGGTACCTGTACTTCACCAACATGCAGGACCGGGCAGCCAAGATCGAACGCGCAGC 3360

Qy       3361 CCTGGACGGCACCGAGCGCGAGGTCCTCTTCACCACCGGCCTCATCCGCCCTGTGGCCCT 3420
Db       3361 CCTGGACGGCACCGAGCGCGAGGTCCTCTTCACCACCGGCCTCATCCGCCCTGTGGCCCT 3420

Qy       3421 GGTGGTGGACAACACACTGGGCAAGCTGTTCTGGGTGGACGCGGACCTGAAGCGCATTGA 3480
Db       3421 GGTGGTGGACAACACACTGGGCAAGCTGTTCTGGGTGGACGCGGACCTGAAGCGCATTGA 3480

Qy       3481 GAGCTGTGACCTGTCAGGGGCCAACCGCCTGACCCTGGAGGACGCCAACATCGTGCAGCC 3540
Db       3481 GAGCTGTGACCTGTCAGGGGCCAACCGCCTGACCCTGGAGGACGCCAACATCGTGCAGCC 3540

Qy       3541 TCTGGGCCTGACCATCCTTGGCAAGCATCTCTACTGGATCGACCGCCAGCAGCAGATGAT 3600
Db       3541 TCTGGGCCTGACCATCCTTGGCAAGCATCTCTACTGGATCGACCGCCAGCAGCAGATGAT 3600

Qy       3601 CGAGCGTGTGGAGAAGACCACCGGGGACAAGCGGACTCGCATCCAGGGCCGTGTCGCCCA 3660
Db       3601 CGAGCGTGTGGAGAAGACCACCGGGGACAAGCGGACTCGCATCCAGGGCCGTGTCGCCCA 3660

Qy       3661 CCTCACTGGCATCCATGCAGTGGAGGAAGTCAGCCTGGAGGAGTTCTCAGCCCACCCATG 3720
Db       3661 CCTCACTGGCATCCATGCAGTGGAGGAAGTCAGCCTGGAGGAGTTCTCAGCCCACCCATG 3720

Qy       3721 TGCCCGTGACAATGGTGGCTGCTCCCACATCTGTATTGCCAAGGGTGATGGGACACCACG 3780
Db       3721 TGCCCGTGACAATGGTGGCTGCTCCCACATCTGTATTGCCAAGGGTGATGGGACACCACG 3780

Qy       3781 GTGCTCATGCCCAGTCCACCTCGTGCTCCTGCAGAACCTGCTGACCTGTGGAGAGCCGCC 3840
Db       3781 GTGCTCATGCCCAGTCCACCTCGTGCTCCTGCAGAACCTGCTGACCTGTGGAGAGCCGCC 3840

Qy       3841 CACCTGCTCCCCGGACCAGTTTGCATGTGCCACAGGGGAGATCGACTGTATCCCCGGGGC 3900
Db       3841 CACCTGCTCCCCGGACCAGTTTGCATGTGCCACAGGGGAGATCGACTGTATCCCCGGGGC 3900

Qy       3901 CTGGCGCTGTGACGGCTTTCCCGAGTGCGATGACCAGAGCGACGAGGAGGGCTGCCCCGT 3960
Db       3901 CTGGCGCTGTGACGGCTTTCCCGAGTGCGATGACCAGAGCGACGAGGAGGGCTGCCCCGT 3960

Qy       3961 GTGCTCCGCCGCCCAGTTCCCCTGCGCGCGGGGTCAGTGTGTGGACCTGCGCCTGCGCTG 4020
Db       3961 GTGCTCCGCCGCCCAGTTCCCCTGCGCGCGGGGTCAGTGTGTGGACCTGCGCCTGCGCTG 4020

Qy       4021 CGACGGCGAGGCAGACTGTCAGGACCGCTCAGACGAGGTGGACTGTGACGCCATCTGCCT 4080
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Db       4021 CGACGGCGAGGCAGACTGTCAGGACCGCTCAGACGAGGTGGACTGTGACGCCATCTGCCT 4080

Qy       4081 GCCCAACCAGTTCCGGTGTGCGAGCGGCCAGTGTGTCCTCATCAAACAGCAGTGCGACTC 4140
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Db       4081 GCCCAACCAGTTCCGGTGTGCGAGCGGCCAGTGTGTCCTCATCAAACAGCAGTGCGACTC 4140

Qy       4141 CTTCCCCGACTGTATCGACGGCTCCGACGAGCTCATGTGTGAAATCACCAAGCCGCCCTC 4200
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Db       4201 AGACGACAGCCCGGCCCACAGCAGTGCCATCGGGCCCGTCATTGGCATCATCCTCTCTCT 4260

Qy       4261 CTTCGTCATGGGTGGTGTCTATTTTGTGTGCCAGCGCGTGGTGTGCCAGCGCTATGCGGG 4320
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Db       4261 CTTCGTCATGGGTGGTGTCTATTTTGTGTGCCAGCGCGTGGTGTGCCAGCGCTATGCGGG 4320

Qy       4321 GGCCAACGGGCCCTTCCCGCACGAGTATGTCAGCGGGACCCCGCACGTGCCCCTCAATTT 4380
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Db       4381 CATAGCCCCGGGCGGTTCCCAGCATGGCCCCTTCACAGGCATCGCATGCGGAAAGTCCAT 4440

Qy       4441 GATGAGCTCCGTGAGCCTGATGGGGGGCCGGGGCGGGGTGCCCCTCTACGACCGGAACCA 4500
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Qy       4501 CGTCACAGGGGCCTCGTCCAGCAGCTCGTCCAGCACGAAGGCCACGCTGTACCCGCCGAT 4560
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Qy       4621 CTCTTCAAACATTCCGGCCACTGCGAGACCGTACAGGCCCTACATCATTCGAGGAATGGC 4680
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Db       4621 CTCTTCAAACATTCCGGCCACTGCGAGACCGTACAGGCCCTACATCATTCGAGGAATGGC 4680

Qy       4681 GCCCCCGACGACGCCCTGCAGCACCGACGTGTGTGACAGCGACTACAGCGCCAGCCGCTG 4740
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Db       4681 GCCCCCGACGACGCCCTGCAGCACCGACGTGTGTGACAGCGACTACAGCGCCAGCCGCTG 4740

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Db       4801 CACGCCCCACAGCCAGTACCTGTCGGCGGAGGACAGCTGCCCGCCCTCGCCCGCCACCGA 4860

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Db       4861 GAGGAGCTACTTCCATCTCTTCCCGCCCCCTCCGTCCCCCTGCACGGACTCATCCTGACC 4920

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RESULT 9
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; Sequence 1, Application US/10731739
; Publication No. US20040176582A1
; GENERAL INFORMATION:
;  APPLICANT: Carulli, John P.
;  APPLICANT:  Little, Randall D.
;  APPLICANT:  Recker, Robert R.
;  APPLICANT:  Johnson, Mark L.
;  TITLE OF INVENTION: High bone mass gene of 11q13.3
;  FILE REFERENCE: 032796-013
;  CURRENT APPLICATION NUMBER: US/10/731,739
;  CURRENT FILING DATE:  2003-12-10
;  PRIOR APPLICATION NUMBER: US/09/544,398B
;  PRIOR FILING DATE: 2002-06-10
;  PRIOR APPLICATION NUMBER: US 09/229,319
;  PRIOR FILING DATE: 1999-01-13
;  PRIOR APPLICATION NUMBER: US 60/071,449
;  PRIOR FILING DATE: 1998-01-13
;  PRIOR APPLICATION NUMBER: US 60/105,511
;  PRIOR FILING DATE: 1998-10-23
;  NUMBER OF SEQ ID NOS: 641
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 5120
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-731-739-1

  Query Match             100.0%;  Score 5118.4;  DB 18;  Length 5120;
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        241 CGTGGTCAGCGGCCTGGAGGATGCGGCCGCAGTGGACTTCCAGTTTTCCAAGGGAGCCGT 300
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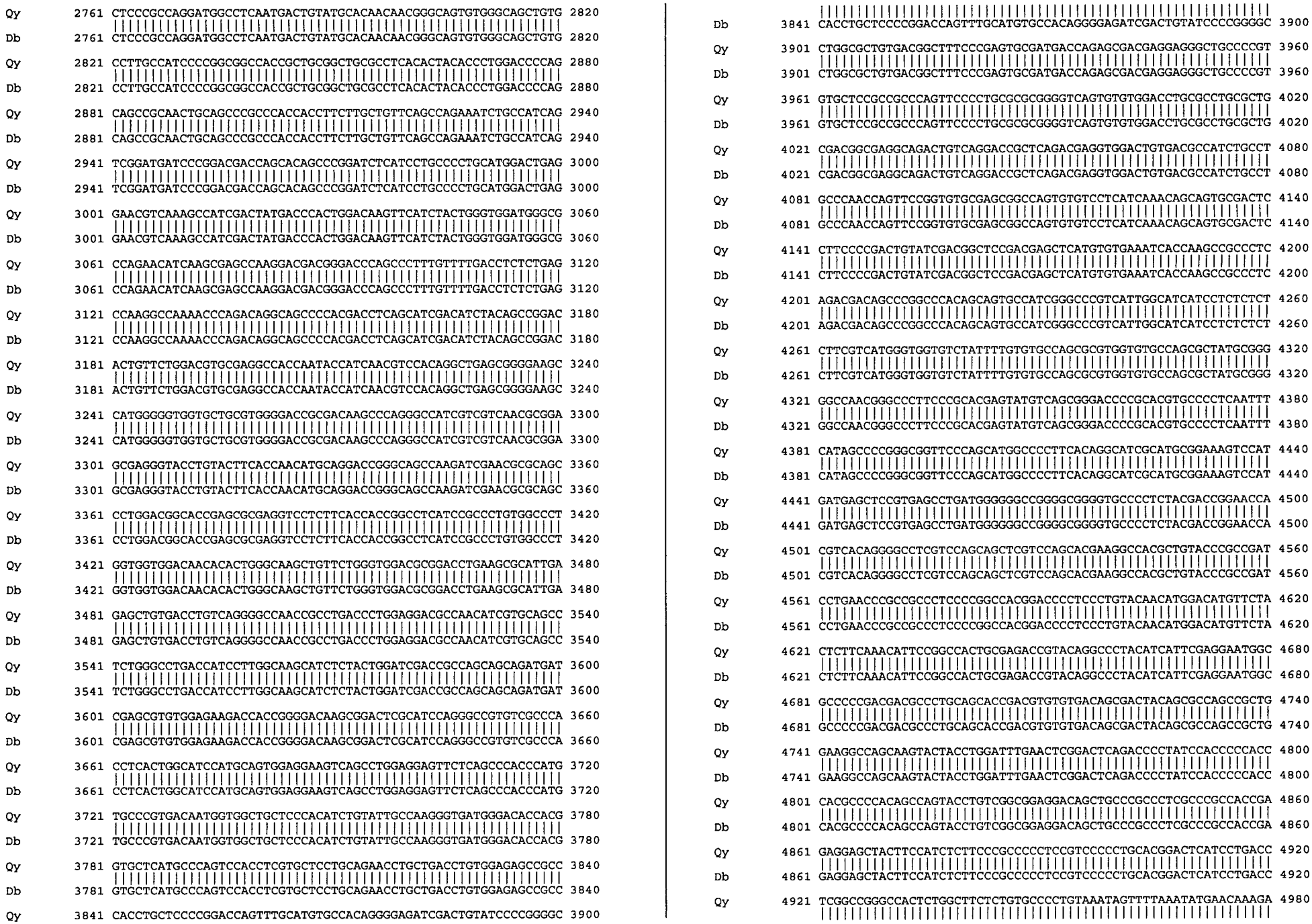
Qy        421 GGTGGGCAAGAAGCTGTACTGGACGGACTCAGAGACCAACCGCATCGAGGTGGCCAACCT 480
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Qy        481 CAATGGCACATCCCGGAAGGTGCTCTTCTGGCAGGACCTTGACCAGCCGAGGGCCATCGC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CAATGGCACATCCCGGAAGGTGCTCTTCTGGCAGGACCTTGACCAGCCGAGGGCCATCGC 540

Qy        541 CTTGGACCCCGCTCACGGGTACATGTACTGGACAGACTGGGTTGAGACGCCCCGGATTGA 600
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Db        541 CTTGGACCCCGCTCACGGGTACATGTACTGGACAGACTGGGGTGAGACGCCCCGGATTGA 600
Qy        601 GCGGGCAGGGATGGATGGCAGCACCCGGAAGATCATTGTGGACTCGGACATTTACTGGCC 660
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Qy        661 CAATGGACTGACCATCGACCTGGAGGAGCAGAAGCTCTACTGGGCTGACGCCAAGCTCAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAATGGACTGACCATCGACCTGGAGGAGCAGAAGCTCTACTGGGCTGACGCCAAGCTCAG 720
Qy        721 CTTCATCCACCGTGCCAACCTGGACGGCTCGTTCCGGCAGAAGGTGGTGGAGGGCAGCCT 780
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Db        721 CTTCATCCACCGTGCCAACCTGGACGGCTCGTTCCGGCAGAAGGTGGTGGAGGGCAGCCT 780
Qy        781 GACGCACCCCTTCGCCCTGACGCTCTCCGGGGACACTCTGTACTGGACAGACTGGCAGAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACGCACCCCTTCGCCCTGACGCTCTCCGGGGACACTCTGTACTGGACAGACTGGCAGAC 840
Qy        841 CCGCTCCATCCATGCCTGCAACAAGCGCACTGGGGGGAAGAGGAAGGAGATCCTGAGTGC 900
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Qy        901 CCTCTACTCACCCATGGACATCCAGGTGCTGAGCCAGGAGCGGCAGCCTTTCTTCCACAC 960
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Db        901 CCTCTACTCACCCATGGACATCCAGGTGCTGAGCCAGGAGCGGCAGCCTTTCTTCCACAC 960
Qy        961 TCGCTGTGAGGAGGACAATGGCGGCTGCTCCCACCTGTGCCTGCTGTCCCCAAGCGAGCC 1020
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Db        961 TCGCTGTGAGGAGGACAATGGCGGCTGCTCCCACCTGTGCCTGCTGTCCCCAAGCGAGCC 1020
Qy       1021 TTTCTACACATGCGCCTGCCCCACGGGTGTGCAGCTGCAGGACAACGGCAGGACGTGTAA 1080
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Db       1021 TTTCTACACATGCGCCTGCCCCACGGGTGTGCAGCTGCAGGACAACGGCAGGACGTGTAA 1080
Qy       1081 GGCAGGAGCCGAGGAGGTGCTGCTGCTGGCCCGGCGGACGGACCTACGGAGGATCTCGCT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 GGCAGGAGCCGAGGAGGTGCTGCTGCTGGCCCGGCGGACGGACCTACGGAGGATCTCGCT 1140
Qy       1141 GGACACGCCGGACTTCACCGACATCGTGCTGCAGGTGGACGACATCCGGCACGCCATTGC 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GGACACGCCGGACTTCACCGACATCGTGCTGCAGGTGGACGACATCCGGCACGCCATTGC 1200
Qy       1201 CATCGACTACGACCCGCTAGAGGGCTATGTCTACTGGACAGATGACGAGGTGCGGGCCAT 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 CATCGACTACGACCCGCTAGAGGGCTATGTCTACTGGACAGATGACGAGGTGCGGGCCAT 1260
Qy       1261 CCGCAGGGCGTACCTGGACGGGTCTGGGGCGCAGACGCTGGTCAACACCGAGATCAACGA 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 CCGCAGGGCGTACCTGGACGGGTCTGGGGCGCAGACGCTGGTCAACACCGAGATCAACGA 1320
Qy       1321 CCCCGATGGCATCGCGGTCGACTGGGTGGCCCGAAACCTCTACTGGACCGACACGGGCAC 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 CCCCGATGGCATCGCGGTCGACTGGGTGGCCCGAAACCTCTACTGGACCGACACGGGCAC 1380
Qy       1381 GGACCGCATCGAGGTGACGCGCCTCAACGGCACCTCCCGCAAGATCCTGGTGTCGGAGGA 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 GGACCGCATCGAGGTGACGCGCCTCAACGGCACCTCCCGCAAGATCCTGGTGTCGGAGGA 1440
Qy       1441 CCTGGACGAGCCCCGAGCCATCGCACTGCACCCCGTGATGGGCCTCATGTACTGGACAGA 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 CCTGGACGAGCCCCGAGCCATCGCACTGCACCCCGTGATGGGCCTCATGTACTGGACAGA 1500
Qy       1501 CTGGGGAGAGAACCCTAAAATCGAGTGTGCCAACTTGGATGGGCAGGAGCGGCGTGTGCT 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 CTGGGGAGAGAACCCTAAAATCGAGTGTGCCAACTTGGATGGGCAGGAGCGGCGTGTGCT 1560
Qy       1561 GGTCAATGCCTCCCTCGGGTGGCCCAACGGCCTGGCCCTGGACCTGCAGGAGGGGAAGCT 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 GGTCAATGCCTCCCTCGGGTGGCCCAACGGCCTGGCCCTGGACCTGCAGGAGGGGAAGCT 1620
Qy       1621 CTACTGGGGAGACGCCAAGACAGACAAGATCGAGGTGATCAATGTTGATGGGACGAAGAG 1680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 CTACTGGGGAGACGCCAAGACAGACAAGATCGAGGTGATCAATGTTGATGGGACGAAGAG 1680
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Qy       1681 GCGGACCCTCCTGGAGGACAAGCTCCCGCACATTTTCGGGTTCACGCTGCTGGGGGACTT 1740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 GCGGACCCTCCTGGAGGACAAGCTCCCGCACATTTTCGGGTTCACGCTGCTGGGGGACTT 1740
Qy       1741 CATCTACTGGACTGACTGGCAGCGCCGCAGCATCGAGCGGGTGCACAAGGTCAAGGCCAG 1800
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 CATCTACTGGACTGACTGGCAGCGCCGCAGCATCGAGCGGGTGCACAAGGTCAAGGCCAG 1800
Qy       1801 CCGGGACGTCATCATTGACCAGCTGCCCGACCTGATGGGGCTCAAAGCTGTGAATGTGGC 1860
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 CCGGGACGTCATCATTGACCAGCTGCCCGACCTGATGGGGCTCAAAGCTGTGAATGTGGC 1860
Qy       1861 CAAGGTCGTCGGAACCAACCCGTGTGCGGACAGGAACGGGGGGTGCAGCCACCTGTGCTT 1920
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1861 CAAGGTCGTCGGAACCAACCCGTGTGCGGACAGGAACGGGGGGTGCAGCCACCTGTGCTT 1920
Qy       1921 CTTCACACCCCACGCAACCCGGTGTGGCTGCCCCATCGGCCTGGAGCTGCTGAGTGACAT 1980
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1921 CTTCACACCCCACGCAACCCGGTGTGGCTGCCCCATCGGCCTGGAGCTGCTGAGTGACAT 1980
Qy       1981 GAAGACCTGCATCGTGCCTGAGGCCTTCTTGGTCTTCACCAGCAGAGCCGCCATCCACAG 2040
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1981 GAAGACCTGCATCGTGCCTGAGGCCTTCTTGGTCTTCACCAGCAGAGCCGCCATCCACAG 2040
Qy       2041 GATCTCCCTCGAGACCAATAACAACGACGTGGCCATCCCGCTCACGGGCGTCAAGGAGGC 2100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2041 GATCTCCCTCGAGACCAATAACAACGACGTGGCCATCCCGCTCACGGGCGTCAAGGAGGC 2100
Qy       2101 CTCAGCCCTGGACTTTGATGTGTCCAACAACCACATCTACTGGACAGACGTCAGCCTGAA 2160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2101 CTCAGCCCTGGACTTTGATGTGTCCAACAACCACATCTACTGGACAGACGTCAGCCTGAA 2160
Qy       2161 GACCATCAGCCGCGCCTTCATGAACGGGAGCTCGGTGGAGCACGTGGTGGAGTTTGGCCT 2220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2161 GACCATCAGCCGCGCCTTCATGAACGGGAGCTCGGTGGAGCACGTGGTGGAGTTTGGCCT 2220
Qy       2221 TGACTACCCCGAGGGCATGGCCGTTGACTGGATGGGCAAGAACCTCTACTGGGCCGACAC 2280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2221 TGACTACCCCGAGGGCATGGCCGTTGACTGGATGGGCAAGAACCTCTACTGGGCCGACAC 2280
Qy       2281 TGGGACCAACAGAATCGAAGTGGCGCGGCTGGACGGGCAGTTCCGGCAAGTCCTCGTGTG 2340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2281 TGGGACCAACAGAATCGAAGTGGCGCGGCTGGACGGGCAGTTCCGGCAAGTCCTCGTGTG 2340
Qy       2341 GAGGGACTTGGACAACCCGAGGTCGCTGGCCCTGGATCCCACCAAGGGCTACATCTACTG 2400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2341 GAGGGACTTGGACAACCCGAGGTCGCTGGCCCTGGATCCCACCAAGGGCTACATCTACTG 2400
Qy       2401 GACCGAGTGGGGCGGCAAGCCGAGGATCGTGCGGGCCTTCATGGACGGGACCAACTGCAT 2460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2401 GACCGAGTGGGGCGGCAAGCCGAGGATCGTGCGGGCCTTCATGGACGGGACCAACTGCAT 2460
Qy       2461 GACGCTGGTGGACAAGGTGGGCCGGGCCAACGACCTCACCATTGACTACGCTGACCAGCG 2520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2461 GACGCTGGTGGACAAGGTGGGCCGGGCCAACGACCTCACCATTGACTACGCTGACCAGCG 2520
Qy       2521 CCTCTACTGGACCGACCTGGACACCAACATGATCGAGTCGTCCAACATGCTGGGTCAGGA 2580
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2521 CCTCTACTGGACCGACCTGGACACCAACATGATCGAGTCGTCCAACATGCTGGGTCAGGA 2580
Qy       2581 GCGGGTCGTGATTGCCGACGATCTCCCGCACCCGTTCGGTCTGACGCAGTACAGCGATTA 2640
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2581 GCGGGTCGTGATTGCCGACGATCTCCCGCACCCGTTCGGTCTGACGCAGTACAGCGATTA 2640
Qy       2641 TATCTACTGGACAGACTGGAATCTGCACAGCATTGAGCGGGCCGACAAGACTAGCGGCCG 2700
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2641 TATCTACTGGACAGACTGGAATCTGCACAGCATTGAGCGGGCCGACAAGACTAGCGGCCG 2700
Qy       2701 GAACCGCACCCTCATCCAGGGCCACCTGGACTTCGTGATGGACATCCTGGTGTTCCACTC 2760
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2701 GAACCGCACCCTCATCCAGGGCCACCTGGACTTCGTGATGGACATCCTGGTGTTCCACTC 2760
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Db       4921 TCGGCCGGGCCACTCTGGCTTCTCTGTGCCCCTGTAAATAGTTTTAAATATGAACAAAGA 4980

Qy       4981 AAAAAATATATTTTATGATTTAAAAAATAAATATAATTGGGATTTTAAAAACATGAGAAA 5040
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4981 AAAAAATATATTTTATGATTTAAAAAATAAATATAATTGGGATTTTAAAAACATGAGAAA 5040

Qy       5041 TGTGAACTGTGATGGGGTGGGCAGGGCTGGGAGAACTTTGTACAGTGGAGAAATATTTAT 5100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5041 TGTGAACTGTGATGGGGTGGGCAGGGCTGGGAGAACTTTGTACAGTGGAGAAATATTTAT 5100

Qy       5101 AAACTTAATTTTGTAAAACA 5120
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Db       5101 AAACTTAATTTTGTAAAACA 5120


RESULT 10
US-10-477-238A-1
; Sequence 1, Application US/10477238A
; Publication No. US20040221326A1
; GENERAL INFORMATION:
;  APPLICANT: Babij, Philip
;  APPLICANT:  Yaworsky, Paul
;  APPLICANT:  Bex, Frederick J. III
;  APPLICANT:  Bodine, Peter Van Nest
;  TITLE OF INVENTION: Transgenic Animal Model of Bone Mass Modulation
;  FILE REFERENCE: 032796-212
;  CURRENT APPLICATION NUMBER: US/10/477,238A
;  CURRENT FILING DATE:  2003-11-10
;  PRIOR APPLICATION NUMBER: US 60/290,071
;  PRIOR FILING DATE: 2001-05-11
;  PRIOR APPLICATION NUMBER: US 60/291,311
;  PRIOR FILING DATE: 2001-05-17
;  PRIOR APPLICATION NUMBER: US 60/353,058
;  PRIOR FILING DATE: 2002-02-01
;  PRIOR APPLICATION NUMBER: US 60/361,293
;  PRIOR FILING DATE: 2002-03-04
;  NUMBER OF SEQ ID NOS: 812
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 5120
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-477-238A-1

  Query Match             100.0%;  Score 5118.4;  DB 18;  Length 5120;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 5119;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ACTAAAGCGCCGCCGCCGCGCCATGGAGCCCGAGTGAGCGCGGCGCGGGCCCGTCCGGCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ACTAAAGCGCCGCCGCCGCGCCATGGAGCCCGAGTGAGCGCGGCGCGGGCCCGTCCGGCC 60

Qy         61 GCCGGACAACATGGAGGCAGCGCCGCCCGGGCCGCCGTGGCCGCTGCTGCTGCTGCTGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCCGGACAACATGGAGGCAGCGCCGCCCGGGCCGCCGTGGCCGCTGCTGCTGCTGCTGCT 120

Qy        121 GCTGCTGCTGGCGCTGTGCGGCTGCCCGGCCCCCGCCGCGGCCTCGCCGCTCCTGCTATT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCTGCTGCTGGCGCTGTGCGGCTGCCCGGCCCCCGCCGCGGCCTCGCCGCTCCTGCTATT 180

Qy        181 TGCCAACCGCCGGGACGTACGGCTGGTGGACGCCGGCGGAGTCAAGCTGGAGTCCACCAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TGCCAACCGCCGGGACGTACGGCTGGTGGACGCCGGCGGAGTCAAGCTGGAGTCCACCAT 240

Qy        241 CGTGGTCAGCGGCCTGGAGGATGCGGCCGCAGTGGACTTCCAGTTTTCCAAGGGAGCCGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CGTGGTCAGCGGCCTGGAGGATGCGGCCGCAGTGGACTTCCAGTTTTCCAAGGGAGCCGT 300

Qy        301 GTACTGGACAGACGTGAGCGAGGAGGCCATCAAGCAGACCTACCTGAACCAGACGGGGGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GTACTGGACAGACGTGAGCGAGGAGGCCATCAAGCAGACCTACCTGAACCAGACGGGGGC 360

Qy        361 CGCCGTGCAGAACGTGGTCATCTCCGGCCTGGTCTCTCCCGACGGCCTCGCCTGCGACTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CGCCGTGCAGAACGTGGTCATCTCCGGCCTGGTCTCTCCCGACGGCCTCGCCTGCGACTG 420

Qy        421 GGTGGGCAAGAAGCTGTACTGGACGGACTCAGAGACCAACCGCATCGAGGTGGCCAACCT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GGTGGGCAAGAAGCTGTACTGGACGGACTCAGAGACCAACCGCATCGAGGTGGCCAACCT 480

Qy        481 CAATGGCACATCCCGGAAGGTGCTCTTCTGGCAGGACCTTGACCAGCCGAGGGCCATCGC 540
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Db        481 CAATGGCACATCCCGGAAGGTGCTCTTCTGGCAGGACCTTGACCAGCCGAGGGCCATCGC 540

Qy        541 CTTGGACCCCGCTCACGGGTACATGTACTGGACAGACTGGGTTGAGACGCCCCGGATTGA 600
              ||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db        541 CTTGGACCCCGCTCACGGGTACATGTACTGGACAGACTGGGGTGAGACGCCCCGGATTGA 600

Qy        601 GCGGGCAGGGATGGATGGCAGCACCCGGAAGATCATTGTGGACTCGGACATTTACTGGCC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GCGGGCAGGGATGGATGGCAGCACCCGGAAGATCATTGTGGACTCGGACATTTACTGGCC 660

Qy        661 CAATGGACTGACCATCGACCTGGAGGAGCAGAAGCTCTACTGGGCTGACGCCAAGCTCAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAATGGACTGACCATCGACCTGGAGGAGCAGAAGCTCTACTGGGCTGACGCCAAGCTCAG 720

Qy        721 CTTCATCCACCGTGCCAACCTGGACGGCTCGTTCCGGCAGAAGGTGGTGGAGGGCAGCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CTTCATCCACCGTGCCAACCTGGACGGCTCGTTCCGGCAGAAGGTGGTGGAGGGCAGCCT 780

Qy        781 GACGCACCCCTTCGCCCTGACGCTCTCCGGGGACACTCTGTACTGGACAGACTGGCAGAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACGCACCCCTTCGCCCTGACGCTCTCCGGGGACACTCTGTACTGGACAGACTGGCAGAC 840

Qy        841 CCGCTCCATCCATGCCTGCAACAAGCGCACTGGGGGGAAGAGGAAGGAGATCCTGAGTGC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CCGCTCCATCCATGCCTGCAACAAGCGCACTGGGGGGAAGAGGAAGGAGATCCTGAGTGC 900

Qy        901 CCTCTACTCACCCATGGACATCCAGGTGCTGAGCCAGGAGCGGCAGCCTTTCTTCCACAC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CCTCTACTCACCCATGGACATCCAGGTGCTGAGCCAGGAGCGGCAGCCTTTCTTCCACAC 960

Qy        961 TCGCTGTGAGGAGGACAATGGCGGCTGCTCCCACCTGTGCCTGCTGTCCCCAAGCGAGCC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TCGCTGTGAGGAGGACAATGGCGGCTGCTCCCACCTGTGCCTGCTGTCCCCAAGCGAGCC 1020

Qy       1021 TTTCTACACATGCGCCTGCCCCACGGGTGTGCAGCTGCAGGACAACGGCAGGACGTGTAA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 TTTCTACACATGCGCCTGCCCCACGGGTGTGCAGCTGCAGGACAACGGCAGGACGTGTAA 1080

Qy       1081 GGCAGGAGCCGAGGAGGTGCTGCTGCTGGCCCGGCGGACGGACCTACGGAGGATCTCGCT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 GGCAGGAGCCGAGGAGGTGCTGCTGCTGGCCCGGCGGACGGACCTACGGAGGATCTCGCT 1140

Qy       1141 GGACACGCCGGACTTCACCGACATCGTGCTGCAGGTGGACGACATCCGGCACGCCATTGC 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GGACACGCCGGACTTCACCGACATCGTGCTGCAGGTGGACGACATCCGGCACGCCATTGC 1200

Qy       1201 CATCGACTACGACCCGCTAGAGGGCTATGTCTACTGGACAGATGACGAGGTGCGGGCCAT 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 CATCGACTACGACCCGCTAGAGGGCTATGTCTACTGGACAGATGACGAGGTGCGGGCCAT 1260

Qy       1261 CCGCAGGGCGTACCTGGACGGGTCTGGGGCGCAGACGCTGGTCAACACCGAGATCAACGA 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 CCGCAGGGCGTACCTGGACGGGTCTGGGGCGCAGACGCTGGTCAACACCGAGATCAACGA 1320

Qy       1321 CCCCGATGGCATCGCGGTCGACTGGGTGGCCCGAAACCTCTACTGGACCGACACGGGCAC 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 CCCCGATGGCATCGCGGTCGACTGGGTGGCCCGAAACCTCTACTGGACCGACACGGGCAC 1380

Qy       1381 GGACCGCATCGAGGTGACGCGCCTCAACGGCACCTCCCGCAAGATCCTGGTGTCGGAGGA 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 GGACCGCATCGAGGTGACGCGCCTCAACGGCACCTCCCGCAAGATCCTGGTGTCGGAGGA 1440

Qy       1441 CCTGGACGAGCCCCGAGCCATCGCACTGCACCCCGTGATGGGCCTCATGTACTGGACAGA 1500
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Db       1441 CCTGGACGAGCCCCGAGCCATCGCACTGCACCCCGTGATGGGCCTCATGTACTGGACAGA 1500
Qy       1501 CTGGGGAGAGAACCCTAAAATCGAGTGTGCCAACTTGGATGGGCAGGAGCGGCGTGTGCT 1560
Db       1501 CTGGGGAGAGAACCCTAAAATCGAGTGTGCCAACTTGGATGGGCAGGAGCGGCGTGTGCT 1560
Qy       1561 GGTCAATGCCTCCCTCGGGTGGCCCAACGGCCTGGCCCTGGACCTGCAGGAGGGGAAGCT 1620
Db       1561 GGTCAATGCCTCCCTCGGGTGGCCCAACGGCCTGGCCCTGGACCTGCAGGAGGGGAAGCT 1620
Qy       1621 CTACTGGGGAGACGCCAAGACAGACAAGATCGAGGTGATCAATGTTGATGGGACGAAGAG 1680
Db       1621 CTACTGGGGAGACGCCAAGACAGACAAGATCGAGGTGATCAATGTTGATGGGACGAAGAG 1680
Qy       1681 GCGGACCCTCCTGGAGGACAAGCTCCCGCACATTTTCGGGTTCACGCTGCTGGGGGACTT 1740
Db       1681 GCGGACCCTCCTGGAGGACAAGCTCCCGCACATTTTCGGGTTCACGCTGCTGGGGGACTT 1740
Qy       1741 CATCTACTGGACTGACTGGCAGCGCCGCAGCATCGAGCGGGTGCACAAGGTCAAGGCCAG 1800
Db       1741 CATCTACTGGACTGACTGGCAGCGCCGCAGCATCGAGCGGGTGCACAAGGTCAAGGCCAG 1800
Qy       1801 CCGGGACGTCATCATTGACCAGCTGCCCGACCTGATGGGGCTCAAAGCTGTGAATGTGGC 1860
Db       1801 CCGGGACGTCATCATTGACCAGCTGCCCGACCTGATGGGGCTCAAAGCTGTGAATGTGGC 1860
Qy       1861 CAAGGTCGTCGGAACCAACCCGTGTGCGGACAGGAACGGGGGGTGCAGCCACCTGTGCTT 1920
Db       1861 CAAGGTCGTCGGAACCAACCCGTGTGCGGACAGGAACGGGGGGTGCAGCCACCTGTGCTT 1920
Qy       1921 CTTCACACCCCACGCAACCCGGTGTGGCTGCCCCATCGGCCTGGAGCTGCTGAGTGACAT 1980
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Qy       1981 GAAGACCTGCATCGTGCCTGAGGCCTTCTTGGTCTTCACCAGCAGAGCCGCCATCCACAG 2040
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Qy       2041 GATCTCCCTCGAGACCAATAACAACGACGTGGCCATCCCGCTCACGGGCGTCAAGGAGGC 2100
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Qy       2101 CTCAGCCCTGGACTTTGATGTGTCCAACAACCACATCTACTGGACAGACGTCAGCCTGAA 2160
Db       2101 CTCAGCCCTGGACTTTGATGTGTCCAACAACCACATCTACTGGACAGACGTCAGCCTGAA 2160
Qy       2161 GACCATCAGCCGCGCCTTCATGAACGGGAGCTCGGTGGAGCACGTGGTGGAGTTTGGCCT 2220
Db       2161 GACCATCAGCCGCGCCTTCATGAACGGGAGCTCGGTGGAGCACGTGGTGGAGTTTGGCCT 2220
Qy       2221 TGACTACCCCGAGGGCATGGCCGTTGACTGGATGGGCAAGAACCTCTACTGGGCCGACAC 2280
Db       2221 TGACTACCCCGAGGGCATGGCCGTTGACTGGATGGGCAAGAACCTCTACTGGGCCGACAC 2280
Qy       2281 TGGGACCAACAGAATCGAAGTGGCGCGGCTGGACGGGCAGTTCCGGCAAGTCCTCGTGTG 2340
Db       2281 TGGGACCAACAGAATCGAAGTGGCGCGGCTGGACGGGCAGTTCCGGCAAGTCCTCGTGTG 2340
Qy       2341 GAGGGACTTGGACAACCCGAGGTCGCTGGCCCTGGATCCCACCAAGGGCTACATCTACTG 2400
Db       2341 GAGGGACTTGGACAACCCGAGGTCGCTGGCCCTGGATCCCACCAAGGGCTACATCTACTG 2400
Qy       2401 GACCGAGTGGGGCGGCAAGCCGAGGATCGTGCGGGCCTTCATGGACGGGACCAACTGCAT 2460
Db       2401 GACCGAGTGGGGCGGCAAGCCGAGGATCGTGCGGGCCTTCATGGACGGGACCAACTGCAT 2460
Qy       2461 GACGCTGGTGGACAAGGTGGGCCGGGCCAACGACCTCACCATTGACTACGCTGACCAGCG 2520
Db       2461 GACGCTGGTGGACAAGGTGGGCCGGGCCAACGACCTCACCATTGACTACGCTGACCAGCG 2520
Qy       2521 CCTCTACTGGACCGACCTGGACACCAACATGATCGAGTCGTCCAACATGCTGGGTCAGGA 2580
Db       2521 CCTCTACTGGACCGACCTGGACACCAACATGATCGAGTCGTCCAACATGCTGGGTCAGGA 2580

Qy       2581 GCGGGTCGTGATTGCCGACGATCTCCCGCACCCGTTCGGTCTGACGCAGTACAGCGATTA 2640
Db       2581 GCGGGTCGTGATTGCCGACGATCTCCCGCACCCGTTCGGTCTGACGCAGTACAGCGATTA 2640
Qy       2641 TATCTACTGGACAGACTGGAATCTGCACAGCATTGAGCGGGCCGACAAGACTAGCGGCCG 2700
Db       2641 TATCTACTGGACAGACTGGAATCTGCACAGCATTGAGCGGGCCGACAAGACTAGCGGCCG 2700
Qy       2701 GAACCGCACCCTCATCCAGGGCCACCTGGACTTCGTGATGGACATCCTGGTGTTCCACTC 2760
Db       2701 GAACCGCACCCTCATCCAGGGCCACCTGGACTTCGTGATGGACATCCTGGTGTTCCACTC 2760
Qy       2761 CTCCCGCCAGGATGGCCTCAATGACTGTATGCACAACAACGGGCAGTGTGGGCAGCTGTG 2820
Db       2761 CTCCCGCCAGGATGGCCTCAATGACTGTATGCACAACAACGGGCAGTGTGGGCAGCTGTG 2820
Qy       2821 CCTTGCCATCCCCGGCGGCCACCGCTGCGGCTGCGCCTCACACTACACCCTGGACCCCAG 2880
Db       2821 CCTTGCCATCCCCGGCGGCCACCGCTGCGGCTGCGCCTCACACTACACCCTGGACCCCAG 2880
Qy       2881 CAGCCGCAACTGCAGCCCGCCCACCACCTTCTTGCTGTTCAGCCAGAAATCTGCCATCAG 2940
Db       2881 CAGCCGCAACTGCAGCCCGCCCACCACCTTCTTGCTGTTCAGCCAGAAATCTGCCATCAG 2940
Qy       2941 TCGGATGATCCCGGACGACCAGCACAGCCCGGATCTCATCCTGCCCCTGCATGGACTGAG 3000
Db       2941 TCGGATGATCCCGGACGACCAGCACAGCCCGGATCTCATCCTGCCCCTGCATGGACTGAG 3000
Qy       3001 GAACGTCAAAGCCATCGACTATGACCCACTGGACAAGTTCATCTACTGGGTGGATGGGCG 3060
Db       3001 GAACGTCAAAGCCATCGACTATGACCCACTGGACAAGTTCATCTACTGGGTGGATGGGCG 3060
Qy       3061 CCAGAACATCAAGCGAGCCAAGGACGACGGGACCCAGCCCTTTGTTTTGACCTCTCTGAG 3120
Db       3061 CCAGAACATCAAGCGAGCCAAGGACGACGGGACCCAGCCCTTTGTTTTGACCTCTCTGAG 3120
Qy       3121 CCAAGGCCAAAACCCAGACAGGCAGCCCCACGACCTCAGCATCGACATCTACAGCCGGAC 3180
Db       3121 CCAAGGCCAAAACCCAGACAGGCAGCCCCACGACCTCAGCATCGACATCTACAGCCGGAC 3180
Qy       3181 ACTGTTCTGGACGTGCGAGGCCACCAATACCATCAACGTCCACAGGCTGAGCGGGGAAGC 3240
Db       3181 ACTGTTCTGGACGTGCGAGGCCACCAATACCATCAACGTCCACAGGCTGAGCGGGGAAGC 3240
Qy       3241 CATGGGGGTGGTGCTGCGTGGGGACCGCGACAAGCCCAGGGCCATCGTCGTCAACGCGGA 3300
Db       3241 CATGGGGGTGGTGCTGCGTGGGGACCGCGACAAGCCCAGGGCCATCGTCGTCAACGCGGA 3300
Qy       3301 GCGAGGGTACCTGTACTTCACCAACATGCAGGACCGGGCAGCCAAGATCGAACGCGCAGC 3360
Db       3301 GCGAGGGTACCTGTACTTCACCAACATGCAGGACCGGGCAGCCAAGATCGAACGCGCAGC 3360
Qy       3361 CCTGGACGGCACCGAGCGCGAGGTCCTCTTCACCACCGGCCTCATCCGCCCTGTGGCCCT 3420
Db       3361 CCTGGACGGCACCGAGCGCGAGGTCCTCTTCACCACCGGCCTCATCCGCCCTGTGGCCCT 3420
Qy       3421 GGTGGTGGACAACACACTGGGCAAGCTGTTCTGGGTGGACGCGGACCTGAAGCGCATTGA 3480
Db       3421 GGTGGTGGACAACACACTGGGCAAGCTGTTCTGGGTGGACGCGGACCTGAAGCGCATTGA 3480
Qy       3481 GAGCTGTGACCTGTCAGGGGCCAACCGCCTGACCCTGGAGGACGCCAACATCGTGCAGCC 3540
Db       3481 GAGCTGTGACCTGTCAGGGGCCAACCGCCTGACCCTGGAGGACGCCAACATCGTGCAGCC 3540
Qy       3541 TCTGGGCCTGACCATCCTTGGCAAGCATCTCTACTGGATCGACCGCCAGCAGCAGATGAT 3600
Db       3541 TCTGGGCCTGACCATCCTTGGCAAGCATCTCTACTGGATCGACCGCCAGCAGCAGATGAT 3600
Qy       3601 CGAGCGTGTGGAGAAGACCACCGGGGACAAGCGGACTCGCATCCAGGGCCGTGTCGCCCA 3660
Db       3601 CGAGCGTGTGGAGAAGACCACCGGGGACAAGCGGACTCGCATCCAGGGCCGTGTCGCCCA 3660
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Qy       3661 CCTCACTGGCATCCATGCAGTGGAGGAAGTCAGCCTGGAGGAGTTCTCAGCCCACCCATG 3720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3661 CCTCACTGGCATCCATGCAGTGGAGGAAGTCAGCCTGGAGGAGTTCTCAGCCCACCCATG 3720

Qy       3721 TGCCCGTGACAATGGTGGCTGCTCCCACATCTGTATTGCCAAGGGTGATGGGACACCACG 3780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3721 TGCCCGTGACAATGGTGGCTGCTCCCACATCTGTATTGCCAAGGGTGATGGGACACCACG 3780

Qy       3781 GTGCTCATGCCCAGTCCACCTCGTGCTCCTGCAGAACCTGCTGACCTGTGGAGAGCCGCC 3840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3781 GTGCTCATGCCCAGTCCACCTCGTGCTCCTGCAGAACCTGCTGACCTGTGGAGAGCCGCC 3840

Qy       3841 CACCTGCTCCCCGGACCAGTTTGCATGTGCCACAGGGGAGATCGACTGTATCCCCGGGGC 3900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3841 CACCTGCTCCCCGGACCAGTTTGCATGTGCCACAGGGGAGATCGACTGTATCCCCGGGGC 3900

Qy       3901 CTGGCGCTGTGACGGCTTTCCCGAGTGCGATGACCAGAGCGACGAGGAGGGCTGCCCCGT 3960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3901 CTGGCGCTGTGACGGCTTTCCCGAGTGCGATGACCAGAGCGACGAGGAGGGCTGCCCCGT 3960

Qy       3961 GTGCTCCGCCGCCCAGTTCCCCTGCGCGCGGGGTCAGTGTGTGGACCTGCGCCTGCGCTG 4020
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Db       3961 GTGCTCCGCCGCCCAGTTCCCCTGCGCGCGGGGTCAGTGTGTGGACCTGCGCCTGCGCTG 4020

Qy       4021 CGACGGCGAGGCAGACTGTCAGGACCGCTCAGACGAGGTGGACTGTGACGCCATCTGCCT 4080
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Db       4021 CGACGGCGAGGCAGACTGTCAGGACCGCTCAGACGAGGTGGACTGTGACGCCATCTGCCT 4080

Qy       4081 GCCCAACCAGTTCCGGTGTGCGAGCGGCCAGTGTGTCCTCATCAAACAGCAGTGCGACTC 4140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4081 GCCCAACCAGTTCCGGTGTGCGAGCGGCCAGTGTGTCCTCATCAAACAGCAGTGCGACTC 4140

Qy       4141 CTTCCCCGACTGTATCGACGGCTCCGACGAGCTCATGTGTGAAATCACCAAGCCGCCCTC 4200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4141 CTTCCCCGACTGTATCGACGGCTCCGACGAGCTCATGTGTGAAATCACCAAGCCGCCCTC 4200

Qy       4201 AGACGACAGCCCGGCCCACAGCAGTGCCATCGGGCCCGTCATTGGCATCATCCTCTCTCT 4260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4201 AGACGACAGCCCGGCCCACAGCAGTGCCATCGGGCCCGTCATTGGCATCATCCTCTCTCT 4260

Qy       4261 CTTCGTCATGGGTGGTGTCTATTTTGTGTGCCAGCGCGTGGTGTGCCAGCGCTATGCGGG 4320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4261 CTTCGTCATGGGTGGTGTCTATTTTGTGTGCCAGCGCGTGGTGTGCCAGCGCTATGCGGG 4320

Qy       4321 GGCCAACGGGCCCTTCCCGCACGAGTATGTCAGCGGGACCCCGCACGTGCCCCTCAATTT 4380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4321 GGCCAACGGGCCCTTCCCGCACGAGTATGTCAGCGGGACCCCGCACGTGCCCCTCAATTT 4380

Qy       4381 CATAGCCCCGGGCGGTTCCCAGCATGGCCCCTTCACAGGCATCGCATGCGGAAAGTCCAT 4440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4381 CATAGCCCCGGGCGGTTCCCAGCATGGCCCCTTCACAGGCATCGCATGCGGAAAGTCCAT 4440

Qy       4441 GATGAGCTCCGTGAGCCTGATGGGGGGCCGGGGCGGGGTGCCCCTCTACGACCGGAACCA 4500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4441 GATGAGCTCCGTGAGCCTGATGGGGGGCCGGGGCGGGGTGCCCCTCTACGACCGGAACCA 4500

Qy       4501 CGTCACAGGGGCCTCGTCCAGCAGCTCGTCCAGCACGAAGGCCACGCTGTACCCGCCGAT 4560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4501 CGTCACAGGGGCCTCGTCCAGCAGCTCGTCCAGCACGAAGGCCACGCTGTACCCGCCGAT 4560

Qy       4561 CCTGAACCCGCCGCCCTCCCCGGCCACGGACCCCTCCCTGTACAACATGGACATGTTCTA 4620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4561 CCTGAACCCGCCGCCCTCCCCGGCCACGGACCCCTCCCTGTACAACATGGACATGTTCTA 4620

Qy       4621 CTCTTCAAACATTCCGGCCACTGCGAGACCGTACAGGCCCTACATCATTCGAGGAATGGC 4680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4621 CTCTTCAAACATTCCGGCCACTGCGAGACCGTACAGGCCCTACATCATTCGAGGAATGGC 4680

Qy       4681 GCCCCCGACGACGCCCTGCAGCACCGACGTGTGTGACAGCGACTACAGCGCCAGCCGCTG 4740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4681 GCCCCCGACGACGCCCTGCAGCACCGACGTGTGTGACAGCGACTACAGCGCCAGCCGCTG 4740

Qy       4741 GAAGGCCAGCAAGTACTACCTGGATTTGAACTCGGACTCAGACCCCTATCCACCCCCACC 4800
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4741 GAAGGCCAGCAAGTACTACCTGGATTTGAACTCGGACTCAGACCCCTATCCACCCCCACC 4800

Qy       4801 CACGCCCCACAGCCAGTACCTGTCGGCGGAGGACAGCTGCCCGCCCTCGCCCGCCACCGA 4860
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4801 CACGCCCCACAGCCAGTACCTGTCGGCGGAGGACAGCTGCCCGCCCTCGCCCGCCACCGA 4860

Qy       4861 GAGGAGCTACTTCCATCTCTTCCCGCCCCCTCCGTCCCCCTGCACGGACTCATCCTGACC 4920
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4861 GAGGAGCTACTTCCATCTCTTCCCGCCCCCTCCGTCCCCCTGCACGGACTCATCCTGACC 4920

Qy       4921 TCGGCCGGGCCACTCTGGCTTCTCTGTGCCCCTGTAAATAGTTTTAAATATGAACAAAGA 4980
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4921 TCGGCCGGGCCACTCTGGCTTCTCTGTGCCCCTGTAAATAGTTTTAAATATGAACAAAGA 4980

Qy       4981 AAAAAATATATTTTATGATTTAAAAAATAAATATAATTGGGATTTTAAAAACATGAGAAA 5040
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4981 AAAAAATATATTTTATGATTTAAAAAATAAATATAATTGGGATTTTAAAAACATGAGAAA 5040

Qy       5041 TGTGAACTGTGATGGGGTGGGCAGGGCTGGGAGAACTTTGTACAGTGGAGAAATATTTAT 5100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5041 TGTGAACTGTGATGGGGTGGGCAGGGCTGGGAGAACTTTGTACAGTGGAGAAATATTTAT 5100

Qy       5101 AAACTTAATTTTGTAAAACA 5120
             ||||||||||||||||||||
Db       5101 AAACTTAATTTTGTAAAACA 5120
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RESULT 11
US-10-680-287A-1
; Sequence 1, Application US/10680287A
; Publication No. US20040244069A1
; GENERAL INFORMATION:
; APPLICANT: Babij, Philip
; APPLICANT: Yaworsky, Paul
; APPLICANT: Bex, Frederick J. III
; APPLICANT: Bodine, Peter Van Nest
; TITLE OF INVENTION: Transgenic Animal Model of Bone Mass Modulation
; FILE REFERENCE: 032796-179
; CURRENT APPLICATION NUMBER: US/10/680,287A
; CURRENT FILING DATE: 2003-10-08
; PRIOR APPLICATION NUMBER: PCT/US02/14876
; PRIOR FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: US 60/290,071
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US 60/291,311
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: US 60/353,058
; PRIOR FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: US 60/361,293
; PRIOR FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 812
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 5120
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-680-287A-1

Query Match 100.0%; Score 5118.4; DB 18; Length 5120;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5119; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 ACTAAAGCGCCGCCGCCGCGCCATGGAGCCCGAGTGAGCGCGGCGCGGGCCCGTCCGGCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ACTAAAGCGCCGCCGCCGCGCCATGGAGCCCGAGTGAGCGCGGCGCGGGCCCGTCCGGCC 60

Qy         61 GCCGGACAACATGGAGGCAGCGCCGCCCGGGCCGCCGTGGCCGCTGCTGCTGCTGCTGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCCGGACAACATGGAGGCAGCGCCGCCCGGGCCGCCGTGGCCGCTGCTGCTGCTGCTGCT 120

Qy        121 GCTGCTGCTGGCGCTGTGCGGCTGCCCGGCCCCCGCCGCGGCCTCGCCGCTCCTGCTATT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        121 GCTGCTGCTGGCGCTGTGCGGCTGCCCGGCCCCCGCCGCGGCCTCGCCGCTCCTGCTATT 180

Qy        181 TGCCAACCGCCGGGACGTACGGCTGGTGGACGCCGGCGGAGTCAAGCTGGAGTCCACCAT 240

Db        181 TGCCAACCGCCGGGACGTACGGCTGGTGGACGCCGGCGGAGTCAAGCTGGAGTCCACCAT 240

Qy        241 CGTGGTCAGCGGCCTGGAGGATGCGGCCGCAGTGGACTTCCAGTTTTCCAAGGGAGCCGT 300

Db        241 CGTGGTCAGCGGCCTGGAGGATGCGGCCGCAGTGGACTTCCAGTTTTCCAAGGGAGCCGT 300

Qy        301 GTACTGGACAGACGTGAGCGAGGAGGCCATCAAGCAGACCTACCTGAACCAGACGGGGGC 360

Db        301 GTACTGGACAGACGTGAGCGAGGAGGCCATCAAGCAGACCTACCTGAACCAGACGGGGGC 360

Qy        361 CGCCGTGCAGAACGTGGTCATCTCCGGCCTGGTCTCTCCCGACGGCCTCGCCTGCGACTG 420

Db        361 CGCCGTGCAGAACGTGGTCATCTCCGGCCTGGTCTCTCCCGACGGCCTCGCCTGCGACTG 420

Qy        421 GGTGGGCAAGAAGCTGTACTGGACGGACTCAGAGACCAACCGCATCGAGGTGGCCAACCT 480

Db        421 GGTGGGCAAGAAGCTGTACTGGACGGACTCAGAGACCAACCGCATCGAGGTGGCCAACCT 480

Qy        481 CAATGGCACATCCCGGAAGGTGCTCTTCTGGCAGGACCTTGACCAGCCGAGGGCCATCGC 540

Db        481 CAATGGCACATCCCGGAAGGTGCTCTTCTGGCAGGACCTTGACCAGCCGAGGGCCATCGC 540

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Db        541 CTTGGACCCCGCTCACGGGTACATGTACTGGACAGACTGGGGTGAGACGCCCCGGATTGA 600

Qy        601 GCGGGCAGGGATGGATGGCAGCACCCGGAAGATCATTGTGGACTCGGACATTTACTGGCC 660

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Qy        661 CAATGGACTGACCATCGACCTGGAGGAGCAGAAGCTCTACTGGGCTGACGCCAAGCTCAG 720

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Qy        721 CTTCATCCACCGTGCCAACCTGGACGGCTCGTTCCGGCAGAAGGTGGTGGAGGGCAGCCT 780

Db        721 CTTCATCCACCGTGCCAACCTGGACGGCTCGTTCCGGCAGAAGGTGGTGGAGGGCAGCCT 780

Qy        781 GACGCACCCCTTCGCCCTGACGCTCTCCGGGGACACTCTGTACTGGACAGACTGGCAGAC 840

Db        781 GACGCACCCCTTCGCCCTGACGCTCTCCGGGGACACTCTGTACTGGACAGACTGGCAGAC 840

Qy        841 CCGCTCCATCCATGCCTGCAACAAGCGCACTGGGGGGAAGAGGAAGGAGATCCTGAGTGC 900

Db        841 CCGCTCCATCCATGCCTGCAACAAGCGCACTGGGGGGAAGAGGAAGGAGATCCTGAGTGC 900

Qy        901 CCTCTACTCACCCATGGACATCCAGGTGCTGAGCCAGGAGCGGCAGCCTTTCTTCCACAC 960

Db        901 CCTCTACTCACCCATGGACATCCAGGTGCTGAGCCAGGAGCGGCAGCCTTTCTTCCACAC 960

Qy        961 TCGCTGTGAGGAGGACAATGGCGGCTGCTCCCACCTGTGCCTGCTGTCCCCAAGCGAGCC 1020

Db        961 TCGCTGTGAGGAGGACAATGGCGGCTGCTCCCACCTGTGCCTGCTGTCCCCAAGCGAGCC 1020

Qy       1021 TTTCTACACATGCGCCTGCCCCACGGGTGTGCAGCTGCAGGACAACGGCAGGACGTGTAA 1080

Db       1021 TTTCTACACATGCGCCTGCCCCACGGGTGTGCAGCTGCAGGACAACGGCAGGACGTGTAA 1080

Qy       1081 GGCAGGAGCCGAGGAGGTGCTGCTGCTGGCCCGGCGGACGGACCTACGGAGGATCTCGCT 1140

Db       1081 GGCAGGAGCCGAGGAGGTGCTGCTGCTGGCCCGGCGGACGGACCTACGGAGGATCTCGCT 1140

Qy       1141 GGACACGCCGGACTTCACCGACATCGTGCTGCAGGTGGACGACATCCGGCACGCCATTGC 1200

Db       1141 GGACACGCCGGACTTCACCGACATCGTGCTGCAGGTGGACGACATCCGGCACGCCATTGC 1200

Qy       1201 CATCGACTACGACCCGCTAGAGGGCTATGTCTACTGGACAGATGACGAGGTGCGGGCCAT 1260

Db       1201 CATCGACTACGACCCGCTAGAGGGCTATGTCTACTGGACAGATGACGAGGTGCGGGCCAT 1260

Qy       1261 CCGCAGGGCGTACCTGGACGGGTCTGGGGCGCAGACGCTGGTCAACACCGAGATCAACGA 1320

Db       1261 CCGCAGGGCGTACCTGGACGGGTCTGGGGCGCAGACGCTGGTCAACACCGAGATCAACGA 1320

Qy       1321 CCCCGATGGCATCGCGGTCGACTGGGTGGCCCGAAACCTCTACTGGACCGACACGGGCAC 1380

Db       1321 CCCCGATGGCATCGCGGTCGACTGGGTGGCCCGAAACCTCTACTGGACCGACACGGGCAC 1380

Qy       1381 GGACCGCATCGAGGTGACGCGCCTCAACGGCACCTCCCGCAAGATCCTGGTGTCGGAGGA 1440

Db       1381 GGACCGCATCGAGGTGACGCGCCTCAACGGCACCTCCCGCAAGATCCTGGTGTCGGAGGA 1440

Qy       1441 CCTGGACGAGCCCCGAGCCATCGCACTGCACCCCGTGATGGGCCTCATGTACTGGACAGA 1500

Db       1441 CCTGGACGAGCCCCGAGCCATCGCACTGCACCCCGTGATGGGCCTCATGTACTGGACAGA 1500

Qy       1501 CTGGGGAGAGAACCCTAAAATCGAGTGTGCCAACTTGGATGGGCAGGAGCGGCGTGTGCT 1560

Db       1501 CTGGGGAGAGAACCCTAAAATCGAGTGTGCCAACTTGGATGGGCAGGAGCGGCGTGTGCT 1560

Qy       1561 GGTCAATGCCTCCCTCGGGTGGCCCAACGGCCTGGCCCTGGACCTGCAGGAGGGGAAGCT 1620

Db       1561 GGTCAATGCCTCCCTCGGGTGGCCCAACGGCCTGGCCCTGGACCTGCAGGAGGGGAAGCT 1620

Qy       1621 CTACTGGGGAGACGCCAAGACAGACAAGATCGAGGTGATCAATGTTGATGGGACGAAGAG 1680

Db       1621 CTACTGGGGAGACGCCAAGACAGACAAGATCGAGGTGATCAATGTTGATGGGACGAAGAG 1680

Qy       1681 GCGGACCCTCCTGGAGGACAAGCTCCCGCACATTTTCGGGTTCACGCTGCTGGGGGACTT 1740

Db       1681 GCGGACCCTCCTGGAGGACAAGCTCCCGCACATTTTCGGGTTCACGCTGCTGGGGGACTT 1740

Qy       1741 CATCTACTGGACTGACTGGCAGCGCCGCAGCATCGAGCGGGTGCACAAGGTCAAGGCCAG 1800

Db       1741 CATCTACTGGACTGACTGGCAGCGCCGCAGCATCGAGCGGGTGCACAAGGTCAAGGCCAG 1800

Qy       1801 CCGGGACGTCATCATTGACCAGCTGCCCGACCTGATGGGGCTCAAAGCTGTGAATGTGGC 1860

Db       1801 CCGGGACGTCATCATTGACCAGCTGCCCGACCTGATGGGGCTCAAAGCTGTGAATGTGGC 1860

Qy       1861 CAAGGTCGTCGGAACCAACCCGTGTGCGGACAGGAACGGGGGGTGCAGCCACCTGTGCTT 1920

Db       1861 CAAGGTCGTCGGAACCAACCCGTGTGCGGACAGGAACGGGGGGTGCAGCCACCTGTGCTT 1920

Qy       1921 CTTCACACCCCACGCAACCCGGTGTGGCTGCCCCATCGGCCTGGAGCTGCTGAGTGACAT 1980

Db       1921 CTTCACACCCCACGCAACCCGGTGTGGCTGCCCCATCGGCCTGGAGCTGCTGAGTGACAT 1980

Qy       1981 GAAGACCTGCATCGTGCCTGAGGCCTTCTTGGTCTTCACCAGCAGAGCCGCCATCCACAG 2040

Db       1981 GAAGACCTGCATCGTGCCTGAGGCCTTCTTGGTCTTCACCAGCAGAGCCGCCATCCACAG 2040

Qy       2041 GATCTCCCTCGAGACCAATAACAACGACGTGGCCATCCCGCTCACGGGCGTCAAGGAGGC 2100

Db       2041 GATCTCCCTCGAGACCAATAACAACGACGTGGCCATCCCGCTCACGGGCGTCAAGGAGGC 2100

Qy       2101 CTCAGCCCTGGACTTTGATGTGTCCAACAACCACATCTACTGGACAGACGTCAGCCTGAA 2160

Db       2101 CTCAGCCCTGGACTTTGATGTGTCCAACAACCACATCTACTGGACAGACGTCAGCCTGAA 2160

Qy       2161 GACCATCAGCCGCGCCTTCATGAACGGGAGCTCGGTGGAGCACGTGGTGGAGTTTGGCCT 2220

Db       2161 GACCATCAGCCGCGCCTTCATGAACGGGAGCTCGGTGGAGCACGTGGTGGAGTTTGGCCT 2220

Qy       2221 TGACTACCCCGAGGGCATGGCCGTTGACTGGATGGGCAAGAACCTCTACTGGGCCGACAC 2280

Db       2221 TGACTACCCCGAGGGCATGGCCGTTGACTGGATGGGCAAGAACCTCTACTGGGCCGACAC 2280

Qy       2281 TGGGACCAACAGAATCGAAGTGGCGCGGCTGGACGGGCAGTTCCGGCAAGTCCTCGTGTG 2340

Db       2281 TGGGACCAACAGAATCGAAGTGGCGCGGCTGGACGGGCAGTTCCGGCAAGTCCTCGTGTG 2340
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Qy       2341 GAGGGACTTGGACAACCCGAGGTCGCTGGCCCTGGATCCCACCAAGGGCTACATCTACTG 2400
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2341 GAGGGACTTGGACAACCCGAGGTCGCTGGCCCTGGATCCCACCAAGGGCTACATCTACTG 2400

Qy       2401 GACCGAGTGGGGCGGCAAGCCGAGGATCGTGCGGGCCTTCATGGACGGGACCAACTGCAT 2460
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2401 GACCGAGTGGGGCGGCAAGCCGAGGATCGTGCGGGCCTTCATGGACGGGACCAACTGCAT 2460

Qy       2461 GACGCTGGTGGACAAGGTGGGCCGGGCCAACGACCTCACCATTGACTACGCTGACCAGCG 2520
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Db       2461 GACGCTGGTGGACAAGGTGGGCCGGGCCAACGACCTCACCATTGACTACGCTGACCAGCG 2520

Qy       2521 CCTCTACTGGACCGACCTGGACACCAACATGATCGAGTCGTCCAACATGCTGGGTCAGGA 2580
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Db       2521 CCTCTACTGGACCGACCTGGACACCAACATGATCGAGTCGTCCAACATGCTGGGTCAGGA 2580

Qy       2581 GCGGGTCGTGATTGCCGACGATCTCCCGCACCCGTTCGGTCTGACGCAGTACAGCGATTA 2640
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2581 GCGGGTCGTGATTGCCGACGATCTCCCGCACCCGTTCGGTCTGACGCAGTACAGCGATTA 2640

Qy       2641 TATCTACTGGACAGACTGGAATCTGCACAGCATTGAGCGGGCCGACAAGACTAGCGGCCG 2700
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2641 TATCTACTGGACAGACTGGAATCTGCACAGCATTGAGCGGGCCGACAAGACTAGCGGCCG 2700

Qy       2701 GAACCGCACCCTCATCCAGGGCCACCTGGACTTCGTGATGGACATCCTGGTGTTCCACTC 2760
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Db       2701 GAACCGCACCCTCATCCAGGGCCACCTGGACTTCGTGATGGACATCCTGGTGTTCCACTC 2760

Qy       2761 CTCCCGCCAGGATGGCCTCAATGACTGTATGCACAACAACGGGCAGTGTGGGCAGCTGTG 2820
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Db       2761 CTCCCGCCAGGATGGCCTCAATGACTGTATGCACAACAACGGGCAGTGTGGGCAGCTGTG 2820

Qy       2821 CCTTGCCATCCCCGGCGGCCACCGCTGCGGCTGCGCCTCACACTACACCCTGGACCCCAG 2880
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2821 CCTTGCCATCCCCGGCGGCCACCGCTGCGGCTGCGCCTCACACTACACCCTGGACCCCAG 2880

Qy       2881 CAGCCGCAACTGCAGCCCGCCCACCACCTTCTTGCTGTTCAGCCAGAAATCTGCCATCAG 2940
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Db       2881 CAGCCGCAACTGCAGCCCGCCCACCACCTTCTTGCTGTTCAGCCAGAAATCTGCCATCAG 2940

Qy       2941 TCGGATGATCCCGGACGACCAGCACAGCCCGGATCTCATCCTGCCCCTGCATGGACTGAG 3000
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2941 TCGGATGATCCCGGACGACCAGCACAGCCCGGATCTCATCCTGCCCCTGCATGGACTGAG 3000

Qy       3001 GAACGTCAAAGCCATCGACTATGACCCACTGGACAAGTTCATCTACTGGGTGGATGGGCG 3060
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3001 GAACGTCAAAGCCATCGACTATGACCCACTGGACAAGTTCATCTACTGGGTGGATGGGCG 3060

Qy       3061 CCAGAACATCAAGCGAGCCAAGGACGACGGGACCCAGCCCTTTGTTTTGACCTCTCTGAG 3120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3061 CCAGAACATCAAGCGAGCCAAGGACGACGGGACCCAGCCCTTTGTTTTGACCTCTCTGAG 3120

Qy       3121 CCAAGGCCAAAACCCAGACAGGCAGCCCCACGACCTCAGCATCGACATCTACAGCCGGAC 3180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3121 CCAAGGCCAAAACCCAGACAGGCAGCCCCACGACCTCAGCATCGACATCTACAGCCGGAC 3180

Qy       3181 ACTGTTCTGGACGTGCGAGGCCACCAATACCATCAACGTCCACAGGCTGAGCGGGGAAGC 3240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3181 ACTGTTCTGGACGTGCGAGGCCACCAATACCATCAACGTCCACAGGCTGAGCGGGGAAGC 3240

Qy       3241 CATGGGGGTGGTGCTGCGTGGGGACCGCGACAAGCCCAGGGCCATCGTCGTCAACGCGGA 3300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3241 CATGGGGGTGGTGCTGCGTGGGGACCGCGACAAGCCCAGGGCCATCGTCGTCAACGCGGA 3300

Qy       3301 GCGAGGGTACCTGTACTTCACCAACATGCAGGACCGGGCAGCCAAGATCGAACGCGCAGC 3360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3301 GCGAGGGTACCTGTACTTCACCAACATGCAGGACCGGGCAGCCAAGATCGAACGCGCAGC 3360

Qy       3361 CCTGGACGGCACCGAGCGCGAGGTCCTCTTCACCACCGGCCTCATCCGCCCTGTGGCCCT 3420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3361 CCTGGACGGCACCGAGCGCGAGGTCCTCTTCACCACCGGCCTCATCCGCCCTGTGGCCCT 3420

Qy       3421 GGTGGTGGACAACACACTGGGCAAGCTGTTCTGGGTGGACGCGGACCTGAAGCGCATTGA 3480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3421 GGTGGTGGACAACACACTGGGCAAGCTGTTCTGGGTGGACGCGGACCTGAAGCGCATTGA 3480

Qy       3481 GAGCTGTGACCTGTCAGGGGCCAACCGCCTGACCCTGGAGGACGCCAACATCGTGCAGCC 3540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3481 GAGCTGTGACCTGTCAGGGGCCAACCGCCTGACCCTGGAGGACGCCAACATCGTGCAGCC 3540

Qy       3541 TCTGGGCCTGACCATCCTTGGCAAGCATCTCTACTGGATCGACCGCCAGCAGCAGATGAT 3600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3541 TCTGGGCCTGACCATCCTTGGCAAGCATCTCTACTGGATCGACCGCCAGCAGCAGATGAT 3600

Qy       3601 CGAGCGTGTGGAGAAGACCACCGGGGACAAGCGGACTCGCATCCAGGGCCGTGTCGCCCA 3660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3601 CGAGCGTGTGGAGAAGACCACCGGGGACAAGCGGACTCGCATCCAGGGCCGTGTCGCCCA 3660

Qy       3661 CCTCACTGGCATCCATGCAGTGGAGGAAGTCAGCCTGGAGGAGTTCTCAGCCCACCCATG 3720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3661 CCTCACTGGCATCCATGCAGTGGAGGAAGTCAGCCTGGAGGAGTTCTCAGCCCACCCATG 3720

Qy       3721 TGCCCGTGACAATGGTGGCTGCTCCCACATCTGTATTGCCAAGGGTGATGGGACACCACG 3780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3721 TGCCCGTGACAATGGTGGCTGCTCCCACATCTGTATTGCCAAGGGTGATGGGACACCACG 3780

Qy       3781 GTGCTCATGCCCAGTCCACCTCGTGCTCCTGCAGAACCTGCTGACCTGTGGAGAGCCGCC 3840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3781 GTGCTCATGCCCAGTCCACCTCGTGCTCCTGCAGAACCTGCTGACCTGTGGAGAGCCGCC 3840

Qy       3841 CACCTGCTCCCCGGACCAGTTTGCATGTGCCACAGGGGAGATCGACTGTATCCCCGGGGC 3900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3841 CACCTGCTCCCCGGACCAGTTTGCATGTGCCACAGGGGAGATCGACTGTATCCCCGGGGC 3900

Qy       3901 CTGGCGCTGTGACGGCTTTCCCGAGTGCGATGACCAGAGCGACGAGGAGGGCTGCCCCGT 3960
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Db       3901 CTGGCGCTGTGACGGCTTTCCCGAGTGCGATGACCAGAGCGACGAGGAGGGCTGCCCCGT 3960

Qy       3961 GTGCTCCGCCGCCCAGTTCCCCTGCGCGCGGGGTCAGTGTGTGGACCTGCGCCTGCGCTG 4020
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Qy       4141 CTTCCCCGACTGTATCGACGGCTCCGACGAGCTCATGTGTGAAATCACCAAGCCGCCCTC 4200
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Db       4141 CTTCCCCGACTGTATCGACGGCTCCGACGAGCTCATGTGTGAAATCACCAAGCCGCCCTC 4200

Qy       4201 AGACGACAGCCCGGCCCACAGCAGTGCCATCGGGCCCGTCATTGGCATCATCCTCTCTCT 4260
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Db       4201 AGACGACAGCCCGGCCCACAGCAGTGCCATCGGGCCCGTCATTGGCATCATCCTCTCTCT 4260

Qy       4261 CTTCGTCATGGGTGGTGTCTATTTTGTGTGCCAGCGCGTGGTGTGCCAGCGCTATGCGGG 4320
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Db       4261 CTTCGTCATGGGTGGTGTCTATTTTGTGTGCCAGCGCGTGGTGTGCCAGCGCTATGCGGG 4320

Qy       4321 GGCCAACGGGCCCTTCCCGCACGAGTATGTCAGCGGGACCCCGCACGTGCCCCTCAATTT 4380
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Qy       4381 CATAGCCCCGGGCGGTTCCCAGCATGGCCCCTTCACAGGCATCGCATGCGGAAAGTCCAT 4440
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Db       4381 CATAGCCCCGGGCGGTTCCCAGCATGGCCCCTTCACAGGCATCGCATGCGGAAAGTCCAT 4440

Qy       4441 GATGAGCTCCGTGAGCCTGATGGGGGGCCGGGGCGGGGTGCCCCTCTACGACCGGAACCA 4500
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Db       4441 GATGAGCTCCGTGAGCCTGATGGGGGGCCGGGGCGGGGTGCCCCTCTACGACCGGAACCA 4500

Qy       4501 CGTCACAGGGGCCTCGTCCAGCAGCTCGTCCAGCACGAAGGCCACGCTGTACCCGCCGAT 4560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       4501 CGTCACAGGGGCCTCGTCCAGCAGCTCGTCCAGCACGAAGGCCACGCTGTACCCGCCGAT 4560

Qy       4561 CCTGAACCCGCCGCCCTCCCCGGCCACGGACCCCTCCCTGTACAACATGGACATGTTCTA 4620
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Db       4561 CCTGAACCCGCCGCCCTCCCCGGCCACGGACCCCTCCCTGTACAACATGGACATGTTCTA 4620

Qy       4621 CTCTTCAAACATTCCGGCCACTGCGAGACCGTACAGGCCCTACATCATTCGAGGAATGGC 4680
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Db       4621 CTCTTCAAACATTCCGGCCACTGCGAGACCGTACAGGCCCTACATCATTCGAGGAATGGC 4680

Qy       4681 GCCCCCGACGACGCCCTGCAGCACCGACGTGTGTGACAGCGACTACAGCGCCAGCCGCTG 4740
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Db       4681 GCCCCCGACGACGCCCTGCAGCACCGACGTGTGTGACAGCGACTACAGCGCCAGCCGCTG 4740

Qy       4741 GAAGGCCAGCAAGTACTACCTGGATTTGAACTCGGACTCAGACCCCTATCCACCCCCACC 4800
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Qy       4801 CACGCCCCACAGCCAGTACCTGTCGGCGGAGGACAGCTGCCCGCCCTCGCCCGCCACCGA 4860
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Qy       4861 GAGGAGCTACTTCCATCTCTTCCCGCCCCCTCCGTCCCCCTGCACGGACTCATCCTGACC 4920
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4861 GAGGAGCTACTTCCATCTCTTCCCGCCCCCTCCGTCCCCCTGCACGGACTCATCCTGACC 4920

Qy       4921 TCGGCCGGGCCACTCTGGCTTCTCTGTGCCCCTGTAAATAGTTTTAAATATGAACAAAGA 4980
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Db       4921 TCGGCCGGGCCACTCTGGCTTCTCTGTGCCCCTGTAAATAGTTTTAAATATGAACAAAGA 4980

Qy       4981 AAAAAATATATTTTATGATTTAAAAAATAAATATAATTGGGATTTTAAAAACATGAGAAA 5040
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Db       4981 AAAAAATATATTTTATGATTTAAAAAATAAATATAATTGGGATTTTAAAAACATGAGAAA 5040

Qy       5041 TGTGAACTGTGATGGGGTGGGCAGGGCTGGGAGAACTTTGTACAGTGGAGAAATATTTAT 5100
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RESULT 12
US-10-477-173-1
; Sequence 1, Application US/10477173
; Publication No. US20050070699A1
; GENERAL INFORMATION:
;  APPLICANT: Genome Therapeutics Corporation and
;  APPLICANT:  Allen, Kristina M.
;  APPLICANT:  Yaworsky, Paul
;  APPLICANT:  Morales, Arturo J.
;  APPLICANT:  Graham, James R.
;  APPLICANT:  Anisowicz, Anthony
;  APPLICANT:  Liu, Wei
;  TITLE OF INVENTION: HBM Variants that Modulate Bone Mass and Lipid Levels
;  FILE REFERENCE: 032796-135
;  CURRENT APPLICATION NUMBER: US/10/477,173
;  CURRENT FILING DATE:  2003-11-10
;  PRIOR APPLICATION NUMBER: US 60/290,071
;  PRIOR FILING DATE: 2001-05-11
;  PRIOR APPLICATION NUMBER: US 60/291,311
;  PRIOR FILING DATE: 2001-05-17
;  PRIOR APPLICATION NUMBER: US 60/353,058
;  PRIOR FILING DATE: 2002-02-01
;  PRIOR APPLICATION NUMBER: US 60/361,293
;  PRIOR FILING DATE: 2002-03-04
;  NUMBER OF SEQ ID NOS: 1086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 5120
;   TYPE: DNA
;   ORGANISM: Homo sapiens
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US-10-477-173-1

  Query Match             100.0%;  Score 5118.4;  DB 19;  Length 5120;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 5119;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ACTAAAGCGCCGCCGCCGCGCCATGGAGCCCGAGTGAGCGCGGCGCGGGCCCGTCCGGCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy         61 GCCGGACAACATGGAGGCAGCGCCGCCCGGGCCGCCGTGGCCGCTGCTGCTGCTGCTGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        121 GCTGCTGCTGGCGCTGTGCGGCTGCCCGGCCCCCGCCGCGGCCTCGCCGCTCCTGCTATT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        181 TGCCAACCGCCGGGACGTACGGCTGGTGGACGCCGGCGGAGTCAAGCTGGAGTCCACCAT 240
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Db        181 TGCCAACCGCCGGGACGTACGGCTGGTGGACGCCGGCGGAGTCAAGCTGGAGTCCACCAT 240

Qy        241 CGTGGTCAGCGGCCTGGAGGATGCGGCCGCAGTGGACTTCCAGTTTTCCAAGGGAGCCGT 300
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Qy        301 GTACTGGACAGACGTGAGCGAGGAGGCCATCAAGCAGACCTACCTGAACCAGACGGGGGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GTACTGGACAGACGTGAGCGAGGAGGCCATCAAGCAGACCTACCTGAACCAGACGGGGGC 360

Qy        361 CGCCGTGCAGAACGTGGTCATCTCCGGCCTGGTCTCTCCCGACGGCCTCGCCTGCGACTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CGCCGTGCAGAACGTGGTCATCTCCGGCCTGGTCTCTCCCGACGGCCTCGCCTGCGACTG 420

Qy        421 GGTGGGCAAGAAGCTGTACTGGACGGACTCAGAGACCAACCGCATCGAGGTGGCCAACCT 480
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Qy        481 CAATGGCACATCCCGGAAGGTGCTCTTCTGGCAGGACCTTGACCAGCCGAGGGCCATCGC 540
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Db        481 CAATGGCACATCCCGGAAGGTGCTCTTCTGGCAGGACCTTGACCAGCCGAGGGCCATCGC 540

Qy        541 CTTGGACCCCGCTCACGGGTACATGTACTGGACAGACTGGGTTGAGACGCCCCGGATTGA 600
              |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        541 CTTGGACCCCGCTCACGGGTACATGTACTGGACAGACTGGGGTGAGACGCCCCGGATTGA 600

Qy        601 GCGGGCAGGGATGGATGGCAGCACCCGGAAGATCATTGTGGACTCGGACATTTACTGGCC 660
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Db        601 GCGGGCAGGGATGGATGGCAGCACCCGGAAGATCATTGTGGACTCGGACATTTACTGGCC 660

Qy        661 CAATGGACTGACCATCGACCTGGAGGAGCAGAAGCTCTACTGGGCTGACGCCAAGCTCAG 720
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Qy        721 CTTCATCCACCGTGCCAACCTGGACGGCTCGTTCCGGCAGAAGGTGGTGGAGGGCAGCCT 780
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Db        721 CTTCATCCACCGTGCCAACCTGGACGGCTCGTTCCGGCAGAAGGTGGTGGAGGGCAGCCT 780

Qy        781 GACGCACCCCTTCGCCCTGACGCTCTCCGGGGACACTCTGTACTGGACAGACTGGCAGAC 840
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Db        781 GACGCACCCCTTCGCCCTGACGCTCTCCGGGGACACTCTGTACTGGACAGACTGGCAGAC 840

Qy        841 CCGCTCCATCCATGCCTGCAACAAGCGCACTGGGGGGAAGAGGAAGGAGATCCTGAGTGC 900
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Db        841 CCGCTCCATCCATGCCTGCAACAAGCGCACTGGGGGGAAGAGGAAGGAGATCCTGAGTGC 900

Qy        901 CCTCTACTCACCCATGGACATCCAGGTGCTGAGCCAGGAGCGGCAGCCTTTCTTCCACAC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CCTCTACTCACCCATGGACATCCAGGTGCTGAGCCAGGAGCGGCAGCCTTTCTTCCACAC 960

Qy        961 TCGCTGTGAGGAGGACAATGGCGGCTGCTCCCACCTGTGCCTGCTGTCCCCAAGCGAGCC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TCGCTGTGAGGAGGACAATGGCGGCTGCTCCCACCTGTGCCTGCTGTCCCCAAGCGAGCC 1020
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Qy       1021 TTTCTACACATGCGCCTGCCCCACGGGTGTGCAGCTGCAGGACAACGGCAGGACGTGTAA 1080
Db       1021 TTTCTACACATGCGCCTGCCCCACGGGTGTGCAGCTGCAGGACAACGGCAGGACGTGTAA 1080

Qy       1081 GGCAGGAGCCGAGGAGGTGCTGCTGCTGGCCCGGCGGACGGACCTACGGAGGATCTCGCT 1140
Db       1081 GGCAGGAGCCGAGGAGGTGCTGCTGCTGGCCCGGCGGACGGACCTACGGAGGATCTCGCT 1140

Qy       1141 GGACACGCCGGACTTCACCGACATCGTGCTGCAGGTGGACGACATCCGGCACGCCATTGC 1200
Db       1141 GGACACGCCGGACTTCACCGACATCGTGCTGCAGGTGGACGACATCCGGCACGCCATTGC 1200

Qy       1201 CATCGACTACGACCCGCTAGAGGGCTATGTCTACTGGACAGATGACGAGGTGCGGGCCAT 1260
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Qy       1261 CCGCAGGGCGTACCTGGACGGGTCTGGGGCGCAGACGCTGGTCAACACCGAGATCAACGA 1320
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Qy       1321 CCCCGATGGCATCGCGGTCGACTGGGTGGCCCGAAACCTCTACTGGACCGACACGGGCAC 1380
Db       1321 CCCCGATGGCATCGCGGTCGACTGGGTGGCCCGAAACCTCTACTGGACCGACACGGGCAC 1380

Qy       1381 GGACCGCATCGAGGTGACGCGCCTCAACGGCACCTCCCGCAAGATCCTGGTGTCGGAGGA 1440
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Qy       1441 CCTGGACGAGCCCCGAGCCATCGCACTGCACCCCGTGATGGGCCTCATGTACTGGACAGA 1500
Db       1441 CCTGGACGAGCCCCGAGCCATCGCACTGCACCCCGTGATGGGCCTCATGTACTGGACAGA 1500

Qy       1501 CTGGGGAGAGAACCCTAAAATCGAGTGTGCCAACTTGGATGGGCAGGAGCGGCGTGTGCT 1560
Db       1501 CTGGGGAGAGAACCCTAAAATCGAGTGTGCCAACTTGGATGGGCAGGAGCGGCGTGTGCT 1560

Qy       1561 GGTCAATGCCTCCCTCGGGTGGCCCAACGGCCTGGCCCTGGACCTGCAGGAGGGGAAGCT 1620
Db       1561 GGTCAATGCCTCCCTCGGGTGGCCCAACGGCCTGGCCCTGGACCTGCAGGAGGGGAAGCT 1620

Qy       1621 CTACTGGGGAGACGCCAAGACAGACAAGATCGAGGTGATCAATGTTGATGGGACGAAGAG 1680
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Qy       1681 GCGGACCCTCCTGGAGGACAAGCTCCCGCACATTTTCGGGTTCACGCTGCTGGGGGACTT 1740
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Qy       1741 CATCTACTGGACTGACTGGCAGCGCCGCAGCATCGAGCGGGTGCACAAGGTCAAGGCCAG 1800
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Qy       1801 CCGGGACGTCATCATTGACCAGCTGCCCGACCTGATGGGGCTCAAAGCTGTGAATGTGGC 1860
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Qy       1861 CAAGGTCGTCGGAACCAACCCGTGTGCGGACAGGAACGGGGGGGTGCAGCCACCTGTGCTT 1920
Db       1861 CAAGGTCGTCGGAACCAACCCGTGTGCGGACAGGAACGGGGGGTGCAGCCACCTGTGCTT 1920

Qy       1921 CTTCACACCCCACGCAACCCGGTGTGGCTGCCCCATCGGCCTGGAGCTGCTGAGTGACAT 1980
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Qy       1981 GAAGACCTGCATCGTGCCTGAGGCCTTCTTGGTCTTCACCAGCAGAGCCGCCATCCACAG 2040
Db       1981 GAAGACCTGCATCGTGCCTGAGGCCTTCTTGGTCTTCACCAGCAGAGCCGCCATCCACAG 2040

Qy       2041 GATCTCCCTCGAGACCAATAACAACGACGTGGCCATCCCGCTCACGGGCGTCAAGGAGGC 2100
Db       2041 GATCTCCCTCGAGACCAATAACAACGACGTGGCCATCCCGCTCACGGGCGTCAAGGAGGC 2100

Qy       2101 CTCAGCCCTGGACTTTGATGTGTCCAACAACCACATCTACTGGACAGACGTCAGCCTGAA 2160
Db       2101 CTCAGCCCTGGACTTTGATGTGTCCAACAACCACATCTACTGGACAGACGTCAGCCTGAA 2160

Qy       2161 GACCATCAGCCGCGCCTTCATGAACGGGAGCTCGGTGGAGCACGTGGTGGAGTTTGGCCT 2220
Db       2161 GACCATCAGCCGCGCCTTCATGAACGGGAGCTCGGTGGAGCACGTGGTGGAGTTTGGCCT 2220

Qy       2221 TGACTACCCCGAGGGCATGGCCGTTGACTGGATGGGCAAGAACCTCTACTGGGCCGACAC 2280
Db       2221 TGACTACCCCGAGGGCATGGCCGTTGACTGGATGGGCAAGAACCTCTACTGGGCCGACAC 2280

Qy       2281 TGGGACCAACAGAATCGAAGTGGCGCGGCTGGACGGGCAGTTCCGGCAAGTCCTCGTGTG 2340
Db       2281 TGGGACCAACAGAATCGAAGTGGCGCGGCTGGACGGGCAGTTCCGGCAAGTCCTCGTGTG 2340

Qy       2341 GAGGGACTTGGACAACCCGAGGTCGCTGGCCCTGGATCCCACCAAGGGCTACATCTACTG 2400
Db       2341 GAGGGACTTGGACAACCCGAGGTCGCTGGCCCTGGATCCCACCAAGGGCTACATCTACTG 2400

Qy       2401 GACCGAGTGGGGCGGCAAGCCGAGGATCGTGCGGGCCTTCATGGACGGGACCAACTGCAT 2460
Db       2401 GACCGAGTGGGGCGGCAAGCCGAGGATCGTGCGGGCCTTCATGGACGGGACCAACTGCAT 2460

Qy       2461 GACGCTGGTGGACAAGGTGGGCCGGGCCAACGACCTCACCATTGACTACGCTGACCAGCG 2520
Db       2461 GACGCTGGTGGACAAGGTGGGCCGGGCCAACGACCTCACCATTGACTACGCTGACCAGCG 2520

Qy       2521 CCTCTACTGGACCGACCTGGACACCAACATGATCGAGTCGTCCAACATGCTGGGTCAGGA 2580
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Qy       2581 GCGGGTCGTGATTGCCGACGATCTCCCGCACCCGTTCGGTCTGACGCAGTACAGCGATTA 2640
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Qy       2641 TATCTACTGGACAGACTGGAATCTGCACAGCATTGAGCGGGCCGACAAGACTAGCGGCCG 2700
Db       2641 TATCTACTGGACAGACTGGAATCTGCACAGCATTGAGCGGGCCGACAAGACTAGCGGCCG 2700

Qy       2701 GAACCGCACCCTCATCCAGGGCCACCTGGACTTCGTGATGGACATCCTGGTGTTCCACTC 2760
Db       2701 GAACCGCACCCTCATCCAGGGCCACCTGGACTTCGTGATGGACATCCTGGTGTTCCACTC 2760

Qy       2761 CTCCCGCCAGGATGGCCTCAATGACTGTATGCACAACAACGGGCAGTGTGGGCAGCTGTG 2820
Db       2761 CTCCCGCCAGGATGGCCTCAATGACTGTATGCACAACAACGGGCAGTGTGGGCAGCTGTG 2820

Qy       2821 CCTTGCCATCCCCGGCGGCCACCGCTGCGGCTGCGCCTCACACTACACCCTGGACCCCAG 2880
Db       2821 CCTTGCCATCCCCGGCGGCCACCGCTGCGGCTGCGCCTCACACTACACCCTGGACCCCAG 2880

Qy       2881 CAGCCGCAACTGCAGCCCGCCCACCACCTTCTTGCTGTTCAGCCAGAAATCTGCCATCAG 2940
Db       2881 CAGCCGCAACTGCAGCCCGCCCACCACCTTCTTGCTGTTCAGCCAGAAATCTGCCATCAG 2940

Qy       2941 TCGGATGATCCCGGACGACCAGCACAGCCCGGATCTCATCCTGCCCCTGCATGGACTGAG 3000
Db       2941 TCGGATGATCCCGGACGACCAGCACAGCCCGGATCTCATCCTGCCCCTGCATGGACTGAG 3000

Qy       3001 GAACGTCAAAGCCATCGACTATGACCCACTGGACAAGTTCATCTACTGGGTGGATGGGCG 3060
Db       3001 GAACGTCAAAGCCATCGACTATGACCCACTGGACAAGTTCATCTACTGGGTGGATGGGCG 3060

Qy       3061 CCAGAACATCAAGCGAGCCAAGGACGACGGGACCCAGCCCTTTGTTTTGACCTCTCTGAG 3120
Db       3061 CCAGAACATCAAGCGAGCCAAGGACGACGGGACCCAGCCCTTTGTTTTGACCTCTCTGAG 3120

Qy       3121 CCAAGGCCAAAACCCAGACAGGCAGCCCCACGACCTCAGCATCGACATCTACAGCCGGAC 3180
Db       3121 CCAAGGCCAAAACCCAGACAGGCAGCCCCACGACCTCAGCATCGACATCTACAGCCGGAC 3180

Qy       3181 ACTGTTCTGGACGTGCGAGGCCACCAATACCATCAACGTCCACAGGCTGAGCGGGGAAGC 3240
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Db       3181 ACTGTTCTGGACGTGCGAGGCCACCAATACCATCAACGTCCACAGGCTGAGCGGGGAAGC 3240

Qy       3241 CATGGGGGTGGTGCTGCGTGGGGACCGCGACAAGCCCAGGGCCATCGTCGTCAACGCGGA 3300
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Db       3241 CATGGGGGTGGTGCTGCGTGGGGACCGCGACAAGCCCAGGGCCATCGTCGTCAACGCGGA 3300

Qy       3301 GCGAGGGTACCTGTACTTCACCAACATGCAGGACCGGGCAGCCAAGATCGAACGCGCAGC 3360
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Db       3301 GCGAGGGTACCTGTACTTCACCAACATGCAGGACCGGGCAGCCAAGATCGAACGCGCAGC 3360

Qy       3361 CCTGGACGGCACCGAGCGCGAGGTCCTCTTCACCACCGGCCTCATCCGCCCTGTGGCCCT 3420
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Db       3361 CCTGGACGGCACCGAGCGCGAGGTCCTCTTCACCACCGGCCTCATCCGCCCTGTGGCCCT 3420

Qy       3421 GGTGGTGGACAACACACTGGGCAAGCTGTTCTGGGTGGACGCGGACCTGAAGCGCATTGA 3480
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Db       3421 GGTGGTGGACAACACACTGGGCAAGCTGTTCTGGGTGGACGCGGACCTGAAGCGCATTGA 3480

Qy       3481 GAGCTGTGACCTGTCAGGGGCCAACCGCCTGACCCTGGAGGACGCCAACATCGTGCAGCC 3540
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Db       3481 GAGCTGTGACCTGTCAGGGGCCAACCGCCTGACCCTGGAGGACGCCAACATCGTGCAGCC 3540

Qy       3541 TCTGGGCCTGACCATCCTTGGCAAGCATCTCTACTGGATCGACCGCCAGCAGCAGATGAT 3600
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Qy       3601 CGAGCGTGTGGAGAAGACCACCGGGGACAAGCGGACTCGCATCCAGGGCCGTGTCGCCCA 3660
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Qy       3661 CCTCACTGGCATCCATGCAGTGGAGGAAGTCAGCCTGGAGGAGTTCTCAGCCCACCCATG 3720
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Db       3661 CCTCACTGGCATCCATGCAGTGGAGGAAGTCAGCCTGGAGGAGTTCTCAGCCCACCCATG 3720

Qy       3721 TGCCCGTGACAATGGTGGCTGCTCCCACATCTGTATTGCCAAGGGTGATGGGACACCACG 3780
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Db       3721 TGCCCGTGACAATGGTGGCTGCTCCCACATCTGTATTGCCAAGGGTGATGGGACACCACG 3780

Qy       3781 GTGCTCATGCCCAGTCCACCTCGTGCTCCTGCAGAACCTGCTGACCTGTGGAGAGCCGCC 3840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3781 GTGCTCATGCCCAGTCCACCTCGTGCTCCTGCAGAACCTGCTGACCTGTGGAGAGCCGCC 3840

Qy       3841 CACCTGCTCCCCGGACCAGTTTGCATGTGCCACAGGGGAGATCGACTGTATCCCCGGGGC 3900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3841 CACCTGCTCCCCGGACCAGTTTGCATGTGCCACAGGGGAGATCGACTGTATCCCCGGGGC 3900

Qy       3901 CTGGCGCTGTGACGGCTTTCCCGAGTGCGATGACCAGAGCGACGAGGAGGGCTGCCCCGT 3960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3901 CTGGCGCTGTGACGGCTTTCCCGAGTGCGATGACCAGAGCGACGAGGAGGGCTGCCCCGT 3960

Qy       3961 GTGCTCCGCCGCCCAGTTCCCCTGCGCGCGGGGTCAGTGTGTGGACCTGCGCCTGCGCTG 4020
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Db       3961 GTGCTCCGCCGCCCAGTTCCCCTGCGCGCGGGGTCAGTGTGTGGACCTGCGCCTGCGCTG 4020

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Qy       4081 GCCCAACCAGTTCCGGTGTGCGAGCGGCCAGTGTGTCCTCATCAAACAGCAGTGCGACTC 4140
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Db       4081 GCCCAACCAGTTCCGGTGTGCGAGCGGCCAGTGTGTCCTCATCAAACAGCAGTGCGACTC 4140

Qy       4141 CTTCCCCGACTGTATCGACGGCTCCGACGAGCTCATGTGTGAAATCACCAAGCCGCCCTC 4200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4141 CTTCCCCGACTGTATCGACGGCTCCGACGAGCTCATGTGTGAAATCACCAAGCCGCCCTC 4200

Qy       4201 AGACGACAGCCCGGCCCACAGCAGTGCCATCGGGCCCGTCATTGGCATCATCCTCTCTCT 4260
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Db       4201 AGACGACAGCCCGGCCCACAGCAGTGCCATCGGGCCCGTCATTGGCATCATCCTCTCTCT 4260

Qy       4261 CTTCGTCATGGGTGGTGTCTATTTTGTGTGCCAGCGCGTGGTGTGCCAGCGCTATGCGGG 4320
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Db       4261 CTTCGTCATGGGTGGTGTCTATTTTGTGTGCCAGCGCGTGGTGTGCCAGCGCTATGCGGG 4320

Qy       4321 GGCCAACGGGCCCTTCCCGCACGAGTATGTCAGCGGGACCCCGCACGTGCCCCTCAATTT 4380
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Qy       4381 CATAGCCCCGGGCGGTTCCCAGCATGGCCCCTTCACAGGCATCGCATGCGGAAAGTCCAT 4440
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Qy       4441 GATGAGCTCCGTGAGCCTGATGGGGGGCCGGGGCGGGGTGCCCCTCTACGACCGGAACCA 4500
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Qy       4501 CGTCACAGGGGCCTCGTCCAGCAGCTCGTCCAGCACGAAGGCCACGCTGTACCCGCCGAT 4560
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Qy       4561 CCTGAACCCGCCGCCCTCCCCGGCCACGGACCCCTCCCTGTACAACATGGACATGTTCTA 4620
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Db       4561 CCTGAACCCGCCGCCCTCCCCGGCCACGGACCCCTCCCTGTACAACATGGACATGTTCTA 4620

Qy       4621 CTCTTCAAACATTCCGGCCACTGCGAGACCGTACAGGCCCTACATCATTCGAGGAATGGC 4680
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Db       4621 CTCTTCAAACATTCCGGCCACTGCGAGACCGTACAGGCCCTACATCATTCGAGGAATGGC 4680

Qy       4681 GCCCCCGACGACGCCCTGCAGCACCGACGTGTGTGACAGCGACTACAGCGCCAGCCGCTG 4740
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Db       4681 GCCCCCGACGACGCCCTGCAGCACCGACGTGTGTGACAGCGACTACAGCGCCAGCCGCTG 4740

Qy       4741 GAAGGCCAGCAAGTACTACCTGGATTTGAACTCGGACTCAGACCCCTATCCACCCCCACC 4800
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4741 GAAGGCCAGCAAGTACTACCTGGATTTGAACTCGGACTCAGACCCCTATCCACCCCCACC 4800

Qy       4801 CACGCCCCACAGCCAGTACCTGTCGGCGGAGGACAGCTGCCCGCCCTCGCCCGCCACCGA 4860
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4801 CACGCCCCACAGCCAGTACCTGTCGGCGGAGGACAGCTGCCCGCCCTCGCCCGCCACCGA 4860

Qy       4861 GAGGAGCTACTTCCATCTCTTCCCGCCCCCTCCGTCCCCCTGCACGGACTCATCCTGACC 4920
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Db       4861 GAGGAGCTACTTCCATCTCTTCCCGCCCCCTCCGTCCCCCTGCACGGACTCATCCTGACC 4920

Qy       4921 TCGGCCGGGCCACTCTGGCTTCTCTGTGCCCCTGTAAATAGTTTTAAATATGAACAAAGA 4980
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             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4981 AAAAAATATATTTTATGATTTAAAAAATAAATATAATTGGGATTTTAAAAACATGAGAAA 5040

Qy       5041 TGTGAACTGTGATGGGGTGGGCAGGGCTGGGAGAACTTTGTACAGTGGAGAAATATTTAT 5100
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Db       5041 TGTGAACTGTGATGGGGTGGGCAGGGCTGGGAGAACTTTGTACAGTGGAGAAATATTTAT 5100

Qy       5101 AAACTTAATTTTGTAAAACA 5120
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Db       5101 AAACTTAATTTTGTAAAACA 5120
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RESULT 13
US-10-477-238A-806
; Sequence 806, Application US/10477238A
; Publication No. US20040221326A1
; GENERAL INFORMATION:
; APPLICANT: Babij, Philip
; APPLICANT: Yaworsky, Paul
; APPLICANT: Bex, Frederick J. III
; APPLICANT: Bodine, Peter Van Nest
; TITLE OF INVENTION: Transgenic Animal Model of Bone Mass Modulation
; FILE REFERENCE: 032796-212
; CURRENT APPLICATION NUMBER: US/10/477,238A
; CURRENT FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: US 60/290,071

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;  PRIOR FILING DATE: 2001-05-11
;  PRIOR APPLICATION NUMBER: US 60/291,311
;  PRIOR FILING DATE: 2001-05-17
;  PRIOR APPLICATION NUMBER: US 60/353,058
;  PRIOR FILING DATE: 2002-02-01
;  PRIOR APPLICATION NUMBER: US 60/361,293
;  PRIOR FILING DATE: 2002-03-04
;  NUMBER OF SEQ ID NOS: 812
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 806
;   LENGTH: 5278
;   TYPE: DNA
;   ORGANISM: Mouse
US-10-477-238A-806

  Query Match             99.9%;  Score 5116.8;  DB 18;  Length 5278;
  Best Local Similarity   100.0%;  Pred. No. 0;
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Db        570 CTTGGACCCCGCTCACGGGTACATGTACTGGACAGACTGGGTTGAGACGCCCCGGATTGA 629

Qy        601 GCGGGCAGGGATGGATGGCAGCACCCGGAAGATCATTGTGGACTCGGACATTTACTGGCC 660
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Qy        661 CAATGGACTGACCATCGACCTGGAGGAGCAGAAGCTCTACTGGGCTGACGCCAAGCTCAG 720
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Qy        721 CTTCATCCACCGTGCCAACCTGGACGGCTCGTTCCGGCAGAAGGTGGTGGAGGGCAGCCT 780
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Qy        781 GACGCACCCCTTCGCCCTGACGCTCTCCGGGGACACTCTGTACTGGACAGACTGGCAGAC 840
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Db        810 GACGCACCCCTTCGCCCTGACGCTCTCCGGGGACACTCTGTACTGGACAGACTGGCAGAC 869

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Db        870 CCGCTCCATCCATGCCTGCAACAAGCGCACTGGGGGGAAGAGGAAGGAGATCCTGAGTGC 929

Qy        901 CCTCTACTCACCCATGGACATCCAGGTGCTGAGCCAGGAGCGGCAGCCTTTCTTCCACAC 960
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Qy       1021 TTTCTACACATGCGCCTGCCCCACGGGTGTGCAGCTGCAGGACAACGGCAGGACGTGTAA 1080
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Qy       1081 GGCAGGAGCCGAGGAGGTGCTGCTGCTGGCCCGGCGGACGGACCTACGGAGGATCTCGCT 1140
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Db       1110 GGCAGGAGCCGAGGAGGTGCTGCTGCTGGCCCGGCGGACGGACCTACGGAGGATCTCGCT 1169

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Db       1170 GGACACGCCGGACTTCACCGACATCGTGCTGCAGGTGGACGACATCCGGCACGCCATTGC 1229

Qy       1201 CATCGACTACGACCCGCTAGAGGGCTATGTCTACTGGACAGATGACGAGGTGCGGGCCAT 1260
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Db       1230 CATCGACTACGACCCGCTAGAGGGCTATGTCTACTGGACAGATGACGAGGTGCGGGCCAT 1289

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Qy       1441 CCTGGACGAGCCCCGAGCCATCGCACTGCACCCCGTGATGGGCCTCATGTACTGGACAGA 1500
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Qy       1501 CTGGGGAGAGAACCCTAAAATCGAGTGTGCCAACTTGGATGGGCAGGAGCGGCGTGTGCT 1560
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Db       1530 CTGGGGAGAGAACCCTAAAATCGAGTGTGCCAACTTGGATGGGCAGGAGCGGCGTGTGCT 1589

Qy       1561 GGTCAATGCCTCCCTCGGGTGGCCCAACGGCCTGGCCCTGGACCTGCAGGAGGGGAAGCT 1620
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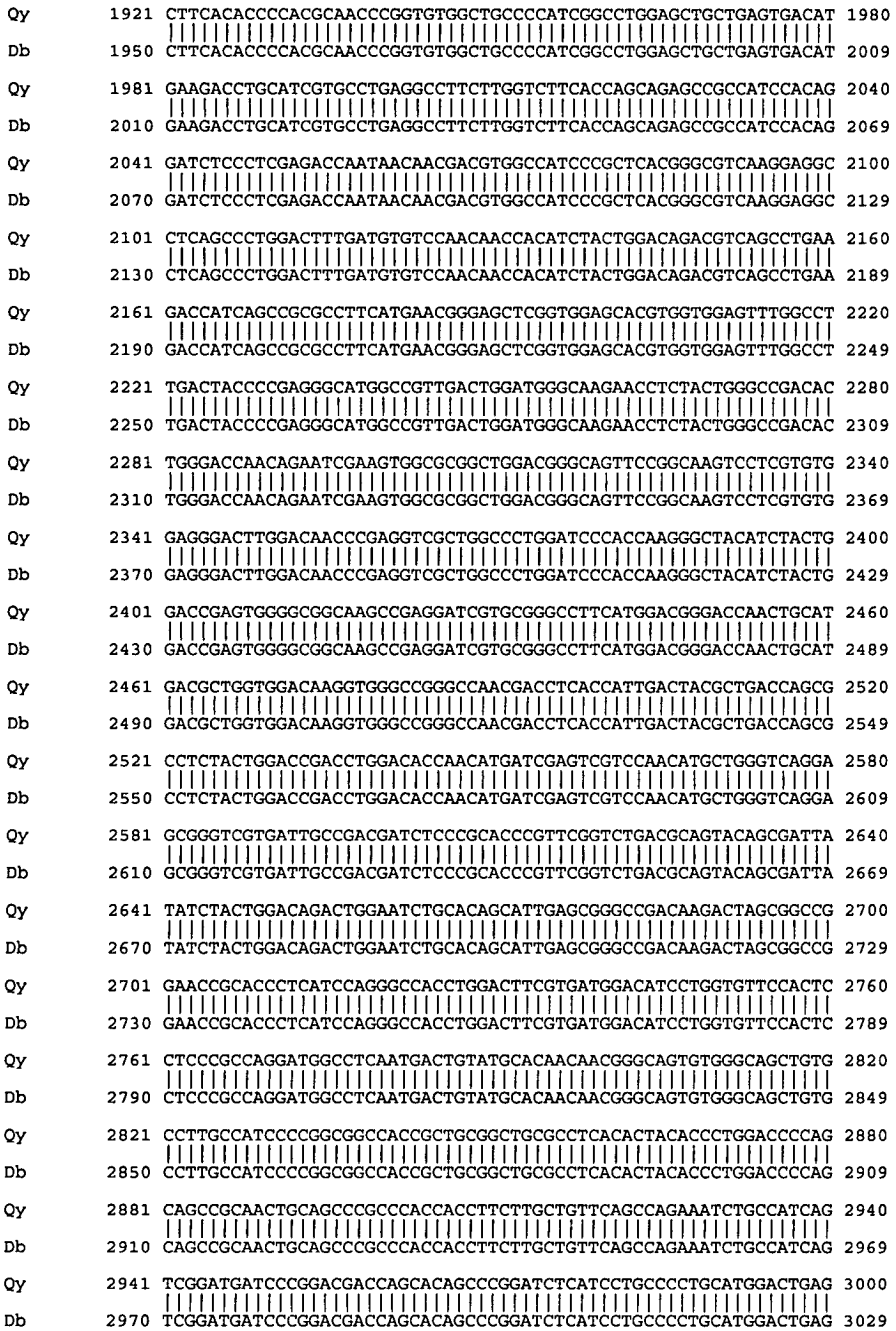
Qy       1621 CTACTGGGGAGACGCCAAGACAGACAAGATCGAGGTGATCAATGTTGATGGGACGAAGAG 1680
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Db       1650 CTACTGGGGAGACGCCAAGACAGACAAGATCGAGGTGATCAATGTTGATGGGACGAAGAG 1709

Qy       1681 GCGGACCCTCCTGGAGGACAAGCTCCCGCACATTTTCGGGTTCACGCTGCTGGGGGACTT 1740
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Db       1710 GCGGACCCTCCTGGAGGACAAGCTCCCGCACATTTTCGGGTTCACGCTGCTGGGGGACTT 1769

Qy       1741 CATCTACTGGACTGACTGGCAGCGCCGCAGCATCGAGCGGGTGCACAAGGTCAAGGCCAG 1800
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Db       1770 CATCTACTGGACTGACTGGCAGCGCCGCAGCATCGAGCGGGTGCACAAGGTCAAGGCCAG 1829

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Db       1830 CCGGGACGTCATCATTGACCAGCTGCCCGACCTGATGGGGCTCAAAGCTGTGAATGTGGC 1889

Qy       1861 CAAGGTCGTCGGAACCAACCCGTGTGCGGACAGGAACGGGGGGGTGCAGCCACCTGTGCTT 1920
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1890 CAAGGTCGTCGGAACCAACCCGTGTGCGGACAGGAACGGGGGGGTGCAGCCACCTGTGCTT 1949
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Db 1950 CTTCACACCCCACGCAACCCGGTGTGGCTGCCCCATCGGCCTGGAGCTGCTGAGTGACAT 2009
Qy 1981 GAAGACCTGCATCGTGCCTGAGGCCTTCTTGGTCTTCACCAGCAGAGCCGCCATCCACAG 2040
Db 2010 GAAGACCTGCATCGTGCCTGAGGCCTTCTTGGTCTTCACCAGCAGAGCCGCCATCCACAG 2069
Qy 2041 GATCTCCCTCGAGACCAATAACAACGACGTGGCCATCCCGCTCACGGGCGTCAAGGAGGC 2100
Db 2070 GATCTCCCTCGAGACCAATAACAACGACGTGGCCATCCCGCTCACGGGCGTCAAGGAGGC 2129
Qy 2101 CTCAGCCCTGGACTTTGATGTGTCCAACAACCACATCTACTGGACAGACGTCAGCCTGAA 2160
Db 2130 CTCAGCCCTGGACTTTGATGTGTCCAACAACCACATCTACTGGACAGACGTCAGCCTGAA 2189
Qy 2161 GACCATCAGCCGCGCCTTCATGAACGGGAGCTCGGTGGAGCACGTGGTGGAGTTTGGCCT 2220
Db 2190 GACCATCAGCCGCGCCTTCATGAACGGGAGCTCGGTGGAGCACGTGGTGGAGTTTGGCCT 2249
Qy 2221 TGACTACCCCGAGGGCATGGCCGTTGACTGGATGGGCAAGAACCTCTACTGGGCCGACAC 2280
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RESULT 14

US-10-680-287A-806
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; Publication No. US20040244069A1
; GENERAL INFORMATION:
; APPLICANT: Babij, Philip
; APPLICANT: Yaworsky, Paul
; APPLICANT: Bex, Frederick J. III
; APPLICANT: Bodine, Peter Van Nest
; TITLE OF INVENTION: Transgenic Animal Model of Bone Mass Modulation
; FILE REFERENCE: 032796-179
; CURRENT APPLICATION NUMBER: US/10/680,287A
; CURRENT FILING DATE: 2003-10-08
; PRIOR APPLICATION NUMBER: PCT/US02/14876
; PRIOR FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: US 60/290,071
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US 60/291,311
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: US 60/353,058
; PRIOR FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: US 60/361,293
; PRIOR FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 812
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 806
; LENGTH: 5278
; TYPE: DNA
; ORGANISM: Mouse
US-10-680-287A-806

Query Match 99.9%; Score 5116.8; DB 18; Length 5278;
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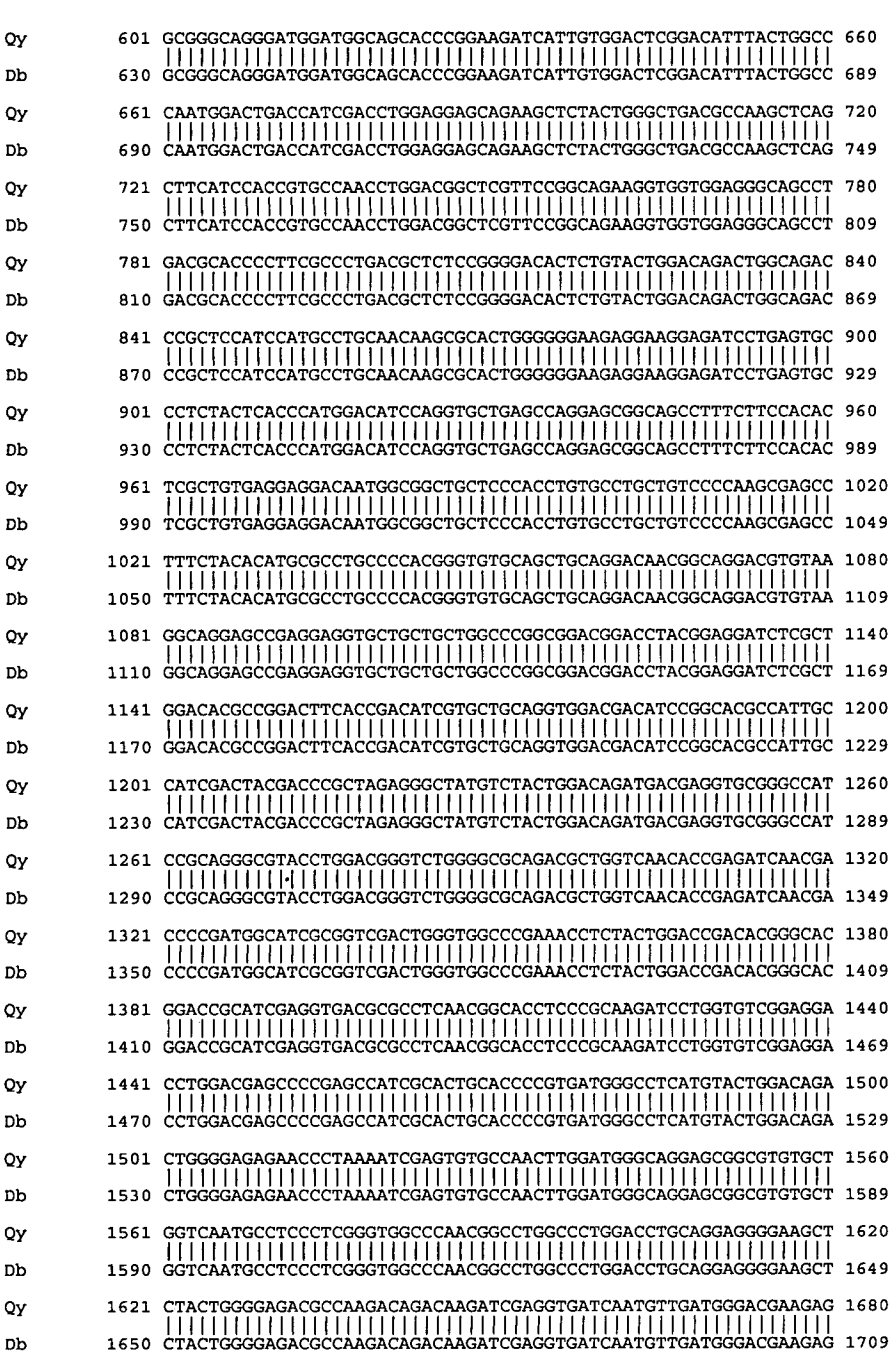
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Db      3690 CCTCACTGGCATCCATGCAGTGGAGGAAGTCAGCCTGGAGGAGTTCTCAGCCCACCCATG 3749
Qy      3721 TGCCCGTGACAATGGTGGCTGCTCCCACATCTGTATTGCCAAGGGTGATGGGACACCACG 3780
Db      3750 TGCCCGTGACAATGGTGGCTGCTCCCACATCTGTATTGCCAAGGGTGATGGGACACCACG 3809
Qy      3781 GTGCTCATGCCCAGTCCACCTCGTGCTCCTGCAGAACCTGCTGACCTGTGGAGAGCCGCC 3840
Db      3810 GTGCTCATGCCCAGTCCACCTCGTGCTCCTGCAGAACCTGCTGACCTGTGGAGAGCCGCC 3869
Qy      3841 CACCTGCTCCCCGGACCAGTTTGCATGTGCCACAGGGGAGATCGACTGTATCCCCGGGGC 3900
Db      3870 CACCTGCTCCCCGGACCAGTTTGCATGTGCCACAGGGGAGATCGACTGTATCCCCGGGGC 3929
Qy      3901 CTGGCGCTGTGACGGCTTTCCCGAGTGCGATGACCAGAGCGACGAGGAGGGCTGCCCCGT 3960
Db      3930 CTGGCGCTGTGACGGCTTTCCCGAGTGCGATGACCAGAGCGACGAGGAGGGCTGCCCCGT 3989
Qy      3961 GTGCTCCGCCGCCCAGTTCCCCTGCGCGCGGGGTCAGTGTGTGGACCTGCGCCTGCGCTG 4020
Db      3990 GTGCTCCGCCGCCCAGTTCCCCTGCGCGCGGGGTCAGTGTGTGGACCTGCGCCTGCGCTG 4049
Qy      4021 CGACGGCGAGGCAGACTGTCAGGACCGCTCAGACGAGGTGGACTGTGACGCCATCTGCCT 4080
Db      4050 CGACGGCGAGGCAGACTGTCAGGACCGCTCAGACGAGGCGGACTGTGACGCCATCTGCCT 4109
Qy      4081 GCCCAACCAGTTCCGGTGTGCGAGCGGCCAGTGTGTCCTCATCAAACAGCAGTGCGACTC 4140
Db      4110 GCCCAACCAGTTCCGGTGTGCGAGCGGCCAGTGTGTCCTCATCAAACAGCAGTGCGACTC 4169
Qy      4141 CTTCCCCGACTGTATCGACGGCTCCGACGAGCTCATGTGTGAAATCACCAAGCCGCCCTC 4200
Db      4170 CTTCCCCGACTGTATCGACGGCTCCGACGAGCTCATGTGTGAAATCACCAAGCCGCCCTC 4229
Qy      4201 AGACGACAGCCCGGCCCACAGCAGTGCCATCGGGCCCGTCATTGGCATCATCCTCTCTCT 4260
Db      4230 AGACGACAGCCCGGCCCACAGCAGTGCCATCGGGCCCGTCATTGGCATCATCCTCTCTCT 4289
Qy      4261 CTTCGTCATGGGTGGTGTCTATTTTGTGTGCCAGCGCGTGGTGTGCCAGCGCTATGCGGG 4320
Db      4290 CTTCGTCATGGGTGGTGTCTATTTTGTGTGCCAGCGCGTGGTGTGCCAGCGCTATGCGGG 4349
Qy      4321 GGCCAACGGGCCCTTCCCGCACGAGTATGTCAGCGGGACCCCGCACGTGCCCCTCAATTT 4380
Db      4350 GGCCAACGGGCCCTTCCCGCACGAGTATGTCAGCGGGACCCCGCACGTGCCCCTCAATTT 4409
Qy      4381 CATAGCCCCGGGCGGTTCCCAGCATGGCCCCTTCACAGGCATCGCATGCGGAAAGTCCAT 4440
Db      4410 CATAGCCCCGGGCGGTTCCCAGCATGGCCCCTTCACAGGCATCGCATGCGGAAAGTCCAT 4469
Qy      4441 GATGAGCTCCGTGAGCCTGATGGGGGGCCGGGGCGGGGTGCCCCCTCTACGACCGGAACCA 4500
Db      4470 GATGAGCTCCGTGAGCCTGATGGGGGGCCGGGGCGGGGTGCCCCCTCTACGACCGGAACCA 4529
Qy      4501 CGTCACAGGGGCCTCGTCCAGCAGCTCGTCCAGCACGAAGGCCACGCTGTACCCGCCGAT 4560
Db      4530 CGTCACAGGGGCCTCGTCCAGCAGCTCGTCCAGCACGAAGGCCACGCTGTACCCGCCGAT 4589
Qy      4561 CCTGAACCCGCCGCCCTCCCCGGCCACGGACCCCTCCCTGTACAACATGGACATGTTCTA 4620
Db      4590 CCTGAACCCGCCGCCCTCCCCGGCCACGGACCCCTCCCTGTACAACATGGACATGTTCTA 4649
Qy      4621 CTCTTCAAACATTCCGGCCACTGCGAGACCGTACAGGCCCTACATCATTCGAGGAATGGC 4680
Db      4650 CTCTTCAAACATTCCGGCCACTGCGAGACCGTACAGGCCCTACATCATTCGAGGAATGGC 4709
Qy      4681 GCCCCCGACGACGCCCTGCAGCACCGACGTGTGTGACAGCGACTACAGCGCCAGCCGCTG 4740
Db      4710 GCCCCCGACGACGCCCTGCAGCACCGACGTGTGTGACAGCGACTACAGCGCCAGCCGCTG 4769
Qy      4741 GAAGGCCAGCAAGTACTACCTGGATTTGAACTCGGACTCAGACCCCTATCCACCCCCACC 4800
Db      4770 GAAGGCCAGCAAGTACTACCTGGATTTGAACTCGGACTCAGACCCCTATCCACCCCCACC 4829
Qy      4801 CACGCCCCACAGCCAGTACCTGTCGGCGGAGGACAGCTGCCCGCCCTCGCCCGCCACCGA 4860
Db      4830 CACGCCCCACAGCCAGTACCTGTCGGCGGAGGACAGCTGCCCGCCCTCGCCCGCCACCGA 4889
Qy      4861 GAGGAGCTACTTCCATCTCTTCCCGCCCCCTCCGTCCCCCTGCACGGACTCATCCTGACC 4920
Db      4890 GAGGAGCTACTTCCATCTCTTCCCGCCCCCTCCGTCCCCCTGCACGGACTCATCCTGACC 4949
Qy      4921 TCGGCCGGGCCACTCTGGCTTCTCTGTGCCCCTGTAAATAGTTTTAAATATGAACAAAGA 4980
Db      4950 TCGGCCGGGCCACTCTGGCTTCTCTGTGCCCCTGTAAATAGTTTTAAATATGAACAAAGA 5009
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Qy       4981 AAAAAATATATTTTATGATTTAAAAAATAAATATAATTGGGATTTTAAAAACATGAGAAA 5040
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5010 AAAAAATATATTTTATGATTTAAAAAATAAATATAATTGGGATTTTAAAAACATGAGAAA 5069

Qy       5041 TGTGAACTGTGATGGGGTGGGCAGGGCTGGGAGAACTTTGTACAGTGGAGAAATATTTAT 5100
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Db       5070 TGTGAACTGTGATGGGGTGGGCAGGGCTGGGAGAACTTTGTACAGTGGAGAAATATTTAT 5129

Qy       5101 AAACTTAATTTTGTAAAACA 5120
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Db       5130 AAACTTAATTTTGTAAAACA 5149


RESULT 15
US-10-477-173-759
; Sequence 759, Application US/10477173
; Publication No. US20050070699A1
; GENERAL INFORMATION:
;  APPLICANT: Genome Therapeutics Corporation and
;  APPLICANT:  Allen, Kristina M.
;  APPLICANT:  Yaworsky, Paul
;  APPLICANT:  Morales, Arturo J.
;  APPLICANT:  Graham, James R.
;  APPLICANT:  Anisowicz, Anthony
;  APPLICANT:  Liu, Wei
;  TITLE OF INVENTION: HBM Variants that Modulate Bone Mass and Lipid Levels
;  FILE REFERENCE: 032796-135
;  CURRENT APPLICATION NUMBER: US/10/477,173
;  CURRENT FILING DATE:  2003-11-10
;  PRIOR APPLICATION NUMBER: US 60/290,071
;  PRIOR FILING DATE: 2001-05-11
;  PRIOR APPLICATION NUMBER: US 60/291,311
;  PRIOR FILING DATE: 2001-05-17
;  PRIOR APPLICATION NUMBER: US 60/353,058
;  PRIOR FILING DATE: 2002-02-01
;  PRIOR APPLICATION NUMBER: US 60/361,293
;  PRIOR FILING DATE: 2002-03-04
;  NUMBER OF SEQ ID NOS: 1086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 759
;   LENGTH: 5278
;   TYPE: DNA
;   ORGANISM: Mouse
US-10-477-173-759

  Query Match             99.9%;  Score 5116.8;  DB 19;  Length 5278;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 5118;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ACTAAAGCGCCGCCGCCGCGCCATGGAGCCCGAGTGAGCGCGGCGCGGGCCCGTCCGGCC 60
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Db         30 ACTAAAGCGCCGCCGCCGCGCCATGGAGCCCGAGTGAGCGCGGCGCGGGCCCGTCCGGCC 89

Qy         61 GCCGGACAACATGGAGGCAGCGCCGCCCGGGCCGCCGTGGCCGCTGCTGCTGCTGCTGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         90 GCCGGACAACATGGAGGCAGCGCCGCCCGGGCCGCCGTGGCCGCTGCTGCTGCTGCTGCT 149

Qy        121 GCTGCTGCTGGCGCTGTGCGGCTGCCCGGCCCCCGCCGCGGCCTCGCCGCTCCTGCTATT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        150 GCTGCTGCTGGCGCTGTGCGGCTGCCCGGCCCCCGCCGCGGCCTCGCCGCTCCTGCTATT 209

Qy        181 TGCCAACCGCCGGGACGTACGGCTGGTGGACGCCGGCGGAGTCAAGCTGGAGTCCACCAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        210 TGCCAACCGCCGGGACGTACGGCTGGTGGACGCCGGCGGAGTCAAGCTGGAGTCCACCAT 269

Qy        241 CGTGGTCAGCGGCCTGGAGGATGCGGCCGCAGTGGACTTCCAGTTTTCCAAGGGAGCCGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        270 CGTGGTCAGCGGCCTGGAGGATGCGGCCGCAGTGGACTTCCAGTTTTCCAAGGGAGCCGT 329

Qy        301 GTACTGGACAGACGTGAGCGAGGAGGCCATCAAGCAGACCTACCTGAACCAGACGGGGGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        330 GTACTGGACAGACGTGAGCGAGGAGGCCATCAAGCAGACCTACCTGAACCAGACGGGGGC 389

Qy        361 CGCCGTGCAGAACGTGGTCATCTCCGGCCTGGTCTCTCCCGACGGCCTCGCCTGCGACTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        390 CGCCGTGCAGAACGTGGTCATCTCCGGCCTGGTCTCTCCCGACGGCCTCGCCTGCGACTG 449

Qy        421 GGTGGGCAAGAAGCTGTACTGGACGGACTCAGAGACCAACCGCATCGAGGTGGCCAACCT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        450 GGTGGGCAAGAAGCTGTACTGGACGGACTCAGAGACCAACCGCATCGAGGTGGCCAACCT 509

Qy        481 CAATGGCACATCCCGGAAGGTGCTCTTCTGGCAGGACCTTGACCAGCCGAGGGCCATCGC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        510 CAATGGCACATCCCGGAAGGTGCTCTTCTGGCAGGACCTTGACCAGCCGAGGGCCATCGC 569

Qy        541 CTTGGACCCCGCTCACGGGTACATGTACTGGACAGACTGGGTTGAGACGCCCCGGATTGA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        570 CTTGGACCCCGCTCACGGGTACATGTACTGGACAGACTGGGTTGAGACGCCCCGGATTGA 629

Qy        601 GCGGGCAGGGATGGATGGCAGCACCCGGAAGATCATTGTGGACTCGGACATTTACTGGCC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        630 GCGGGCAGGGATGGATGGCAGCACCCGGAAGATCATTGTGGACTCGGACATTTACTGGCC 689

Qy        661 CAATGGACTGACCATCGACCTGGAGGAGCAGAAGCTCTACTGGGCTGACGCCAAGCTCAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        690 CAATGGACTGACCATCGACCTGGAGGAGCAGAAGCTCTACTGGGCTGACGCCAAGCTCAG 749

Qy        721 CTTCATCCACCGTGCCAACCTGGACGGCTCGTTCCGGCAGAAGGTGGTGGAGGGCAGCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        750 CTTCATCCACCGTGCCAACCTGGACGGCTCGTTCCGGCAGAAGGTGGTGGAGGGCAGCCT 809

Qy        781 GACGCACCCCTTCGCCCTGACGCTCTCCGGGGACACTCTGTACTGGACAGACTGGCAGAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        810 GACGCACCCCTTCGCCCTGACGCTCTCCGGGGACACTCTGTACTGGACAGACTGGCAGAC 869

Qy        841 CCGCTCCATCCATGCCTGCAACAAGCGCACTGGGGGGAAGAGGAAGGAGATCCTGAGTGC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        870 CCGCTCCATCCATGCCTGCAACAAGCGCACTGGGGGGAAGAGGAAGGAGATCCTGAGTGC 929

Qy        901 CCTCTACTCACCCATGGACATCCAGGTGCTGAGCCAGGAGCGGCAGCCTTTCTTCCACAC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        930 CCTCTACTCACCCATGGACATCCAGGTGCTGAGCCAGGAGCGGCAGCCTTTCTTCCACAC 989

Qy        961 TCGCTGTGAGGAGGACAATGGCGGCTGCTCCCACCTGTGCCTGCTGTCCCCAAGCGAGCC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        990 TCGCTGTGAGGAGGACAATGGCGGCTGCTCCCACCTGTGCCTGCTGTCCCCAAGCGAGCC 1049

Qy       1021 TTTCTACACATGCGCCTGCCCCACGGGTGTGCAGCTGCAGGACAACGGCAGGACGTGTAA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1050 TTTCTACACATGCGCCTGCCCCACGGGTGTGCAGCTGCAGGACAACGGCAGGACGTGTAA 1109

Qy       1081 GGCAGGAGCCGAGGAGGTGCTGCTGCTGGCCCGGCGGACGGACCTACGGAGGATCTCGCT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1110 GGCAGGAGCCGAGGAGGTGCTGCTGCTGGCCCGGCGGACGGACCTACGGAGGATCTCGCT 1169

Qy       1141 GGACACGCCGGACTTCACCGACATCGTGCTGCAGGTGGACGACATCCGGCACGCCATTGC 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1170 GGACACGCCGGACTTCACCGACATCGTGCTGCAGGTGGACGACATCCGGCACGCCATTGC 1229

Qy       1201 CATCGACTACGACCCGCTAGAGGGCTATGTCTACTGGACAGATGACGAGGTGCGGGCCAT 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1230 CATCGACTACGACCCGCTAGAGGGCTATGTCTACTGGACAGATGACGAGGTGCGGGCCAT 1289

Qy       1261 CCGCAGGGCGTACCTGGACGGGTCTGGGGCGCAGACGCTGGTCAACACCGAGATCAACGA 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1290 CCGCAGGGCGTACCTGGACGGGTCTGGGGCGCAGACGCTGGTCAACACCGAGATCAACGA 1349

Qy       1321 CCCCGATGGCATCGCGGTCGACTGGGTGGCCCGAAACCTCTACTGGACCGACACGGGCAC 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1350 CCCCGATGGCATCGCGGTCGACTGGGTGGCCCGAAACCTCTACTGGACCGACACGGGCAC 1409

Qy       1381 GGACCGCATCGAGGTGACGCGCCTCAACGGCACCTCCCGCAAGATCCTGGTGTCGGAGGA 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1410 GGACCGCATCGAGGTGACGCGCCTCAACGGCACCTCCCGCAAGATCCTGGTGTCGGAGGA 1469
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Qy      1441 CCTGGACGAGCCCCCGAGCCATCGCACTGCACCCCGTGATGGGCCTCATGTACTGGACAGA 1500
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Db      1470 CCTGGACGAGCCCCGAGCCATCGCACTGCACCCCGTGATGGGCCTCATGTACTGGACAGA 1529

Qy      1501 CTGGGGAGAGAACCCTAAAATCGAGTGTGCCAACTTGGATGGGCAGGAGCGGCGTGTGCT 1560
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Db      1530 CTGGGGAGAGAACCCTAAAATCGAGTGTGCCAACTTGGATGGGCAGGAGCGGCGTGTGCT 1589

Qy      1561 GGTCAATGCCTCCCTCGGGTGGCCCAACGGCCTGGCCCTGGACCTGCAGGAGGGGAAGCT 1620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1590 GGTCAATGCCTCCCTCGGGTGGCCCAACGGCCTGGCCCTGGACCTGCAGGAGGGGAAGCT 1649

Qy      1621 CTACTGGGGAGACGCCAAGACAGACAAGATCGAGGTGATCAATGTTGATGGGACGAAGAG 1680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy      1681 GCGGACCCTCCTGGAGGACAAGCTCCCGCACATTTTCGGGTTCACGCTGCTGGGGGACTT 1740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1710 GCGGACCCTCCTGGAGGACAAGCTCCCGCACATTTTCGGGTTCACGCTGCTGGGGGACTT 1769

Qy      1741 CATCTACTGGACTGACTGGCAGCGCCGCAGCATCGAGCGGGTGCACAAGGTCAAGGCCAG 1800
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Db      1770 CATCTACTGGACTGACTGGCAGCGCCGCAGCATCGAGCGGGTGCACAAGGTCAAGGCCAG 1829

Qy      1801 CCGGGACGTCATCATTGACCAGCTGCCCGACCTGATGGGGCTCAAAGCTGTGAATGTGGC 1860
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1830 CCGGGACGTCATCATTGACCAGCTGCCCGACCTGATGGGGCTCAAAGCTGTGAATGTGGC 1889

Qy      1861 CAAGGTCGTCGGAACCAACCCGTGTGCGGACAGGAACGGGGGGTGCAGCCACCTGTGCTT 1920
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1890 CAAGGTCGTCGGAACCAACCCGTGTGCGGACAGGAACGGGGGGTGCAGCCACCTGTGCTT 1949

Qy      1921 CTTCACACCCCACGCAACCCGGTGTGGCTGCCCCATCGGCCTGGAGCTGCTGAGTGACAT 1980
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1950 CTTCACACCCCACGCAACCCGGTGTGGCTGCCCCATCGGCCTGGAGCTGCTGAGTGACAT 2009

Qy      1981 GAAGACCTGCATCGTGCCTGAGGCCTTCTTGGTCTTCACCAGCAGAGCCGCCATCCACAG 2040
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2010 GAAGACCTGCATCGTGCCTGAGGCCTTCTTGGTCTTCACCAGCAGAGCCGCCATCCACAG 2069

Qy      2041 GATCTCCCTCGAGACCAATAACAACGACGTGGCCATCCCGCTCACGGGCGTCAAGGAGGC 2100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2070 GATCTCCCTCGAGACCAATAACAACGACGTGGCCATCCCGCTCACGGGCGTCAAGGAGGC 2129

Qy      2101 CTCAGCCCTGGACTTTGATGTGTCCAACAACCACATCTACTGGACAGACGTCAGCCTGAA 2160
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2130 CTCAGCCCTGGACTTTGATGTGTCCAACAACCACATCTACTGGACAGACGTCAGCCTGAA 2189

Qy      2161 GACCATCAGCCGCGCCTTCATGAACGGGAGCTCGGTGGAGCACGTGGTGGAGTTTGGCCT 2220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2190 GACCATCAGCCGCGCCTTCATGAACGGGAGCTCGGTGGAGCACGTGGTGGAGTTTGGCCT 2249

Qy      2221 TGACTACCCCGAGGGCATGGCCGTTGACTGGATGGGCAAGAACCTCTACTGGGCCGACAC 2280
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2250 TGACTACCCCGAGGGCATGGCCGTTGACTGGATGGGCAAGAACCTCTACTGGGCCGACAC 2309

Qy      2281 TGGGACCAACAGAATCGAAGTGGCGCGGCTGGACGGGCAGTTCCGGCAAGTCCTCGTGTG 2340
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2310 TGGGACCAACAGAATCGAAGTGGCGCGGCTGGACGGGCAGTTCCGGCAAGTCCTCGTGTG 2369

Qy      2341 GAGGGACTTGGACAACCCGAGGTCGCTGGCCCTGGATCCCACCAAGGGCTACATCTACTG 2400
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2370 GAGGGACTTGGACAACCCGAGGTCGCTGGCCCTGGATCCCACCAAGGGCTACATCTACTG 2429

Qy      2401 GACCGAGTGGGGCGGCAAGCCGAGGATCGTGCGGGCCTTCATGGACGGGACCAACTGCAT 2460
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2430 GACCGAGTGGGGCGGCAAGCCGAGGATCGTGCGGGCCTTCATGGACGGGACCAACTGCAT 2489

Qy      2461 GACGCTGGTGGACAAGGTGGGCCGGGCCAACGACCTCACCATTGACTACGCTGACCAGCG 2520
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2490 GACGCTGGTGGACAAGGTGGGCCGGGCCAACGACCTCACCATTGACTACGCTGACCAGCG 2549

Qy      2521 CCTCTACTGGACCGACCTGGACACCAACATGATCGAGTCGTCCAACATGCTGGGTCAGGA 2580
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Db      2550 CCTCTACTGGACCGACCTGGACACCAACATGATCGAGTCGTCCAACATGCTGGGTCAGGA 2609

Qy      2581 GCGGGTCGTGATTGCCGACGATCTCCCGCACCCGTTCGGTCTGACGCAGTACAGCGATTA 2640
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Db      2610 GCGGGTCGTGATTGCCGACGATCTCCCGCACCCGTTCGGTCTGACGCAGTACAGCGATTA 2669

Qy      2641 TATCTACTGGACAGACTGGAATCTGCACAGCATTGAGCGGGCCGACAAGACTAGCGGCCG 2700
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2670 TATCTACTGGACAGACTGGAATCTGCACAGCATTGAGCGGGCCGACAAGACTAGCGGCCG 2729

Qy      2701 GAACCGCACCCTCATCCAGGGCCACCTGGACTTCGTGATGGACATCCTGGTGTTCCACTC 2760
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Db      2730 GAACCGCACCCTCATCCAGGGCCACCTGGACTTCGTGATGGACATCCTGGTGTTCCACTC 2789

Qy      2761 CTCCCGCCAGGATGGCCTCAATGACTGTATGCACAACAACGGGCAGTGTGGGCAGCTGTG 2820
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Qy      2821 CCTTGCCATCCCCGGCGGCCACCGCTGCGGCTGCGCCTCACACTACACCCTGGACCCCAG 2880
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Qy      2881 CAGCCGCAACTGCAGCCCGCCCACCACCTTCTTGCTGTTCAGCCAGAAATCTGCCATCAG 2940
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Db      2910 CAGCCGCAACTGCAGCCCGCCCACCACCTTCTTGCTGTTCAGCCAGAAATCTGCCATCAG 2969

Qy      2941 TCGGATGATCCCGGACGACCAGCACAGCCCGGATCTCATCCTGCCCCTGCATGGACTGAG 3000
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2970 TCGGATGATCCCGGACGACCAGCACAGCCCGGATCTCATCCTGCCCCTGCATGGACTGAG 3029

Qy      3001 GAACGTCAAAGCCATCGACTATGACCCACTGGACAAGTTCATCTACTGGGTGGATGGGCG 3060
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Db      3030 GAACGTCAAAGCCATCGACTATGACCCACTGGACAAGTTCATCTACTGGGTGGATGGGCG 3089

Qy      3061 CCAGAACATCAAGCGAGCCAAGGACGACGGGACCCAGCCCTTTGTTTTGACCTCTCTGAG 3120
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Db      3090 CCAGAACATCAAGCGAGCCAAGGACGACGGGACCCAGCCCTTTGTTTTGACCTCTCTGAG 3149

Qy      3121 CCAAGGCCAAAACCCAGACAGGCAGCCCCACGACCTCAGCATCGACATCTACAGCCGGAC 3180
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Db      3150 CCAAGGCCAAAACCCAGACAGGCAGCCCCACGACCTCAGCATCGACATCTACAGCCGGAC 3209

Qy      3181 ACTGTTCTGGACGTGCGAGGCCACCAATACCATCAACGTCCACAGGCTGAGCGGGGAAGC 3240
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Db      3210 ACTGTTCTGGACGTGCGAGGCCACCAATACCATCAACGTCCACAGGCTGAGCGGGGAAGC 3269

Qy      3241 CATGGGGGTGGTGCTGCGTGGGGACCGCGACAAGCCCAGGGCCATCGTCGTCAACGCGGA 3300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3270 CATGGGGGTGGTGCTGCGTGGGGACCGCGACAAGCCCAGGGCCATCGTCGTCAACGCGGA 3329

Qy      3301 GCGAGGGTACCTGTACTTCACCAACATGCAGGACCGGGCAGCCAAGATCGAACGCGCAGC 3360
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Qy      3361 CCTGGACGGCACCGAGCGCGAGGTCCTCTTCACCACCGGCCTCATCCGCCCTGTGGCCCT 3420
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Qy      3601 CGAGCGTGTGGAGAAGACCACCGGGGACAAGCGGACTCGCATCCAGGGCCGTGTCGCCCA 3660
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Qy       3961 GTGCTCCGCCGCCCAGTTCCCCTGCGCGCGGGGTCAGTGTGTGGACCTGCGCCTGCGCTG 4020
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Db       3990 GTGCTCCGCCGCCCAGTTCCCCTGCGCGCGGGGTCAGTGTGTGGACCTGCGCCTGCGCTG 4049

Qy       4021 CGACGGCGAGGCAGACTGTCAGGACCGCTCAGACGAGGTGGACTGTGACGCCATCTGCCT 4080
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Qy       4081 GCCCAACCAGTTCCGGTGTGCGAGCGGCCAGTGTGTCCTCATCAAACAGCAGTGCGACTC 4140
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Db       4170 CTTCCCCGACTGTATCGACGGCTCCGACGAGCTCATGTGTGAAATCACCAAGCCGCCCTC 4229

Qy       4201 AGACGACAGCCCGGCCCACAGCAGTGCCATCGGGCCCGTCATTGGCATCATCCTCTCTCT 4260
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Db       4230 AGACGACAGCCCGGCCCACAGCAGTGCCATCGGGCCCGTCATTGGCATCATCCTCTCTCT 4289

Qy       4261 CTTCGTCATGGGTGGTGTCTATTTTGTGTGCCAGCGCGTGGTGTGCCAGCGCTATGCGGG 4320
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Db       4290 CTTCGTCATGGGTGGTGTCTATTTTGTGTGCCAGCGCGTGGTGTGCCAGCGCTATGCGGG 4349

Qy       4321 GGCCAACGGGCCCTTCCCGCACGAGTATGTCAGCGGGACCCCGCACGTGCCCCTCAATTT 4380
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Db       4350 GGCCAACGGGCCCTTCCCGCACGAGTATGTCAGCGGGACCCCGCACGTGCCCCTCAATTT 4409

Qy       4381 CATAGCCCCGGGCGGTTCCCAGCATGGCCCCTTCACAGGCATCGCATGCGGAAAGTCCAT 4440
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Db       4890 GAGGAGCTACTTCCATCTCTTCCCGCCCCCTCCGTCCCCCTGCACGGACTCATCCTGACC 4949

Qy       4921 TCGGCCGGGCCACTCTGGCTTCTCTGTGCCCCTGTAAATAGTTTTAAATATGAACAAAGA 4980
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Qy       5041 TGTGAACTGTGATGGGGTGGGCAGGGCTGGGAGAACTTTGTACAGTGGAGAAATATTTAT 5100
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Db       5070 TGTGAACTGTGATGGGGTGGGCAGGGCTGGGAGAACTTTGTACAGTGGAGAAATATTTAT 5129

Qy       5101 AAACTTAATTTTGTAAAACA 5120
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Db       5130 AAACTTAATTTTGTAAAACA 5149
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Search completed: May 18, 2005, 23:18:28
Job time : 2729 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 18, 2005, 19:16:53 ; Search time 15013 Seconds
(without alignments)
12981.353 Million cell updates/sec

Title: US-10-680-287A-2
Perfect score: 5120
Sequence: 1 actaaagcgccgccgccgcg.....aaacttaatttttgtaaaaca 5120

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	2078.4	40.6	2838	3	AK090382	AK090382 Mus muscu
	2	1367.2	26.7	2752	3	AK081025	AK081025 Mus muscu
	3	933.6	18.2	1045	5	BM920216	BM920216 AGENCOURT
c	4	930.2	18.2	1031	5	BX402084	BX402084 BX402084
	5	919.6	18.0	1032	5	BX439521	BX439521 BX439521
c	6	881	17.2	1052	5	BX439520	BX439520 BX439520
	7	836.4	16.3	888	5	BX431414	BX431414 BX431414
	8	811	15.8	967	5	BX428434	BX428434 BX428434
c	9	805.4	15.7	870	5	BQ687102	BQ687102 AGENCOURT
	10	805	15.7	1001	5	BX402085	BX402085 BX402085
	11	802.2	15.7	986	4	BM561582	BM561582 AGENCOURT
c	12	783.6	15.3	932	4	BM006571	BM006571 603615546
	13	783.4	15.3	855	5	BQ228206	BQ228206 AGENCOURT
	14	782.8	15.3	902	5	BU195422	BU195422 AGENCOURT
c	15	780.6	15.2	911	5	BX453469	BX453469 BX453469
	16	780	15.2	5400	9	AY407796	AY407796 Homo sapi
	17	776.8	15.2	866	5	BU169706	BU169706 AGENCOURT
c	18	776.8	15.2	891	5	BQ691300	BQ691300 AGENCOURT
	19	770	15.0	5400	9	AY407797	AY407797 Pan trogl
	20	766.4	15.0	880	7	CK769878	CK769878 957987 MA
c	21	761.2	14.9	902	5	BQ687648	BQ687648 AGENCOURT
	22	758	14.8	886	6	CA489007	CA489007 AGENCOURT
c	23	730.4	14.3	847	5	BU157972	BU157972 AGENCOURT
	24	722	14.1	5400	9	AY407798	AY407798 Mus muscu
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c	27	709	13.8	943	5	BX428598	BX428598 BX428598
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	40	661.8	12.9	699	7	CF131821	CF131821 UI-HF-FQ0
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	43	636.8	12.4	850	5	BU841341	BU841341 AGENCOURT
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c	45	636.2	12.4	655	6	CA312718	CA312718 UI-CF-FN0

ALIGNMENTS

RESULT 1
AK090382
LOCUS AK090382 2838 bp mRNA linear HTC 03-APR-2004
DEFINITION Mus musculus adult male intestinal mucosa cDNA, RIKEN full-length enriched library, clone:G630070K03 product:low density lipoprotein receptor-related protein 5, full insert sequence.
ACCESSION AK090382
VERSION AK090382.1 GI:26105912
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Carninci,P. and Hayashizaki,Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
REFERENCE 2
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PUBMED 11042159
REFERENCE 3
AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE 20530913
PUBMED 11076861
REFERENCE 4
AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409, 685-690 (2001)
REFERENCE 5
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research

```
            Group Phase I & II Team.
  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
REFERENCE   6  (bases 1 to 2838)
  AUTHORS   Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
            Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
            Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
            Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
            Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
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            Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,
            Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,
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            Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
            Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
            Muramatsu,M. and Hayashizaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
            URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
COMMENT     cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
            Please visit our web site for further details.
            URL:http://genome.gsc.riken.jp/
            URL:http://fantom.gsc.riken.jp/.
FEATURES             Location/Qualifiers
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                     /strain="C57BL/6J"
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                     /dev_stage="adult"
     misc_feature    <1. .2644
                     /note="low density lipoprotein receptor-related protein 5
                     (MGD|MGI:1278315, GB|NM_008513, evidence: BLASTN, 99%,
                     match=2144)
                     putative"
ORIGIN

  Query Match             40.6%;  Score 2078.4;  DB 3;  Length 2838;
  Best Local Similarity   85.5%;  Pred. No. 0;
  Matches 2455;  Conservative    0;  Mismatches  376;  Indels   41;  Gaps   11;

Qy       2249 TGGATGGGCAAGAACCTCTACTGGGCCGACACTGGGACCAACAGAATCGAAGTGGCGCGG 2308
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Db          2 TGGATGGGCAAGAACCTCTATTGGGCGGACACAGGGACCAACAGGATTGAGGTGGCCCGG 61

Qy       2309 CTGGACGGGCAGTTCCGGCAAGTCCTCGTGTGGAGGGACTTGGACAACCCGAGGTCGCT- 2367
             ||||| |||||||||||||| || || |||||||| ||| | |||||||| ||||| ||
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Qy       2368 GGCCCTGGATCCCACCAAGGGCTACATCTACTGGACCGAGTGGGGCGGCAAGCCGAGGAT 2427
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Qy       2487 CCAACGACCTCACCATTGACTACGCTGACCAGCGCCTCTACTGGACCGACCTGGACACCA 2546
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Qy       2607 CGCACCCGTTCGGTCTGACGCAGTACAGCGATTATATCTACTGGACAGACTGGAATCTGC 2666
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Qy       2727 TGGACTTCGTGATGGACATCCTGGTGTTCCACTCCTCCCGCCAGGATGGCCTCAATGACT 2786
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Qy       2787 GTATGCACAACAACGGGCAGTGTGGGCAGCTGTGCCTTGCCATCCCCGGCGGCCACCGCT 2846
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Db        693 AGCCCGGACCTTGTCCTACCCCTTCATGGGCTGAGGAACGTCAAAGCCATCAACTATGAC 752

Qy       3026 CCACTGGACAAGTTCATCTACTGGGTGGATGGGCGCCAGAACATCAAGCGAGCCAAGGAC 3085
              || |||||||||||||||||||||||| |||||||||||||||||| | |||||||||
Db        753 CCGCTGGACAAGTTCATCTACTGGGTGGACGGGCGCCAGAACATCAAGAGGGCCAAGGAC 812

Qy       3086 GACGGGACCCAGCCCTTTGTTTTGACCTCTCTGAGCCAAGGCCAAAACCCAGACAGGCAG 3145
              ||||| |||||||||||    | |||||||||  |||||| |||  | |||||||||| |||
Db        813 GACGGTACCCAGCCCTCCATGCTGACCTCTCCCAGCCAAAGCCTGAGCCCAGACAGACAG 872

Qy       3146 CCCCACGACCTCAGCATCGACATCTACAGCCGGACACTGTTCTGGACGTGCGAGGCCACC 3205
              || |||||||||||||| |||||||||||||||||||||||||||||| || |||||||||
Db        873 CCACACGACCTCAGCATTGACATCTACAGCCGGACACTGTTCTGGACCTGTGAGGCCACC 932

Qy       3206 AATACCATCAACGTCCACAGGCTGAGCGGGGAAGCCATGGGGGTGGTGCTGCGTGGGGAC 3265
              || || ||||| |||||| |||||   ||||| |||||||| |||||||| || ||||||
Db        933 AACACTATCAATGTCCACCGGCTGGATGGGGATGCCATGGGAGTGGTGCTTCGAGGGGAC 992

Qy       3266 CGCGACAAGCCCAGGGCCATCGTCGTCAACGCGGAGCGAGGGTACCTGTACTTCACCAAC 3325
              || |||||||| |||||||| |  ||||| || |||||||||||| ||||||| ||||||
Db        993 CGTGACAAGCCAAGGGCCATTGCTGTCAATGCTGAGCGAGGGTACATGTACTTTACCAAC 1052

Qy       3326 ATGCAGGACCGGGCAGCCAAGATCGAACGCGCAGCCCTGGACGGCACCGAGCGCGAGGTC 3385
              ||||||||||  || |||||||||| || ||  ||||||| ||||| ||||| ||||||
Db        1053 ATGCAGGACCATGCTGCCAAGATCGAGCGAGCCTCCCTGGATGGCACAGAGCGGGAGGTC 1112

Qy       3386 CTCTTCACCACCGGCCTCATCCGCCCTGTGGCCCTGGTGGTGGACAACACACTGGGCAAG 3445
              |||||||||| |||||||||| || |||||||| ||||||||||  | |||||||||
Db        1113 CTCTTCACCACAGGCCTCATCCGTCCCGTGGCCCTTGTGGTGGACAATGCTCTGGGCAAG 1172

Qy       3446 CTGTTCTGGGTGGACGCGGACCTGAAGCGCATTGAGAGCTGTGACCTGTCAGGGGCCAAC 3505
              || |||||||  | || ||||| ||||| || || || |||||||| || |||||||||
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Qy       3506 CGCCTGACCCTGGAGGACGCCAACATCGTGCAGCCTCTGGGCCTGACCATCCTTGGCAAG 3565
              |||||||||||||| || |||||||||| ||||| | || ||||| | || |||| |
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Qy       3566 CATCTCTACTGGATCGACCGCCAGCAGCAGATGATCGAGCGTGTGGAGAAGACCACCGGG 3625
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Db       1291 CACCTCTACTGGATCGACCGCCAGCAGCAGATGATCGAGCGCGTGGAGAAGACCACTGGG 1350
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Db       1351 GACAAGCGGACTAGGGTTCAGGGCCGTGTCACCCACCTGACAGGCATCCATGCCGT-GAG 1409
Qy       3686 GAAGTCAGCCTGGAGGAGTTCTCAGCCCACCCATGTGCCCGTGACAATGGTGGCTGCTCC 3745
Db       1410 GAAGTCAGCCTGGAGGAGTTCTCAGCCCATCCTTGTGCCCGAGACAATGGCGGCTGCTCC 1469
Qy       3746 CACATCTGTATTGCCAAGGGTGATGGGACACCACGGTGCTCATGCCCAGTCCACCTCGTG 3805
Db       1470 CACATCTGTATCGCCAAGGGTGATGGAACACCGCGCTGCTCGTGCCCTGTCCACCTGGTG 1529
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Db       1530 CTCCTGCAGAACCTGCTGACTTGTGGTGAGCCTCCTACCTGCTCCCCTGATCAGTTTGCA 1589
Qy       3866 TGTGCCACAGGGGAGATCGACTGTATCCCCGGGGCCTGGCGCTGTGACGGCTTTCCCGAG 3925
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Qy       3926 TGCGATGACCAGAGCGACGAGGAGGGCTGCCCCGTGTGCTCCGCCGCCCAGTTCCCCTGC 3985
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Qy       4524 GCTCGTCCAGCACGAAGGCCACGCTGTACCCGCCGATCCTGAACCCGCCGCCCTCCCCGG 4583
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Qy       4584 CCACGGACCCCTCCCTGTACAACATGGACATGTTCTACTCTTCAAACATTCCGGCCACTG 4643
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Qy       4644 CGAGACCGTACAGGCCCTACATCATTCGAGGAATGGCGCCCCCGACGACGCCCTGCAGCA 4703
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Qy       4884 CGCCCCCTCCGTCCCCCTGCACGGACTCATCCTGACCTCGGCCGGGCCACTCTGGCTTCT 4943
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Qy       4944 CTGTGCCCCTGTAAATAGTTTTAAATATGAACAAAGAAAAAAATATATTTTATGATTTAA 5003
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Qy       5004 AAAATAAATATAATTGGGATTTTAAAAACATGAGAAATGTGAACTGTGATGGGGTGGGCA 5063
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Qy       5064 GGGCTGGGAGAACTTTGTACAGTGGAG-AAATATTTATAAACTTAATTTTGT 5114
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```

RESULT 2
AK081025

LOCUS	AK081025 2752 bp mRNA linear HTC 03-APR-2004
DEFINITION	Mus musculus 10 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:B930069L06 product:low density lipoprotein receptor-related protein 5, full insert sequence.
ACCESSION	AK081025
VERSION	AK081025.1 GI:26099620
KEYWORDS	HTC; CAP trapper.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE	1
AUTHORS	Carninci,P. and Hayashizaki,Y.
TITLE	High-efficiency full-length cDNA cloning
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)
MEDLINE	99279253
PUBMED	10349636
REFERENCE	2
AUTHORS	Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE	20499374
PUBMED	11042159
REFERENCE	3
AUTHORS	Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE	20530913
PUBMED	11076861
REFERENCE	4
AUTHORS	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.

```
  TITLE     Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409, 685-690 (2001)
REFERENCE   5
  AUTHORS   The FANTOM Consortium and the RIKEN Genome Exploration Research
            Group Phase I & II Team.
  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
REFERENCE   6  (bases 1 to 2752)
  AUTHORS   Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
            Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
            Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
            Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
            Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
            Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
            Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,
            Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,
            Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
            Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
            Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
            Muramatsu,M. and Hayashizaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
            URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
COMMENT     cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
            Please visit our web site for further details.
            URL:http://genome.gsc.riken.jp/
            URL:http://fantom.gsc.riken.jp/.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /strain="C57BL/6J"
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                     /clone="B930069L06"
                     /tissue_type="cerebellum"
                     /clone_lib="RIKEN full-length enriched mouse cDNA library"
                     /dev_stage="10 days neonate"
     misc_feature    1. .2752
                     /note="low density lipoprotein receptor-related protein 5
                     (MGD|MGI:1278315, GB|NM_008513, evidence: BLASTN, 99%,
                     match=2144)"
ORIGIN

  Query Match           26.7%;  Score 1367.2;  DB 3;  Length 2752;
  Best Local Similarity   85.2%;  Pred. No. 2.4e-287;
  Matches 1593;  Conservative    0;  Mismatches  267;  Indels    9;  Gaps    6;

Qy          8 CGCCGCCGCCGCGCCATGGAGCCCGAGTGAGCGCGGCGCGGGCCCGTCCGGCCGCCGGAC 67
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Db         60 CACCGCCGCCGCGCGCGCCATGGAGCCCGAGTGAGCGCGCGGCGCTCCCGGCCGCCGGAC 119

Qy         68 AACATGGAGGCAGCGCCGCCCGGGCCGCCGTGGCCGCTGCTGCTGCTGCTGCTGCTGCTG 127
                |||||||  | ||||| || || | ||    |||| || || || || ||||||||||
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Qy        128 CTGGCGCTGTGCGGCTGCCCGGCCCCCGCCGCGGCCTCGCCGCTCCTGCTATTTGCCAAC 187
              |||| ||||| | || ||  || ||||||||||||||| ||||||| | |||||||||
Db        177 CTGGTGCTGTACTGCAGCTTGGTCCCCGCCGCGGCCTCACCGCTCCTGTTGTTTGCCAAC 236

Qy        188 CGCCGGGACGTACGGCTGGTGGACGCCGGCGGAGTCAAGCTGGAGTCCACCATCGTGGTC 247
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Qy        248 AGCGGCCTGGAGGATGCGGCCGCAGTGGACTTCCAGTTTTCCAAGGGAGCCGTGTACTGG 307
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Qy        308 ACAGACGTGAGCGAGGAGGCCATCAAGCAGACCTACCTGAACCAGACGGGGGCCGCCGTG 367
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Qy        368 CAGAACGTGGTCATCTCCGGCCTGGTCTCTCCCGACGGCCTCGCCTGCGACTGGGTGGGC 427
              |||||| | |||||||| ||||| || || || || ||||| ||||| ||||||||| |||
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Qy        428 AAGAAGCTGTACTGGACGGACTCAGAGACCAACCGCATCGAGGTGGCCAACCTCAATGGC 487
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Qy        488 ACATCCCGGAAGGTGCTCTTCTGGCAGGACCTTGACCAGCCGA--GGGCCATCGCCTTGG 545
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Qy        546 ACCCCGCTCACGGGTACATGTACTGGACAGACTGGGTTGAGACGCCCCGGATTGAGCGGG 605
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Qy        606 CAGGGATGGATGGCAGCACCCGGAAGATCATTGTGGACTCGGACATTTACTGGCCCAATG 665
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Qy        786 ACCCCTTCGCCCTGACGCTCTCCGGGGACACTCTGTACTGGACAGACTGGCAGACCCGCT 845
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Qy        966 GTGAGGAGGACAATGGCGGCTGCTCCCACCTGTGCCTGCTGTCCCCAAGCGAGCCTTTCT 1025
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RESULT 3
BM920216
LOCUS       BM920216                1045 bp    mRNA    linear   EST 12-MAR-2002
DEFINITION  AGENCOURT_6706353 NIH_MGC_120 Homo sapiens cDNA clone IMAGE:5750120
            5', mRNA sequence.
ACCESSION   BM920216
VERSION     BM920216.1  GI:19370595
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1045)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM12780  row: j  column: 09
            High quality sequence start: 29
            High quality sequence stop: 736.
FEATURES             Location/Qualifiers
     source          1. .1045
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                     /mol_type="mRNA"
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                     /clone="IMAGE:5750120"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_120"
                     /note="Organ: pooled pancreas and spleen; Vector:
                     pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
                     source anonymous pool of spleen and pancreas from 28 yo
                     male.  Library is oligo-dT primed and directionally cloned
                     (EcoRV  site is destroyed upon cloning).  Average insert
                     size 1.5 kb, insert size range 1-2.5 kb.  Library is
                     normalized and enriched for  full-length clones and was
                     constructed by C. Gruber (Invitrogen). Research Genetics
                     tracking code 025. Note: this is a NIH_MGC Library."
ORIGIN

  Query Match           18.2%;  Score 933.6;  DB 5;  Length 1045;
  Best Local Similarity   96.7%;  Pred. No. 9.9e-193;
  Matches  973;  Conservative    0;  Mismatches   31;  Indels    2;  Gaps    2;

Qy       3221 CACAGGCTGAGCGGGGAAGCCATGGGGGTGGTGCTGCGTGGGGACCGCGACAAGCCCAGG 3280
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         41 CCCAGGCTGAGCGGGGAAGCCATGGGGGTGGTGCTGCGTGGGGACCGCGACAAGCCCAGG 100

Qy       3281 GCCATCGTCGTCAACGCGGAGCGAGGGTACCTGTACTTCACCAACATGCAGGACCGGGCA 3340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        101 GCCATCGTCGTCAACGCGGAGCGAGGGTACCTGTACTTCACCAACATGCAGGACCGGGCA 160

Qy       3341 GCCAAGATCGAACGCGCAGCCCTGGACGGCACCGAGCGCGAGGTCCTCTTCACCACCGGC 3400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        161 GCCAAGATCGAACGCGCAGCCCTGGACGGCACCGAGCGCGAGGTCCTCTTCACCACCGGC 220

Qy       3401 CTCATCCGCCCTGTGGCCCTGGTGGTGGACAACACACTGGGCAAGCTGTTCTGGGTGGAC 3460
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Db        221 CTCATCCGCCCTGTGGCCCTGGTGGTGGACAACACACTGGGCAAGCTGTTCTGGGTGGAC 280

Qy       3461 GCGGACCTGAAGCGCATTGAGAGCTGTGACCTGTCAGGGGCCAACCGCCTGACCCTGGAG 3520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        281 GCGGACCTGAAGCGCATTGAGAGCTGTGACCTGTCAGGGGCCAACCGCCTGACCCTGGAG 340

Qy       3521 GACGCCAACATCGTGCAGCCTCTGGGCCTGACCATCCTTGGCAAGCATCTCTACTGGATC 3580
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Db        341 GACGCCAACATCGTGCAGCCTCTGGGCCTGACCATCCTTGGCAAGCATCTCTACTGGATC 400

Qy       3581 GACCGCCAGCAGCAGATGATCGAGCGTGTGGAGAAGACCACCGGGGACAAGCGGACTCGC 3640
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Db        401 GACCGCCAGCAGCAGATGATCGAGCGTGTGGAGAAGACCACCGGGGACAAGCGGACTCGC 460

Qy       3641 ATCCAGGGCCGTGTCGCCCACCTCACTGGCATCCATGCAGTGGAGGAAGTCAGCCTGGAG 3700
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        461 ATCCAGGGCCGTGTCGCCCACCTCACTGGCATCCATGCAGTGGAGGAAGTCAGCCTGGAG 520

Qy       3701 GAGTTCTCAGCCCACCCATGTGCCCGTGACAATGGTGGCTGCTCCCACATCTGTATTGCC 3760
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        521 GAGTTCTCAGCCCACCCATGTGCCCGTGACAATGGTGGCTGCTCCCACATCTGTATTGCC 580

Qy       3761 AAGGGTGATGGGACACCACGGTGCTCATGCCCAGTCCACCTCGTGCTCCTGCAGAACCTG 3820
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        581 AAGGGTGATGGGACACCACGGTGCTCATGCCCAGTCCACCTCGTGCTCCTGCAGAACCTG 640

Qy       3821 CTGACCTGTGGAGAGCCGCCCACCTGCTCCCCGGACCAGTTTGCATGTGCCACAGGGGAG 3880
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Db        641 CTGACCTGTGGAGAGCCGCCCACCTGCTCCCCGGACCAGTTTGCATGTGCCACAGGGGAG 700

Qy       3881 ATCGACTGTATCCCCGGGGCCTGGCGCTGTGACGGCTTTCCCGAGTGCGATGACCAGAGC 3940
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Db        701 ATCGACTGTATCCCCGGGGCCTGGCGCTGTGACGGCTTTCCCGAGTGCGATGACCAGAGC 760

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        761 GACGAGGAGGGCTGCCCCGTGTGCTCCGCCGCCCAGTTCCCCTGCGCGCGGGGTCAGTGT 820

Qy       4001 GTGGACCTGCGCCTGCGCTGCGACGGCGAGGCAGACTGTCAGGACCGCTCAGACGAGGTG 4060
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Db        821 GTGGACCTGCGCCTGCGCTGCGACGGCGAAGCAGACTGTCAGGACCGCTCAGACGAGGTG 880

Qy       4061 GACTGTGACGCCATCTGCCTGCCCAACCAGTTCCGGTGTGCGAGCGGCCAGTGTGTCCTC 4120
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Db        881 GACTGTGACGNCATCTGCCTG-CCAAACANTTCCGGTGTGCCAGCGGCCATTGTGTCCTC 939

Qy       4121 ATCAAACAGCAGTGCGACTCCTTCCCCGACTGTATCGACGGCTCCGACGAGCTCATGTGT 4180
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Db        940 ATCAAAC-GCAGTGCGGCTCCTTCCCCGACTGTATCGACGGCTCGAACGAACTCAGTGGG 998

Qy       4181 GAAATCACCAAGCCGCCCTCAGACGACAGCCCGGCCCACAGCAGTG 4226
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Db        999 GAAATCACAAGCCGCCCTCAGAACGAAGCCCCGGCCCCAAACAGTG 1044


RESULT 4
BX402084/c
LOCUS       BX402084               1031 bp    mRNA    linear   EST 29-APR-2004
DEFINITION  BX402084 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens
            cDNA clone CS0DC011YB06 3-PRIME, mRNA sequence.
ACCESSION   BX402084
VERSION     BX402084.2  GI:46874938
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1031)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     On May 13, 2003 this sequence version replaced gi:30618689.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen. This sequence belongs to sequence cluster
            6245.f
            For more information about this cluster, see
            http://www.genoscope.cns.fr/cdna?s=CS1AC003ZF04NP1&c=6245.f.
FEATURES             Location/Qualifiers
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                     /clone="CS0DC011YB06"
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                     /clone_lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
                     /note="1st strand cDNA was primed with a NotI-oligo(dT)
                     primer. Five prime end enriched, double-strand cDNA was
                     digested with Not I and cloned into the Not I and EcoR V
                     sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN

  Query Match             18.2%;  Score 930.2;  DB 5;  Length 1031;
  Best Local Similarity   97.6%;  Pred. No. 5.5e-192;
  Matches  970;  Conservative   13;  Mismatches    7;  Indels    4;  Gaps    4;

Qy       4116 TCCTCATCAAACAGCAGTGCGACTCCTTCCCCGACTGTATCGACGGCTCCGACGAGCTCA 4175
              :|||:|| |||:|| ||||: ||||||||||||||||||||||||||||||||| |||:|
Db        991 KCCTMATAAAAMAGAAGTGY-ACTCCTTCCCCGACTGTATCGACGGCTCCGACGCGCTYA 933

Qy       4176 TGTGTGAAATCACCAAGCCGCCCTCAGACGACAGCCCGGCCCACAGCAGTGCCATCGGGC 4235
              ||:::| |||:|||||||||||||||||||||||||||||||||||||||||||||||||
Db        932 TGYKKG-AATYACCAAGCCGCCCTCAGACGACAGCCCGGCCCACAGCAGTGCCATCGGGC 874

Qy       4236 CCGTCATTGGCATCATCCTCTCTCTCTTCGTCATGGGTGGTGTCTATTTTGTGTGCCAGC 4295
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Db        873 CCGTCATTGGCATCATCCTCTCTCTCTTCGTCATGGGTGGTGTCTATMTTGTGTGCCAGC 814

Qy       4296 GCGTGGTGTGCCAGCGCTATGCGGGGGCCAACGGGCCCTTCCCGCACGAGTATGTCAGCG 4355
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Db        813 GCGTGGTGTGCCAGCGCTATGCGGGGGCCAACGGGCCCTTCCCGCACGAGTATGTCAGCG 754

Qy       4356 GGACCCCGCACGTGCCCCTCAATTTCATAGCCCCGGGCGGTTCCCAGCATGGCCCCTTCA 4415
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Qy       4416 CAGGCATCGCATGCGGAAAGTCCATGATGAGCTCCGTGAGCCTGATGGGGGGCCGGGGCG 4475
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Db        694 CAGGCATCGCATGCGGAAAGTCCATGATGAGCTCCGTGAGCCTGATGGGGGGCCGGGGCG 635

Qy       4476 GGGTGCCCCTCTACGACCGGAACCACGTCACAGGGGCCTCGTCCAGCAGCTCGTCCAGCA 4535
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Db        634 GGGTGCCCCTCTACGACCGGAACCACGTCACAGGGGCCTCGTCCAGCAGCTCGTCCAGCA 575

Qy       4536 CGAAGGCCACGCTGTACCCGCCGATCCTGAACCCGCCGCCCTCCCCGGCCACGGACCCCT 4595
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Db        574 CGAAGGCCACGCTGTACCCGCCGATCCTGAACCCGCCGCCCTCCCCGGCCACGGACCCCT 515

Qy       4596 CCCTGTACAACATGGACATGTTCTACTCTTCAAACATTCCGGCCACTGCGAGACCGTACA 4655
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Db        514 CCCTGTACAACATGGACATGTTCTACTCTTCAAACATTCCGGCCACTGCGAGACCGTACA 455

Qy       4656 GGCCCTACATCATTCGAGGAATGGCGCCCCCGACGACGCCCTGCAGCACCGACGTGTGTG 4715
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Db        454 GGCCCTACATCATTCGAGGAATGGCGCCCCCGACGACGCCCTGCAGCACCGACGTGTGTG 395

Qy       4716 ACAGCGACTACAGCGCCAGCCGCTGGAAGGCCAGCAAGTACTACCTGGATTTGAACTCGG 4775
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Qy       4776 ACTCAGACCCCTATCCACCCCCACCCACGCCCCACAGCCAGTACCTGTCGGCGGAGGACA 4835
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Db        334 ACTCAGACCCCTATCCACCCCCACCCACGCCCCACAGCCAGTACCTGTCGGCGGAGGACA 275

Qy       4836 GCTGCCCGCCCTCGCCCGCCACCGAGAGGAGCTACTTCCATCTCTTCCCGCCCCCTCCGT 4895
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Db        274 GCTGCCCGCCCTCGCCCGCCACCGAGAGGAGCTACTTCCATCTCTTCCCGCCCCCTCCGT 215

Qy       4896 CCCCCTGCACGGACTCATCCTGACCTCGGCCGGGCCACTCTGGCTTCTCTGTGCCCCTGT 4955
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Db        214 CCCCCTGCACGGACTCATCCTGACCTCAGCCGGGCCACTCTGGCTTCTCTGTGCCCCTGT 155

Qy       4956 AAATAGTTTTAAATATGAACAAAGAAAAAAATATATTTTATGATTTAAAAAATAAATATA 5015
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Db        154 AAATAGTKTTAAATATGAACAAAGAAAAAAATATATTTTATGATTTAAAAAATAAATATA 95

Qy       5016 ATTGGGATTTTAAAAACATGAGAAATGTGAACTGTGATGGGGTGGGCAGGGCTGGGAGAA 5075
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Db         94 ATTGGGATTTTAAAAACATGAGAAATGTGAACTGTGATGGGGTGGGCAGGGCTGGGGGAA 35

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Db         34 CTTTGTNNCAGTGGAGAAATWTTTWTARACTTAA 1


RESULT 5
BX439521
LOCUS       BX439521               1032 bp    mRNA    linear   EST 04-MAY-2004
DEFINITION  BX439521 Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DE011YM02
            5-PRIME, mRNA sequence.
ACCESSION   BX439521
VERSION     BX439521.2  GI:47020909
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1032)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
```

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  JOURNAL   Unpublished (2001)
COMMENT     On May 15, 2003 this sequence version replaced gi:30787803.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
            was not normalized. Library was constructed by Life Technologies, a
            division of Invitrogen.
            This sequence belongs to sequence cluster 6245.f
            For more information about this cluster, see
            http://www.genoscope.cns.fr/cdna?s=CS0DE011BG01QP1&c=6245.f.
FEATURES             Location/Qualifiers
     source          1. .1032
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DE011YM02"
                     /tissue_type="PLACENTA"
                     /clone_lib="Homo sapiens PLACENTA"
                     /note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
                     with a NotI-oligo(dT) primer. Five prime end enriched,
                     double-strand cDNA was digested with Not I and cloned into
                     the Not I and EcoRV sites of the pCMVSPORT 6 vector.
                     Library was not normalized."
ORIGIN

  Query Match           18.0%;  Score 919.6;  DB 5;  Length 1032;
  Best Local Similarity   99.4%;  Pred. No. 1.1e-189;
  Matches  930;  Conservative    3;  Mismatches    2;  Indels    1;  Gaps    1;

Qy       1342 CTGGGTGGCCCGAAACCTCTACTGGACCGACACGGGCACGGACCGCATCGAGGTGACGCG 1401
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CTGGGTGGCCCGAAACCTCTACTGGACCGACACGGGCACGGACCGCATCGAGGTGACGCG 60

Qy       1402 CCTCAACGGCACCTCCCGCAAGATCCTGGTGTCGGAGGACCTGGACGAGCCCCGAGCCAT 1461
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Db         61 CCTCAACGGCACCTCCCGCAAGATCCTGGTGTCGGAGGACCTGGACGAGCCCCGAGCCAT 120

Qy       1462 CGCACTGCACCCCGTGATGGGCCTCATGTACTGGACAGACTGGGGAGAGAACCCTAAAAT 1521
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Db        121 CGCACTGCACCCCGTGATGGGCCTCATGTACTGGACAGACTGGGGAGAGAACCCTAAAAT 180

Qy       1522 CGAGTGTGCCAACTTGGATGGGCAGGAGCGGCGTGTGCTGGTCAATGCCTCCCTCGGGTG 1581
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Db        181 CGAGTGTGCCAACTTGGATGGGCAGGAGCGGCGTGTGCTGGTCAATGCCTCCCTCGGGTG 240

Qy       1582 GCCCAACGGCCTGGCCCTGGACCTGCAGGAGGGGAAGCTCTACTGGGGAGACGCCAAGAC 1641
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Db        241 GCCCAACGGCCTGGCCCTGGACCTGCAGGAGGGGAAGCTCTACTGGGGAGACGCCAAGAC 300

Qy       1642 AGACAAGATCGAGGTGATCAATGTTGATGGGACGAAGAGGCGGACCCTCCTGGAGGACAA 1701
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Db        301 AGACAAGATCGAGGTGATCAATGTTGATGGGACGAAGAGGCGGACCCTCCTGGAGGACAA 360

Qy       1702 GCTCCCGCACATTTTCGGGTTCACGCTGCTGGGGGACTTCATCTACTGGACTGACTGGCA 1761
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Db        421 GCGCCGCAGCATCGAGCGGGTGCACAAGGTCAAGGCCAGCCGGGACGTCATCATTGACCA 480

Qy       1822 GCTGCCCGACCTGATGGGGCTCAAAGCTGTGAATGTGGCCAAGGTCGTCGGAACCAACCC 1881
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Qy       1882 GTGTGCGGACAGGAACGGGGGGTGCAGCCACCTGTGCTTCTTCACACCCCACGCAACCCG 1941
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Db        541 GTGTGCGGACAGGAACGGGGGGTGCAGCCACCTGTGCTTCTTCACACCCCACGCAACCCG 600

Qy       1942 GTGTGGCTGCCCCATCGGCCTGGAGCTGCTGAGTGACATGAAGACCTGCATCGTGCCTGA 2001
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Db         601 GTGTGGCTGCCCCATCGGCCTGGAGCTGCTGAGTGACATGAAGACCTGCATCGTGCCTGA 660

Qy       2002 GGCCTTCTTGGTCTTCACCAGCAGAGCCGCCATCCACAGGATCTCCCTCGAGACCAATAA 2061
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       2062 CAACGACGTGGCCATCCCGCTCACGGGCGTCAAGGAGGCCTCAGCCCTGGACTTTGATGT 2121
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Db         721 CAACGACGTGGCCATCCCGCTCACGGGCGTCAAGGAGGCCTCAGCCCTGGACTTTGATGT 780

Qy       2122 GTCCAACAACCACATCTACTGGACAGACGTCAGCCTGAAGACCATCAGCCGCGCCTTCAT 2181
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Db         781 GTCCAACAACCACATCTACTGGACAGACGTCAGCCTGAAGACCATCAGCCGCGCCTTCAT 840

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Qy       2242 CGTTGACTGGATGGGCAAGAACCTCTACTGGGCCGA 2277
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Db         901 CGTTGACTGGATTGGCAA-AAACTCTACTGGGCCRM 935


RESULT 6
BX439520/c
LOCUS       BX439520               1052 bp    mRNA    linear   EST 04-MAY-2004
DEFINITION  BX439520 Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DE011YM02
            3-PRIME, mRNA sequence.
ACCESSION   BX439520
VERSION     BX439520.2  GI:47012605
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1052)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     On May 15, 2003 this sequence version replaced gi:30785796.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
            was not normalized. Library was constructed by Life Technologies, a
            division of Invitrogen.
            This sequence belongs to sequence cluster 6245.f
            For more information about this cluster, see
            http://www.genoscope.cns.fr/cdna?s=CS0DE011BG01NP1&c=6245.f.
FEATURES             Location/Qualifiers
     source          1. .1052
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
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                     /note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
                     with a NotI-oligo(dT) primer. Five prime end enriched,
                     double-strand cDNA was digested with Not I and cloned into
                     the Not I and EcoRV sites of the pCMVSPORT 6 vector.
                     Library was not normalized."
ORIGIN

  Query Match           17.2%;  Score 881;  DB 5;  Length 1052;
  Best Local Similarity   90.8%;  Pred. No. 3.1e-181;
  Matches  945;  Conservative   32;  Mismatches   60;  Indels    4;  Gaps    4;
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Db       1038 CCSAGTCCCTGSGCGGGGGTCAGTKKKGGACTGSGCTKSGYGGGACGGSGAGGCAGATTK 979

Qy       4039 TCAGGACCGCTCAGACGAGGTGGACTGTGACGCCATCTGCCTGCCCAACCAGTTCCGGTG 4098
Db        978 TCA-GACGCGTCAGACGAGGT-GAATTTKACGCCATTTCCTGCCCAAACCAGTTTCGGTG 921

Qy       4099 TGCGAGCGGCCAGTGTGTCCTCATCAAACAGCAGTGCGACTCCTTCCCCGACTGTATCGA 4158
Db        920 TGCGAGCGSCGAGTGTGTCYTCATCAAACAGCAGTGCGACTTCTTCCCCGACTGTATCGA 861

Qy       4159 CGGCTCCGACGAGCTCATGTGTGAAATCACCAAGCCGCCCTCAGACGACAGCCCGGCCCA 4218
Db        860 CGGCTCCGACGGGCTCATATG-KRAATCACCAAGCCGCCCTCAGACGACAGCCCGGCCCA 802

Qy       4219 CAGCAGTGCCATCGGGCCCGTCATTGGCATCATCCTCTCTCTCTTCGTCATGGGTGGTGT 4278
Db        801 CAGCAGTGCCATCGGGCCCGTCATTGGCATCATCCTCTCTCTCTTCGTCATGGGTGGTGT 742

Qy       4279 CTATTTTGTGTGCCAGCGCGTGGTGTGCCAGCGCTAT-GCGGGGGCCAACGGGCCCTTCC 4337
Db        741 CTATTTTGTGTGCCAGCGCGTGGTGTGCCAGCGCTATGGCGGGGGCCAACGGGCCCTTCC 682

Qy       4338 CGCACGAGTATGTCAGCGGGACCCCGCACGTGCCCCTCAATTTCATAGCCCCGGGCGGTT 4397
Db        681 CGCACGAGTATGTCAGCGGGACCCCGCACGTGCCCCTCAATTTCATAGCCCCGGGCGGTT 622

Qy       4398 CCCAGCATGGCCCCTTCACAGGCATCGCATGCGGAAAGTCCATGATGAGCTCCGTGAGCC 4457
Db        621 CCCAGCATGGCCCCTTCACAGGCATCGCATGCGGAAAGTCCATGATGAGCTCCGTGAGCC 562

Qy       4458 TGATGGGGGGCCGGGGCGGGGTGCCCCTCTACGACCGGAACCACGTCACAGGGGCCTCGT 4517
Db        561 TGATGGGGGGCCGGGGCGGGGTGCCCCTCTACGACSGGAACCACGTCACAGGGGCCTCGT 502

Qy       4518 CCAGCAGCTCGTCCAGCACGAAGGCCACGCTGTACCCGCCGATCCTGAACCCGCCGCCCT 4577
Db        501 CCAGCAGCTCGTCCAGCACGAAGGCCACGCTGTACCCGCCGATCCTGAACCCGCCGCCCT 442

Qy       4578 CCCCGGCCACGGACCCCTCCCTGTACAACATGGACATGTTCTACTCTTCAAACATTCCGG 4637
Db        441 CCCCGGCCACGGACCCCTCCCTGTACAACATGGACATGTTYTACTCTTCAAAMATTCCGG 382

Qy       4638 CCACTGCGAGACCGTACAGGCCCTACATCATTCGAGGAATGGCGCCCCCGACGACGCCCT 4697
Db        381 CCACTGSGAGACCGTACAGGCCCTACATCATTCGAGGAATGGCGCCCCCGACGACGCCCT 322

Qy       4698 GCAGCACCGACGTGTGTGACAGCGACTACAGCGCCAGCCGCTGGAAGGCCAGCAAGTACT 4757
Db        321 GCAGCACCGACGTGTGTGACAGCGACTACAGCGCCAGCCGCTGGAAGGCCAGCAAGTACT 262

Qy       4758 ACCTGGATTTGAACTCGGACTCAGACCCCTATCCACCCCCACCCACGCCCCACAGCCAGT 4817
Db        261 ACCTGGATTTGAACTCGGACTCAGACCCCTATCCACCCCMACCCACGCCCCACAGCCAGT 202

Qy       4818 ACCTGTCGGCGGAGGACAGCTGCCCGCCCTCGCCCGCCACCGAGAGGAGCTACTTCCATC 4877
Db        201 ACCTGTCGGCGGAGGACAGCTGCCCGCCCTMRCCCGCCACCGAGAGGAGCTACTTCCATC 142

Qy       4878 TCTTCCCGCCCCCTCCGTCCCCCTGCACGGACTCATCCTGACCTCGGCCGGGCCACTCTG 4937
Db        141 AAAAACCGCCCCCCVCMVACCCCCBBBACGGACTCATCCTGACCTCGGCCGGGCKKKTCTG 82

Qy       4938 GCTTCTCTGTGCCCCCTGTAAATAGTTTTAAATATGAACAAAGAAAAAAATATATTTTATG 4997
Db          81 GCTTCTCTGTGCMCCBGTAAATAGBKTTAAATATGGACAVTGSGKKAAATGTKTTTTATG 22

Qy       4998 ATTTAAAAAATAAATATAATT 5018
Db          21 ATTTTAAAAATDAATATAATT 1
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RESULT 7
BX431414
LOCUS       BX431414                888 bp    mRNA    linear   EST 04-MAY-2004
DEFINITION  BX431414 Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DE011YM02
            5-PRIME, mRNA sequence.
ACCESSION   BX431414
VERSION     BX431414.2  GI:47007686
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 888)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     On May 15, 2003 this sequence version replaced gi:30779003.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
            was not normalized. Library was constructed by Life Technologies, a
            division of Invitrogen.
            This sequence belongs to sequence cluster 6245.f
            For more information about this cluster, see
            http://www.genoscope.cns.fr/cdna?s=CS0BAG013ZC06_CS01195_1&c=6245.f
            .
FEATURES             Location/Qualifiers
     source          1. .888
                     /organism="Homo sapiens"
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                     /db_xref="taxon:9606"
                     /clone="CS0DE011YM02"
                     /tissue_type="PLACENTA"
                     /clone_lib="Homo sapiens PLACENTA"
                     /note="Vector: pCMVSPORT_6; 1st strand cDNA was primed
                     with a NotI-oligo(dT) primer. Five prime end enriched,
                     double-strand cDNA was digested with Not I and cloned into
                     the Not I and EcoRV sites of the pCMVSPORT 6 vector.
                     Library was not normalized."
ORIGIN
```

```
  Query Match           16.3%;  Score 836.4;  DB 5;  Length 888;
  Best Local Similarity   97.9%;  Pred. No. 1.6e-171;
  Matches  854;  Conservative    0;  Mismatches   17;  Indels    1;  Gaps    1;

Qy       2156 CTGAAGACCATCAGCCGCGCCTTCATGAACGGGAGCTCGGTGGAGCACGTGGTGGAGTTT 2215
Db          1 CTGNAANACATCAGCCGCGCCTTCATGAACGGGAGCTCGGTGGAGCACGTGGTGGAGTTT 60

Qy       2216 GGCCTTGACTACCCCGAGGGCATGGCCGTTGACTGGATGGGCAAGAACCTCTACTGGGCC 2275
Db         61 GGCCTTGACTACCCCGAGGGCATGGCCGTTGACTGGATGGGCAAGAACCTCTACTGGGCC 120

Qy       2276 GACACTGGGACCAACAGAATCGAAGTGGCGCGGCTGGACGGGCAGTTCCGGCAAGTCCTC 2335
Db        121 GACACTGGGACCAATAGAATCGAAGTGGCGCGGCTGGACGGGCAGTTCCGGCAAGTCCTC 180

Qy       2336 GTGTGGAGGGACTTGGACAACCCGAGGTCGCTGGCCCTGGATCCCACCAAGGGCTACATC 2395
Db        181 GTGTGGAGGGACTTGGACAACCCGAGGTCGCTGGCCCTGGATCCCACCAAGGGCTACATC 240

Qy       2396 TACTGGACCGAGTGGGGCGGCAAGCCGAGGATCGTGCGGGCCTTCATGGACGGGACCAAC 2455
Db        241 TACTGGACCGAGTGGGGCGGCAAGCCGAGGATCGTGCGGGCCTTCATGGACGGGACCAAC 300

Qy       2456 TGCATGACGCTGGTGGACAAGGTGGGCCGGGCCAACGACCTCACCATTGACTACGCTGAC 2515
Db        301 TGCATGACGCTGGTGGACAAGGTGGGCCGGGCCAACGACCTCACCATTGACTACGCTGAC 360
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Qy       2516 CAGCGCCTCTACTGGACCGACCTGGACACCAACATGATCGAGTCGTCCAACATGCTGGGT 2575
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CAGCGCCTCTACTGGACCGACCTGGACACCAACATGATCGAGTCGTCCAACATGCTGGGT 420

Qy       2576 CAGGAGCGGGTCGTGATTGCCGACGATCTCCCGCACCCGTTCGGTCTGACGCAGTACAGC 2635
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CAGGAGCGGGTCGTGATTGCCGACGATCTCCCGCACCCGTTCGGTCTGACGCAGTACAGC 480

Qy       2636 GATTATATCTACTGGACAGACTGGAATCTGCACAGCATTGAGCGGGCCGACAAGACTAGC 2695
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GATTATATCTACTGGACAGACTGGAATCTGCACAGCATTGAGCGGGCCGACAAGACTAGC 540

Qy       2696 GGCCGGAACCGCACCCTCATCCAGGGCCACCTGGACTTCGTGATGGACATCCTGGTGTTC 2755
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Db        541 GGCCGGAACCGCACCCTCATCCAGGGCCACCTGGACTTCGTGATGGACATCCTGGTGTTC 600

Qy       2756 CACTCCTCCCGCCAGGATGGCCTCAATGACTGTATGCACAACAACGGGCAGTGTGGGCAG 2815
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CACTCCTCCCGCCAGGATGGCCTCAATGACTGTATGCACAACAACGGGCAGTGTGGGCAG 660

Qy       2816 CTGTGCCTTGCCATCCCCGGCGGCCACCGCTGCGGCTGCGCCTCACACTACACCCTGGAC 2875
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CTGTGCCTTGCCATCCCCGGCGGCCACCGCTGCGGCTGCGCCTCACACTACACCCTGGAC 720

Qy       2876 CCCAGCAGCCGCAACTGCAGCCCGCCCACCACCTTCTTGCTGTTCAGCCAGAAATCTGCC 2935
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Db        721 CCCAGCAGCCGCAACTGCAGCCCGNCCCACACCTTCTTGCTGNTCAGCCAGAAATCTGCC 780

Qy       2936 ATCAGTCGGATGATCCCGGACGACCAGCACAGCCC-GGATCTCATCCTGCCCCTGCATGG 2994
             |||||||||||||||||||||||||||||||| || ||||||||| ||||||||||||||
Db        781 ATCAGTCGGATGATCCCGGACGACCAGCACAGNCCGGGATCTCATNCTGCCCCTGCATGG 840

Qy       2995 ACTGAGGAACGTCAAAGCCATCGACTATGACC 3026
                 ||||||||||||||||||||||||||||
Db        841 GACTGAGAACGTCAAAGCCATCGACTATGACC 872
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RESULT 8
BX428434
LOCUS       BX428434                967 bp    mRNA    linear   EST 05-MAY-2004
DEFINITION  BX428434 Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DE011YM02
            5-PRIME, mRNA sequence.
ACCESSION   BX428434
VERSION     BX428434.1  GI:31017882
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 967)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
            was not normalized. Library was constructed by Life Technologies, a
            division of Invitrogen.
            This sequence belongs to sequence cluster 6245.f
            For more information about this cluster, see
            http://www.genoscope.cns.fr/cdna?s=CS0AQ006ZH04_A0512_1&c=6245.f.
FEATURES             Location/Qualifiers
     source          1. .967
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                     /db_xref="taxon:9606"
                     /clone="CS0DE011YM02"
                     /tissue_type="PLACENTA"
                     /clone_lib="Homo sapiens PLACENTA"
                     /note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
                     with a NotI-oligo(dT) primer. Five prime end enriched,
                     double-strand cDNA was digested with Not I and cloned into
                     the Not I and EcoRV sites of the pCMVSPORT 6 vector.
                     Library was not normalized."
ORIGIN
```

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  Query Match             15.8%;  Score 811;  DB 5;  Length 967;
  Best Local Similarity   90.3%;  Pred. No. 5.9e-166;
  Matches  859;  Conservative    0;  Mismatches   92;  Indels    0;  Gaps    0;

Qy       1893 GGAACGGGGGGTGCAGCCACCTGTGCTTCTTCACACCCCACGCAACCCGGTGTGGCTGCC 1952
             || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6 GGTACGGGGGGTGCAGCCACCTGTGCTTCTTCACACCCCACGCAACCCGGTGTGGCTGCC 65

Qy       1953 CCATCGGCCTGGAGCTGCTGAGTGACATGAAGACCTGCATCGTGCCTGAGGCCTTCTTGG 2012
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 CCATCGGCCTGGAGCTGCTGAGTGACATGAAGACCTGCATCGTGCCTGAGGCCTTCTTGG 125

Qy       2013 TCTTCACCAGCAGAGCCGCCATCCACAGGATCTCCCTCGAGACCAATAACAACGACGTGG 2072
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         126 TCTTCACCAGCAGAGCCGCCATCCACAGGATCTCCCTCGAGACCAATAACAACGACGTGG 185

Qy       2073 CCATCCCGCTCACGGGCGTCAAGGAGGCCTCAGCCCTGGACTTTGATGTGTCCAACAACC 2132
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         186 CCATCCCGCTCACGGGCGTCAAGGAGGCCTCAGCCCTGGACTTTGATGTGTCCAACAACC 245

Qy       2133 ACATCTACTGGACAGACGTCAGCCTGAAGACCATCAGCCGCGCCTTCATGAACGGGAGCT 2192
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Db         246 ACATCTACTGGACAGACGTCAGCCTGAAGACCATCAGCCGCGCCTTCATGAACGGGAGCT 305

Qy       2193 CGGTGGAGCACGTGGTGGAGTTTGGCCTTGACTACCCCGAGGGCATGGCCGTTGACTGGA 2252
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Db         306 CGGTGGAGCACGTGGTGGAGTTTGGCCTTGACTACCCCGAGGGCATGGCCGTTGACTGGA 365

Qy       2253 TGGGCAAGAACCTCTACTGGGCCGACACTGGGACCAACAGAATCGAAGTGGCGCGGCTGG 2312
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Db         366 TGGGCAAGAACCTCTACTGGGCCGACACTGGGACCAATAGAATCGAAGTGGCGCGGCTGG 425

Qy       2313 ACGGGCAGTTCCGGCAAGTCCTCGTGTGGAGGGACTTGGACAACCCGAGGTCGCTGGCCC 2372
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Db         426 ACGGGCAGTTCCGGCAAGTCCTCGTGTGGAGGGACTTGGACAACCCGAGGTCGCTGGCCC 485

Qy       2373 TGGATCCCACCAAGGGCTACATCTACTGGACCGAGTGGGGCGGCAAGCCGAGGATCGTGC 2432
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         486 TGGATCCCACCAAGGGCTACATCTACTGGACCGAGTGGGGCGGCAAGCCGAGGATCGTGC 545

Qy       2433 GGGCCTTCATGGACGGGACCAACTGCATGACGCTGGTGGACAAGGTGGGCCGGGCCAACG 2492
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         546 GGGCCTTCATGGACGGGACCAACTGCATGACGCTGGTGGACAAGGTGGGCCGGGCCAACG 605

Qy       2493 ACCTCACCATTGACTACGCTGACCAGCGCCTCTACTGGACCGACCTGGACACCAACATGA 2552
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         606 ACCTCACCATTGACTACGCTGACCAGCGCCTCTACTGGACCGACCTGGACACCAACATGA 665

Qy       2553 TCGAGTCGTCCAACATGCTGGGTCAGGAGCGGGTCGTGATTGCCGACGATCTCCCGCACC 2612
             |||||||||||||||||| ||||||||||||||||||||||           |||||||
Db         666 TCGAGTCGTCCAACATGCTGNGTCAGGAGCGGGTCGTGATTGCACGACGATCTCCGCACC 725

Qy       2613 CGTTCGGTCTGACGCAGTACAGCGATTATATCTACTGGACAGACTGGAATCTGCACAGCA 2672
             || |  |||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db         726 CGCTTCGTCTGACGCAGTACAGCGATTATTTCTACTGGACAGACTGGAATCTGCACAGCA 785

Qy       2673 TTGAGCGGGCCGACAAGACTAGCGGCCGGAACCGCACCCTCATCCAGGGCCACCTGGACT 2732
             |||||||| |||| |||||||||| |||| |||| |||||| |||| | |||| |||||||
Db         786 TTGAGCGGCGCGACATGACTAGCGGNCGGAAACGCATCCTCATNCAGGNNCCCCTGNACT 845

Qy       2733 TCGTGATGGACATCCTGGTGTTCCACTCCTCCCGCCAGGATGGCCTCAATGACTGTATGC 2792
             ||||||||    |  |   | || |    ||||    |    | | | ||    | | |
Db         846 NCGTGATGGCATACTGGTGTTCCCTCCTNNCCCGAGNAGCNCTCATGACTGTTGCCAACC 905

Qy       2793 ACAACAACGGGCAGTGTGGGCAGCTGTGCCTTGCCATCCCCGGCGGCCACC 2843
               |  ||  | |     |||||      | |      | || | |||   | |
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Db        906 TCGGCAGTGTGGCAGTTGGGCTTGCCTTTCCGCGGACCCGCTGCGNTTAGC 956


RESULT 9
BQ687102/c
LOCUS       BQ687102                870 bp    mRNA    linear   EST 15-JUL-2002
DEFINITION  AGENCOURT_8046500 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6209180
            5', mRNA sequence.
ACCESSION   BQ687102
VERSION     BQ687102.1  GI:21812406
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 870)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2368  row: a  column: 21
            High quality sequence stop: 680.
FEATURES             Location/Qualifiers
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                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_110"
                     /note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI;
                     Site_2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G). Library constructed  by
                     Ling Hong in the laboratory of Gerald M. Rubin (University
                     of  California, Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             15.7%;  Score 805.4;  DB 5;  Length 870;
  Best Local Similarity   98.6%;  Pred. No. 9.6e-165;
  Matches  823;  Conservative    0;  Mismatches   11;  Indels    1;  Gaps    1;

Qy       3415 GGCCCTGGTGGTGGACAACACACT-GGGCAAGCTGTTCTGGGTGGACGCGGACCTGAAGC 3473
              | || |||||||||||||||||||| |||||||||||||||||| |     ||||||||||
Db        835 GCCCGTGGTGGTGGACAACACACTGGGGCAAGCTGTTCTGGGGGACGCGGGACCTGAAGC 776

Qy       3474 GCATTGAGAGCTGTGACCTGTCAGGGGCCAACCGCCTGACCCTGGAGGACGCCAACATCG 3533
              |||||||||||||||||||||||||||||||||| ||| ||||||||||||||||||||
Db        775 GCATTGAGAGCTGTGACCTGTCAGGGGCCAACCGCTTGAACCTGGAGGACGCCAACATCG 716

Qy       3534 TGCAGCCTCTGGGCCTGACCATCCTTGGCAAGCATCTCTACTGGATCGACCGCCAGCAGC 3593
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        715 TGCAGCCTCTGGGCCTGACCATCCTTGGCAAGCATCTCTACTGGATCGACCGCCAGCAGC 656

Qy       3594 AGATGATCGAGCGTGTGGAGAAGACCACCGGGGACAAGCGGACTCGCATCCAGGGCCGTG 3653
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        655 AGATGATCGAGCGTGTGGAGAAGACCACCGGGGACAAGCGGACTCGCATCCAGGGCCGTG 596

Qy       3654 TCGCCCACCTCACTGGCATCCATGCAGTGGAGGAAGTCAGCCTGGAGGAGTTCTCAGCCC 3713
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        595 TCGCCCACCTCACTGGCATCCATGCAGTGGAGGAAGTCAGCCTGGAGGAGTTCTCAGCCC 536

Qy       3714 ACCCATGTGCCCGTGACAATGGTGGCTGCTCCCACATCTGTATTGCCAAGGGTGATGGGA 3773
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        535 ACCCATGTGCCCGTGACAATGGTGGCTGCTCCCACATCTGTATTGCCAAGGGTGATGGGA 476

Qy       3774 CACCACGGTGCTCATGCCCAGTCCACCTCGTGCTCCTGCAGAACCTGCTGACCTGTGGAG 3833
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        475 CACCACGGTGCTCATGCCCAGTCCACCTCGTGCTCCTGCAGAACCTGCTGACCTGTGGAG 416

Qy       3834 AGCCGCCCACCTGCTCCCCGGACCAGTTTGCATGTGCCACAGGGGAGATCGACTGTATCC 3893
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Db        415 AGCCGCCCACCTGCTCCCCGGACCAGTTTGCATGTGCCACAGGGGAGATCGACTGTATCC 356

Qy       3894 CCGGGGCCTGGCGCTGTGACGGCTTTCCCGAGTGCGATGACCAGAGCGACGAGGAGGGCT 3953
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        355 CCGGGGCCTGGCGCTGTGACGGCTTTCCCGAGTGCGATGACCAGAGCGACGAGGAGGGCT 296

Qy       3954 GCCCCGTGTGCTCCGCCGCCCAGTTCCCCTGCGCGCGGGGTCAGTGTGTGGACCTGCGCC 4013
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        295 GCCCCGTGTGCTCCGCCGCCCAGTTCCCCTGCGCGCGGGGTCAGTGTGTGGACCTGCGCC 236

Qy       4014 TGCGCTGCGACGGCGAGGCAGACTGTCAGGACCGCTCAGACGAGGTGGACTGTGACGCCA 4073
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Db        235 TGCGCTGCGACGGCGAGGCAGACTGTCAGGACCGCTCAGACGAGGCGGACTGTGACGCCA 176

Qy       4074 TCTGCCTGCCCAACCAGTTCCGGTGTGCGAGCGGCCAGTGTGTCCTCATCAAACAGCAGT 4133
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Db        175 TCTGCCTGCCCAACCAGTTCCGGTGTGCGAGCGGCCAGTGTGTCCTCATCAAACAGCAGT 116

Qy       4134 GCGACTCCTTCCCCGACTGTATCGACGGCTCCGACGAGCTCATGTGTGAAATCACCAAGC 4193
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Db        115 GCGACTCCTTCCCCGACTGTATCGACGGCTCCGACGAGCTCATGTGTGAAATCACCAAGC 56

Qy       4194 CGCCCTCAGACGACAGCCCGGCCCACAGCAGTGCCATCGGGCCCGTCATTGGCAT 4248
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Db         55 CGCCCTCAGACGACAGCCCGGCCCACAGCAGTGCCATCGGGCCCGTCATTGGCAT 1


RESULT 10
BX402085
LOCUS       BX402085                1001 bp    mRNA    linear   EST 29-APR-2004
DEFINITION  BX402085 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens
            cDNA clone CS0DC011YB06 5-PRIME, mRNA sequence.
ACCESSION   BX402085
VERSION     BX402085.2  GI:46876774
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1001)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     On May 13, 2003 this sequence version replaced gi:30622712.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen. This sequence belongs to sequence cluster
            6245.f
            For more information about this cluster, see
            http://www.genoscope.cns.fr/cdna?s=CS1AC003ZF04QP1&c=6245.f.
FEATURES             Location/Qualifiers
     source          1. .1001
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DC011YB06"
                     /tissue_type="NEUROBLASTOMA COT 25-NORMALIZED"
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/clone_lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 15.7%; Score 805; DB 5; Length 1001;
Best Local Similarity 96.3%; Pred. No. 1.2e-164;
Matches 873; Conservative 5; Mismatches 21; Indels 8; Gaps 5;

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Qy       2997 TGAGGAACGTCAAAGCCATCGACTATGACCCACTGGACAAGTTCATCTACTGGGTGGATG 3056
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Db          4 TGAGGAACGTCAAAGCCATCGACTATGACCCACTGGACAAGTTCATCTACTGGGTGGATG 63

Qy       3057 GGCGCCAGAACATCAAGCGAGCCAAGGACGACGGGACCCAGCCCTTTGTTTTGACCTCTC 3116
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Db         64 GGCGCCAGAACATCAAGCGAGCCAAGGACGACGGGACCCAGCCCTTTGTTTTGACCTCTC 123

Qy       3117 TGAGCCAAGGCCAAAACCCAGACAGGCAGCCCCACGACCTCAGCATCGACATCTACAGCC 3176
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 TGAGCCAAGGCCAAAACCCAGACAGGCAGCCCCACGACCTCAGCATCGACATCTACAGCC 183

Qy       3177 GGACACTGTTCTGGACGTGCGAGGCCACCAATACCATCAACGTCCACAGGCTGAGCGGGG 3236
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        184 GGACACTGTTCTGGACGTGCGAGGCCACCAATACCATCAACGTCCACAGGCTGAGCGGGG 243

Qy       3237 AAGCCATGGGGGTGGTGCTGCGTGGGGACCGCGACAAGCCCAGGGCCATCGTCGTCAACG 3296
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 AAGCCATGGGGGTGGTGCTGCGTGGGGACCGCGACAAGCCCAGGGCCATCGTCGTCAACG 303

Qy       3297 CGGAGCGAGGGTACCTGTACTTCACCAACATGCAGGACCGGGCAGCCAAGATCGAACGCG 3356
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Db        304 CGGA--SAGGGTACCTGTACTTCACCAACATGCAGGACCGGGCAGCCAAGATCGAACGCG 361

Qy       3357 CAGCCCTGGACGGCACCGAGCGCGAGGTCCTCTTCACCACCGGCCTCATCCGCCCTGTGG 3416
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Db        362 CA-CCCTGGACGGCACCGAGCGCGAGGTCCTCTTCACCACCGGCCTCATCCGCCCTGTGG 420

Qy       3417 CCCTGGTGGTGGACAACACACTGGGCAAGCTGTTCTGGGTGGACGCGGACCTGAAGCGCA 3476
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Db        421 CCCTGGTGGTAGACAACACACTGGGCAAGCTGTTCTGGGTGGACGCGGACCTGAAGCGCA 480

Qy       3477 TTGAGAGCTGTGACCTGTCAGGGGCCAACCGCCTGACCCTGGAGGACGCCAACATCGTGC 3536
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Db        481 TTGAGAGCTGTGACCTGTCAGGGGCCAACCGCCTGACCCTGGAGGACGCCAACATCGTGC 540

Qy       3537 AGCCTCTGGGCCTGACCATCCTTGGCAAGCATCTCTACTGGATCGACCGCCAGCAGCAGA 3596
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Db        541 AGCCTCTGGGCCTGACCATCCTTGGCAAGCATCTCTACTGGATCGACCGCCAGCAGCAGA 600

Qy       3597 TGATCGAGCGTGTGGAGAAGACCACCGGGGACAAGCGGACTCGCATCCAGGGCCGTGTCG 3656
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Db        661 CCCACCTCACTGGCATCCATGCAGTGGAGGAAGTCAGCCTGGAGGAGTTCTCAGCCCACC 720

Qy       3717 CATGTGCCCGTGACAATGGTGGCTGCTCCCACATCTGTATTGCCAAGGGTGATGGGACAC 3776
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Qy       3777 CACGGTGCTCATGCCCAGTCCACCTCGTGCTCCTGCAGAACCTGCTGACCTGTGGAGAGC 3836
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Db        780 CACGGTGCTCATGCCCAGTCCACCTCGTGCTCCTGCAGAACCTGCTGACCTGTGGAGAG- 838

Qy       3837 CGCCCACCTGCTCCCCGGACCAGTTTGCATGTGCCACAGGGGAGATCGACTGTATCCCCG 3896
             |||||||||||||| |  |   ||    |  :||:|:||||||||||   |  ||  |
Db        839 CGCCCACCTGCTCCCGGACCAGTTTCATGT---BCAMARGGGAGATCGATGTTTCCCGGG 895

Qy       3897 GGGCCTG 3903
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Db 896 GCTGCTS 902

RESULT 11
BM561582
LOCUS BM561582 986 bp mRNA linear EST 20-FEB-2002
DEFINITION AGENCOURT_6567315 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:5739763 5', mRNA sequence.
ACCESSION BM561582
VERSION BM561582.1 GI:18806953
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 986)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12753 row: j column: 20
High quality sequence stop: 680.

FEATURES Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5739763"
/tissue_type="duodenal adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_88"
/note="Organ: small intestine; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 1.767 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."

ORIGIN

Query Match 15.7%; Score 802.2; DB 4; Length 986;
Best Local Similarity 98.6%; Pred. No. 4.9e-164;
Matches 831; Conservative 0; Mismatches 8; Indels 4; Gaps 2;

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Qy       1797 CCAGCCGGGACGTCATCATTGACCAGCTGCCCGACCTGATGGGGCTCAAAGCTGTGAATG 1856
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Db          1 CCAGCCGGGACGTCATCATTGACCAGCTGCCCGACCTGATGGGGCTCAAAGCTGTGAATG 60

Qy       1857 TGGCCAAGGTCGTCGGAACCAACCCGTGTGCGGACAGGAACGGGGGGTGCAGCCACCTGT 1916
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Db         61 TGGCCAAGGTCGTCGGAACCAACCCGTGTGCGGACAGGAACGGGGGGTGCAGCCACCTGT 120

Qy       1917 GCTTCTTCACACCCCACGCAACCCGGTGTGGCTGCCCCATCGGCCTGGAGCTGCTGAGTG 1976
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Db        121 GCTTCTTCACACCCCACGCAACCCGGTGTGGCTGCCCCATCGGCCTGGAGCTGCTGAGTG 180

Qy       1977 ACATGAAGACCTGCATCGTGCCTGAGGCCTTCTTGGTCTTCACCAGCAGAGCCGCCATCC 2036
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Db        181 ACATGAAGACCTGCATCGTGCCTGAGGCCTTCTTGGTCTTCACCAGCAGAGCCGCCATCC 240

Qy       2037 ACAGGATCTCCCTCGAGACCAATAACAACGACGTGGCCATCCCGCTCACGGGCGTCAAGG 2096
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ACAGGATCTCCCTCGAGACCAATAACAACGACGTGGCCATCCCGCTCACGGGCGTCAAGG 300

Qy       2097 AGGCCTCAGCCCTGGACTTTGATGTGTCCAACAACCACATCTACTGGACAGACGTCAGCC 2156
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AGGCCTCAGCCCTGGACTTTGATGTGTCCAACAACCACATCTACTGGACAGACGTCAGCC 360
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Qy       2157 TGAAGACCATCAGCCGCGCCTTCATGAACGGGAGCTCGGTGGAGCACGTGGTGGAGTTTG 2216
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Db        361 TGAAGACCATCAGCCGCGCCTTCATGAACGGGAGCTCGGTGGAGCACGTGGTGGAGTTTG 420

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Db        421 GCCTTGACTACCCCGAGGGCATGGCCGTTGACTGGATGGGCAAGAACCTCTACTGGGCCG 480

Qy       2277 ACACTGGGACCAACAGAATCGAAGTGGCGCGGCTGGACGGGCAGTTCCGGCAAGTCCTCG 2336
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Db        481 ACACTGGGACCAACAGAATCGAAGTGGCGCGGCTGGACGGGCAGTTCCGGCAAGTCCTCG 540

Qy       2337 TGTGGAGGGACTTGGACAACCCGAGGTCGCTGGCCCTGGATCCCACCAAGGGCTACATCT 2396
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Db        541 TGTGGAGGGACTTGGACAACCCGAGGTCGCTGGCCCTGGATCCCACCAAGGGCTACATCT 600

Qy       2397 ACTGGACCGAGTGGGGCGGCAAGCCGAGGATCGTGCGGGCCTTCATGGACGGGACCAACT 2456
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Db        601 ACTGGACCGAGTGGGGCGGCAAGCCGAGGATCGTGCGGGCCTTCATGGACGGGACCAACT 660

Qy       2457 GCATGACGCTGGTGGACAAGGTGGGCCGGGCCAACGACCTCACCATTGACTACGCTGACC 2516
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Qy       2517 AGCGCCTCTACTGGACCGACCTGGACACCAACATGATCGAGTCGTCCAACATGCTGGG-- 2574
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Db        721 AGCGCCTCTACTGGACCGACCTGGACACCAACATGATCGAGTCGTCCAACATGCTGGGGT 780

Qy       2575 TCAGGAGCGGGTCGTGATTGCCGACGATCTCCCGCA--CCCGTTCGGTCTGACGCAGTAC 2632
                ||||||||||||||||||||||||||||||||  ||  |  || ||||||||||||
Db        781 CAGGGAGCGGGTCGTGATTGCCGACGATCTCCCGCAACCCGTTCGGGCCTGACGCAGTAC 840

Qy       2633 AGC 2635
              |||
Db        841 AGC 843


RESULT 12
BM006571/c
LOCUS       BM006571                 932 bp    mRNA    linear   EST 30-OCT-2001
DEFINITION  603615546F1 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:5421467 5',
            mRNA sequence.
ACCESSION   BM006571
VERSION     BM006571.1  GI:16520925
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 932)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1877  row: 1  column: 12
            High quality sequence stop: 757.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5421467"
                     /tissue_type="ductal carcinoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_110"
                     /note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI;
                     Site_2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G). Library constructed by
                     Ling Hong in the laboratory of Gerald M. Rubin (University
                     of California, Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library."
ORIGIN

  Query Match            15.3%;  Score 783.6;  DB 4;  Length 932;
  Best Local Similarity  96.4%;  Pred. No. 5.6e-160;
  Matches  866;  Conservative    0;  Mismatches   24;  Indels    8;  Gaps    6;

Qy       3356 GCAGCCCTGGACGGCACCGAGCGCGAGGTCCTCTTCACCACCGGCCTCATCCGCCCTGTG 3415
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Db        895 GCCAGCCTGGACGGCAACGAGCGCGGGTCCGTGGTCACCACCGG-CTCAACCGCCCTGTG 837

Qy       3416 GCCCTGGTGGTGGACAACACACTGGGCAAGCT-GTTCTGGGTGGACGCGGACCTGAAGCG 3474
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Db        836 G-CCTGGTGGTGGCAAACACACTGGGCAAGCTGGTTCTGGGGGGACGCGGACCTGAAGCG 778

Qy       3475 CATTGAGAGCTGTGACCTGTCAGGGGCCAACCGCCTGACCCTGGAGGACG-CCAACATCG 3533
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Qy       3534 TGCA--GCCTCTGGGCCTGACCATCCTTGGCAAGCATCTCTACTGGATCGACCGCCAGCA 3591
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Db        719 TGCAAGCCTCTGGGGCCTGACCATCCTTGGCAAGCATCTCTACTGGATCGACCGCCAGCA 660

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Qy       3652 TGTCGCCCACCTCACTGGCATCCATGCAGTGGAGGAAGTCAGCCTGGAGGAGTTCTCAGC 3711
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Db        539 CCACCCATGTGCCCGTGACAATGGTGGCTGCTCCCACATCTGTATTGCCAAGGGTGATGG 480

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Db        479 GACACCACGGTGCTCATGCCCAGTCCACCTCGTGCTCCTGCAGAACCTGCTGACCTGTGG 420

Qy       3832 AGAGCCGCCCACCTGCTCCCCGGACCAGTTTGCATGTGCCACAGGGGAGATCGACTGTAT 3891
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Db        419 AGAGCCGCCCACCTGCTCCCCGGACCAGTTTGCATGTGCCACAGGGGAGATCGACTGTAT 360

Qy       3892 CCCCGGGGCCTGGCGCTGTGACGGCTTTCCCGAGTGCGATGACCAGAGCGACGAGGAGGG 3951
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        359 CCCCGGGGCCTGGCGCTGTGACGGCTTTCCCGAGTGCGATGACCAGAGCGACGAGGAGGG 300

Qy       3952 CTGCCCCGTGTGCTCCGCCGCCCAGTTCCCCTGCGCGCGGGGTCAGTGTGTGGACCTGCG 4011
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Qy       4012 CCTGCGCTGCGACGGCGAGGCAGACTGTCAGGACCGCTCAGACGAGGTGGACTGTGACGC 4071
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Db        119 GTGCGACTCCTTCCCCGACTGTATCGACGGCTCCGACGAGCTCATGTGTGAAATCACCAA 60

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RESULT 13
BQ228206
LOCUS       BQ228206                855 bp    mRNA    linear   EST 02-MAY-2002
DEFINITION  AGENCOURT_7593499 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:6020654
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ACCESSION   BQ228206
VERSION     BQ228206.1  GI:20409606
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 855)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM13225  row: b  column: 15
            High quality sequence stop: 608.
FEATURES             Location/Qualifiers
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                     /lab_host="DH10B (phage-resistant)"
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                     /note="Organ: pancreas; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.1 kb.   Library constructed by Life
                     Technologies."
ORIGIN

  Query Match            15.3%;  Score 783.4;  DB 5;  Length 855;
  Best Local Similarity  97.9%;  Pred. No. 6.1e-160;
  Matches  836;  Conservative    0;  Mismatches   12;  Indels    6;  Gaps    4;

Qy       3089 GGGACCCAGCCCTTTGTTTTGACCTCTCTGAGCCAAGGCCAAAACCCAGACAGGCAGCCC 3148
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Db          1 GGGACCCAGCCCTTTGTTTTGACCTCTCTGAGCCAAGGCCAAAACCCAGACAGGCAGCCC 60

Qy       3149 CACGACCTCAGCATCGACATCTACAGCCGGACACTGTTCTGGACGTGCGAGGCCACCAAT 3208
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Db         61 CACGACCTCAGCATCGACATCTACAGCCGGACACTGTTCTGGACGTGCGAGGCCACCAAT 120

Qy       3209 ACCATCAACGTCCACAGGCTGAGCGGGGAAGCCATGGGGGTGGTGCTGCGTGGGGACCGC 3268
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Db        121 ACCATCAACGTCCACAGGCTGAGCGGGGAAGCCATGGGGGTGGTGCTGCGTGGGGACCGC 180

Qy       3269 GACAAGCCCAGGGCCATCGTCGTCAACGCGGAGCGAGGGTACCTGTACTTCACCAACATG 3328
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Qy       3329 CAGGACCGGGCAGCCAAGATCGAACGCGCAGCCCTGGACGGCACCGAGCGCGAGGTCCTC 3388
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Qy       3449 TTCTGGGTGGACGCGGACCTGAAGCGCATTGAGAGCTGTGACCTGTCAGGGGCCAACCGC 3508
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Db        361 TTCTGGGTGGACGCGGACCTGAAGCGCATTGAGAGCTGTGACCTGTCAGGGGCCAACCGC 420

Qy       3509 CTGACCCTGGAGGACGCCAACATCGTGCAGCCTCTGGGCCTGACCATCCTTGGCAAGCAT 3568
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Db        421 CTGACCCTGGAGGACGCCAACATCGTGCAGCCTCTGGGCCTGACCATCCTTGGCAAGCAT 480

Qy       3569 CTCTACTGGATCGACCGCCAGCAGCAGATGATCGAGCGTGTGGAGAAGACCACCGGGGAC 3628
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Db        481 CTCTACTGGATCGACCGCCAGCAGCAGATGATCGAGCGTGTGGAGAAGACCACCGGGGAC 540

Qy       3629 AAGCGGACTCGCATCCAGGGCCGTGTCGCCCACCTCACTGGCATCCATGCAGTGGAGGAA 3688
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Qy       3809 CTGCAGAACCTGCTGACCTGTGGAGAGCCGCCCACCT-GCTCCCCGGACCAGTTTGCATG 3867
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Db        721 CTGCAGAACCTGCTGACCTGTGGAGAGCCGCCCACCTGGCTCCCCGNACCAGTTTGCATT 780

Qy       3868 TGCC--ACAGGGGAGATCGACTGTATCCCC--GGGGCCTGGCGCTGTGACGGCTTT-CCC 3922
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Db        781 GCCCCACAGGGGAAGATCGACTGTATCCCCCGGGGGCTGGGCGCTGTGACGGCTTTCCCC 840

Qy       3923 GAGTGCGATGACCA 3936
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RESULT 14
BU195422
LOCUS       BU195422                902 bp    mRNA    linear   EST 04-SEP-2002
DEFINITION  AGENCOURT_7951926 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:6171960
            5', mRNA sequence.
ACCESSION   BU195422
VERSION     BU195422.1  GI:22709406
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 902)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM13541  row: c  column: 01
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                Technologies."
ORIGIN

  Query Match           15.3%;  Score 782.8;  DB 5;  Length 902;
  Best Local Similarity   95.5%;  Pred. No. 8.3e-160;
  Matches  861;  Conservative    0;  Mismatches   32;  Indels    9;  Gaps    5;

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Db        181 TGTGCCCGTGACAATGGTGGCTGCTCCCACATCTGTATTGCCAAGGGTGATGGGACACCA 240

Qy       3779 CGGTGCTCATGCCCAGTCCACCTCGTGCTCCTGCAGAACCTGCTGACCTGTGGAGAGCCG 3838
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Qy       3899 GCCTGGCGCTGTGACGGCTTTCCCGAGTGCGATGACCAGAGCGACGAGGAGGGCTGCCCC 3958
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Qy       3959 GTGTGCTCCGCCGCCCAGTTCCCCTGCGCGCGGGGTCAGTGTGTGGACCTGCGCCTGCGC 4018
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Qy       4019 TGCGACGGCGAGGCAGACTGTCAGGACCGCTCAGACGAGGTGGACTGTGACGCCATCTGC 4078
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Qy       4430 GG 4431
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RESULT 15
BX453469/c
LOCUS       BX453469                911 bp    mRNA    linear   EST 05-MAY-2004
DEFINITION  BX453469 Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DE011YM02
            3-PRIME, mRNA sequence.
ACCESSION   BX453469
VERSION     BX453469.2  GI:47056383
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 911)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     On May 22, 2003 this sequence version replaced gi:31024493.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
            was not normalized. Library was constructed by Life Technologies, a
            division of Invitrogen.
            This sequence belongs to sequence cluster 6245.f
            For more information about this cluster, see
            http://www.genoscope.cns.fr/cdna?s=CS0BAI009ZA06_CS00809_2&c=6245.f
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                     /clone="CS0DE011YM02"
                     /tissue_type="PLACENTA"
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                     /note="Vector: pCMVSPORT_6; 1st strand cDNA was primed
                     with a NotI-oligo(dT) primer. Five prime end enriched,
                     double-strand cDNA was digested with Not I and cloned into
                     the Not I and EcoRV sites of the pCMVSPORT 6 vector.
                     Library was not normalized."
ORIGIN

  Query Match           15.2%;  Score 780.6;  DB 5;  Length 911;
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Qy       3364 GGACGGCACCGAGCGCG--AGGTCCTCTTCACCACCGGCCTCAT-CCGCCCTGTGGCCCT 3420
             |||| |   |||| |||  ||||| | || |||||||| ||||| ||||||||||||||||
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Qy       3421 GGTGGTGGACAACACACTGGGCAAGCTGTTCT-GGGTGGACGCGGACCTGAAGCGCATTG 3479
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Db        491 GTGCCCGTGACAATGGTGGCTGCTCCCACATCTGTATTGCCAAGGGTGATGGGACACCAC 432

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Db        431 GGTGCTCATGCCCAGTCCACCTCGTGCTCCTGCAGAACCTGCTGACCTGTGGAGAGCCGC 372

Qy       3840 CCACCTGCTCCCCGGACCAGTTTGCATGTGCCACAGGGGAGATCGACTGTATCCCCGGGG 3899
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Qy       3900 CCTGGCGCTGTGACGGCTTTCCCGAGTGCGATGACCAGAGCGACGAGGAGGGCTGCCCCG 3959
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Qy       4140 CCTTCCCCGACTGTATCGACGGCTCCGACGAGCTCATGTGTGAAATCACCAAGCCGCCCT 4199
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Job time : 15029 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 18, 2005, 19:27:08 ; Search time 21134 Seconds
(without alignments)
11738.938 Million cell updates/sec

Title: US-10-680-287A-2
Perfect score: 5120
Sequence: 1 actaaagcgccgccgccgcg.....aaacttaatttttgtaaaaca 5120

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: gb_htg:*
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5: gb_ov:*
6: gb_pat:*
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10: gb_ro:*
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12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	5120	100.0	5120	6	AR567476	AR567476 Sequence
2	5120	100.0	5120	6	AX277523	AX277523 Sequence
3	5120	100.0	5120	6	AX418087	AX418087 Sequence
4	5118.4	100.0	5120	6	AR567475	AR567475 Sequence
5	5118.4	100.0	5120	6	AX277522	AX277522 Sequence
6	5118.4	100.0	5120	6	AX418086	AX418086 Sequence
7	5094.8	99.5	5099	6	CQ870240	CQ870240 Sequence
8	5091.6	99.4	5135	6	AX658229	AX658229 Sequence
9	5091.6	99.4	5135	9	AF077820	AF077820 Homo sapi
10	5077.4	99.2	5100	6	AX821900	AX821900 Sequence
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12	5053.4	98.7	5098	6	AR305075	AR305075 Sequence
13	5053.4	98.7	5098	6	AR309179	AR309179 Sequence
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15	5048.8	98.6	5135	6	CQ870242	CQ870242 Sequence
16	5014.2	97.9	5059	9	AB017498	AB017498 Homo sapi
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ALIGNMENTS

RESULT 1
AR567476
LOCUS AR567476 5120 bp DNA linear PAT 08-OCT-2004
DEFINITION Sequence 2 from patent US 6780609.
ACCESSION AR567476
VERSION AR567476.1 GI:53985258
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 5120)
AUTHORS Carulli,J.P., Little,R.D., Recker,R.R. and Johnson,M.L.
TITLE High bone mass gene of 1.1q13.3
JOURNAL Patent: US 6780609-A 2 24-AUG-2004;
FEATURES Location/Qualifiers
source 1. .5120
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ORIGIN

Query Match 100.0%; Score 5120; DB 6; Length 5120;
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Matches 5120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        481 CAATGGCACATCCCGGAAGGTGCTCTTCTGGCAGGACCTTGACCAGCCGAGGGCCATCGC 540
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Qy        541 CTTGGACCCCGCTCACGGGTACATGTACTGGACAGACTGGGTTGAGACGCCCCGGATTGA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        601 GCGGGCAGGGATGGATGGCAGCACCCGGAAGATCATTGTGGACTCGGACATTTACTGGCC 660
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Db        601 GCGGGCAGGGATGGATGGCAGCACCCGGAAGATCATTGTGGACTCGGACATTTACTGGCC 660

Qy        661 CAATGGACTGACCATCGACCTGGAGGAGCAGAAGCTCTACTGGGCTGACGCCAAGCTCAG 720
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Qy        721 CTTCATCCACCGTGCCAACCTGGACGGCTCGTTCCGGCAGAAGGTGGTGGAGGGCAGCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CTTCATCCACCGTGCCAACCTGGACGGCTCGTTCCGGCAGAAGGTGGTGGAGGGCAGCCT 780

Qy        781 GACGCACCCCTTCGCCCTGACGCTCTCCGGGGACACTCTGTACTGGACAGACTGGCAGAC 840
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Db        781 GACGCACCCCTTCGCCCTGACGCTCTCCGGGGACACTCTGTACTGGACAGACTGGCAGAC 840

Qy        841 CCGCTCCATCCATGCCTGCAACAAGCGCACTGGGGGGAAGAGGAAGGAGATCCTGAGTGC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CCGCTCCATCCATGCCTGCAACAAGCGCACTGGGGGGAAGAGGAAGGAGATCCTGAGTGC 900

Qy        901 CCTCTACTCACCCATGGACATCCAGGTGCTGAGCCAGGAGCGGCAGCCTTTCTTCCACAC 960
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Qy        961 TCGCTGTGAGGAGGACAATGGCGGCTGCTCCCACCTGTGCCTGCTGTCCCCAAGCGAGCC 1020
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Qy       1021 TTTCTACACATGCGCCTGCCCCACGGGTGTGCAGCTGCAGGACAACGGCAGGACGTGTAA 1080
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Qy       1081 GGCAGGAGCCGAGGAGGTGCTGCTGCTGGCCCGGCGGACGGACCTACGGAGGATCTCGCT 1140
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Qy       1201 CATCGACTACGACCCGCTAGAGGGCTATGTCTACTGGACAGATGACGAGGTGCGGGCCAT 1260
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Db       1261 CCGCAGGGCGTACCTGGACGGGTCTGGGGCGCAGACGCTGGTCAACACCGAGATCAACGA 1320

Qy       1321 CCCCGATGGCATCGCGGTCGACTGGGTGGCCCGAAACCTCTACTGGACCGACACGGGCAC 1380
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Db       1321 CCCCGATGGCATCGCGGTCGACTGGGTGGCCCGAAACCTCTACTGGACCGACACGGGCAC 1380

Qy       1381 GGACCGCATCGAGGTGACGCGCCTCAACGGCACCTCCCGCAAGATCCTGGTGTCGGAGGA 1440
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Qy       1921 CTTCACACCCCACGCAACCCGGTGTGGCTGCCCCATCGGCCTGGAGCTGCTGAGTGACAT 1980
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Db       1981 GAAGACCTGCATCGTGCCTGAGGCCTTCTTGGTCTTCACCAGCAGAGCCGCCATCCACAG 2040

Qy       2041 GATCTCCCTCGAGACCAATAACAACGACGTGGCCATCCCGCTCACGGGCGTCAAGGAGGC 2100
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Qy       2341 GAGGGACTTGGACAACCCGAGGTCGCTGGCCCTGGATCCCACCAAGGGCTACATCTACTG 2400
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Db       2341 GAGGGACTTGGACAACCCGAGGTCGCTGGCCCTGGATCCCACCAAGGGCTACATCTACTG 2400

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Qy      2461 GACGCTGGTGGACAAGGTGGGCCGGGCCAACGACCTCACCATTGACTACGCTGACCAGCG 2520
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Qy      2581 GCGGGTCGTGATTGCCGACGATCTCCCGCACCCGTTCGGTCTGACGCAGTACAGCGATTA 2640
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Qy      3001 GAACGTCAAAGCCATCGACTATGACCCACTGGACAAGTTCATCTACTGGGTGGATGGGCG 3060
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Qy      3241 CATGGGGGTGGTGCTGCGTGGGGACCGCGACAAGCCCAGGGCCATCGTCGTCAACGCGGA 3300
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Qy      3301 GCGAGGGTACCTGTACTTCACCAACATGCAGGACCGGGCAGCCAAGATCGAACGCGCAGC 3360
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DEFINITION  Sequence 2 from Patent WO0177327.
ACCESSION   AX277523
VERSION     AX277523.1  GI:16604716
KEYWORDS    .
SOURCE      Homo sapiens (human)
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            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE   1
  AUTHORS   Carulli,J.P., Little,R.D., Recker,R.R. and Johnson,M.L.
  TITLE     The high bone mass gene of 11q13.3
  JOURNAL   Patent: WO 0177327-A 2 18-OCT-2001;
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FEATURES             Location/Qualifiers
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ORIGIN

  Query Match             100.0%;  Score 5120;  DB 6;  Length 5120;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 5120;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy        241 CGTGGTCAGCGGCCTGGAGGATGCGGCCGCAGTGGACTTCCAGTTTTCCAAGGGAGCCGT 300

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Db        361 CGCCGTGCAGAACGTGGTCATCTCCGGCCTGGTCTCTCCCGACGGCCTCGCCTGCGACTG 420

Qy        421 GGTGGGCAAGAAGCTGTACTGGACGGACTCAGAGACCAACCGCATCGAGGTGGCCAACCT 480

Db        421 GGTGGGCAAGAAGCTGTACTGGACGGACTCAGAGACCAACCGCATCGAGGTGGCCAACCT 480

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Db       1201 CATCGACTACGACCCGCTAGAGGGCTATGTCTACTGGACAGATGACGAGGTGCGGGCCAT 1260
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Qy       1261 CCGCAGGGCGTACCTGGACGGGTCTGGGGCGCAGACGCTGGTCAACACCGAGATCAACGA 1320
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Qy       4981 AAAAAATATATTTTATGATTTAAAAAATAAATATAATTGGGATTTTAAAAACATGAGAAA 5040
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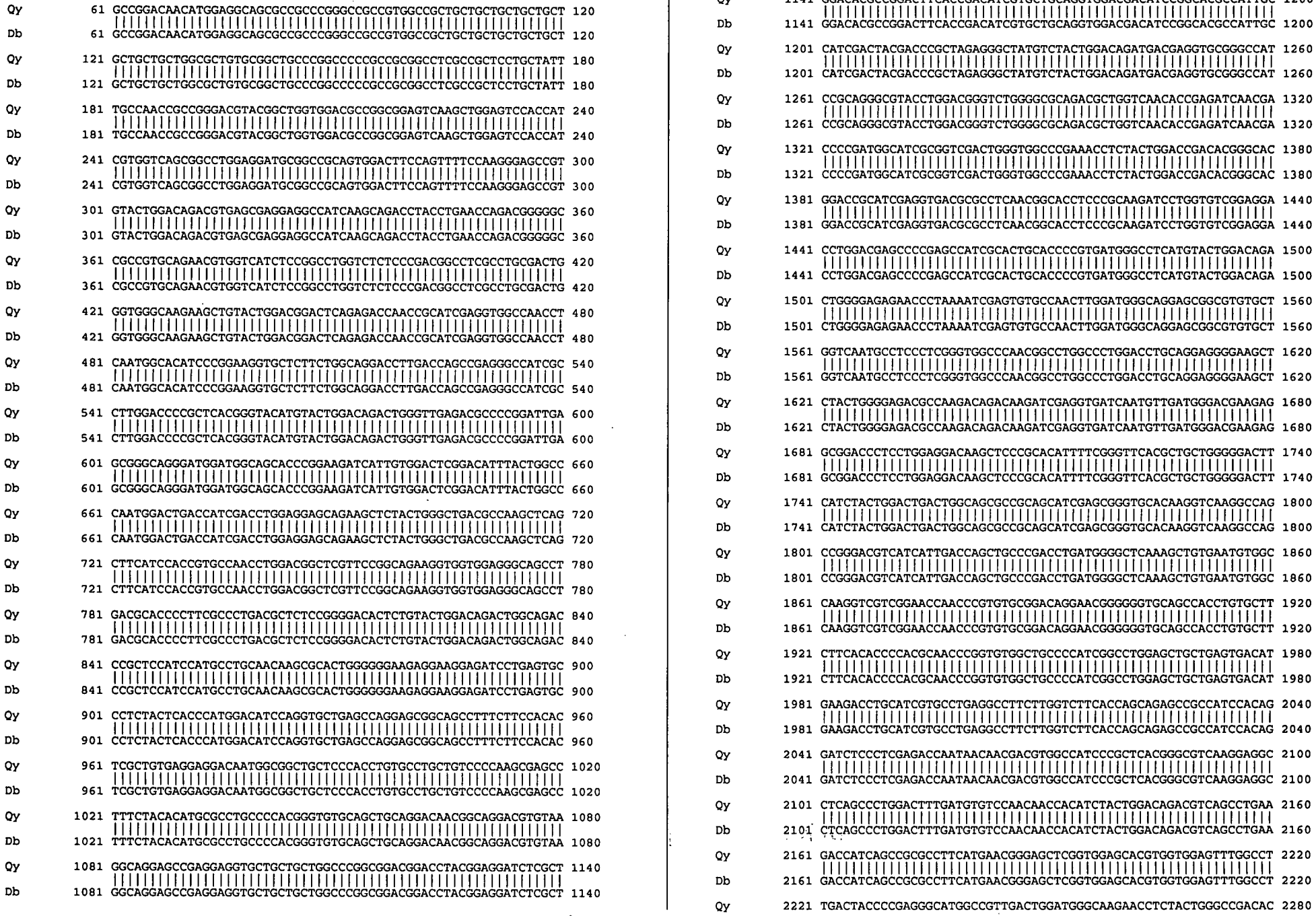
Qy       5041 TGTGAACTGTGATGGGGTGGGCAGGGCTGGGAGAACTTTGTACAGTGGAGAAATATTTAT 5100
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Qy       5101 AAACTTAATTTTGTAAAACA 5120
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Db       5101 AAACTTAATTTTGTAAAACA 5120


RESULT 3
AX418087
LOCUS       AX418087               5120 bp    DNA     linear   PAT 18-JUN-2002
DEFINITION  Sequence 2 from Patent WO0192891.
ACCESSION   AX418087
VERSION     AX418087.1  GI:21523101
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Carulli,J.P., Little,R.D., Recker,R.R. and Johnson,M.L.
  TITLE     Regulating lipid levels via the Zmax1 or HBM gene
  JOURNAL   Patent: WO 0192891-A 2 06-DEC-2001;
            Genome Therapeutics Corporation (US) ; Creighton University School
            of Medicine (US)
FEATURES             Location/Qualifiers
     source          1. .5120
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                     /mol_type="unassigned DNA"
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ORIGIN

  Query Match            100.0%;  Score 5120;  DB 6;  Length 5120;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 5120;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ACTAAAGCGCCGCCGCCGCGCCATGGAGCCCGAGTGAGCGCGGCGCGGGCCCGTCCGGCC 60
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Qy      2341 GAGGGACTTGGACAACCCGAGGTCGCTGGCCCTGGATCCCACCAAGGGCTACATCTACTG 2400
Db      2341 GAGGGACTTGGACAACCCGAGGTCGCTGGCCCTGGATCCCACCAAGGGCTACATCTACTG 2400
Qy      2401 GACCGAGTGGGGCGGCAAGCCGAGGATCGTGCGGGCCTTCATGGACGGGACCAACTGCAT 2460
Db      2401 GACCGAGTGGGGCGGCAAGCCGAGGATCGTGCGGGCCTTCATGGACGGGACCAACTGCAT 2460
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Qy      2521 CCTCTACTGGACCGACCTGGACACCAACATGATCGAGTCGTCCAACATGCTGGGTCAGGA 2580
Db      2521 CCTCTACTGGACCGACCTGGACACCAACATGATCGAGTCGTCCAACATGCTGGGTCAGGA 2580
Qy      2581 GCGGGTCGTGATTGCCGACGATCTCCCGCACCCGTTCGGTCTGACGCAGTACAGCGATTA 2640
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Qy      2641 TATCTACTGGACAGACTGGAATCTGCACAGCATTGAGCGGGCCGACAAGACTAGCGGCCG 2700
Db      2641 TATCTACTGGACAGACTGGAATCTGCACAGCATTGAGCGGGCCGACAAGACTAGCGGCCG 2700
Qy      2701 GAACCGCACCCTCATCCAGGGCCACCTGGACTTCGTGATGGACATCCTGGTGTTCCACTC 2760
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Qy      2761 CTCCCGCCAGGATGGCCTCAATGACTGTATGCACAACAACGGGCAGTGTGGGCAGCTGTG 2820
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Qy      2881 CAGCCGCAACTGCAGCCCGCCCACCACCTTCTTGCTGTTCAGCCAGAAATCTGCCATCAG 2940
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Qy      2941 TCGGATGATCCCGGACGACCAGCACAGCCCGGATCTCATCCTGCCCCTGCATGGACTGAG 3000
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Qy      3001 GAACGTCAAAGCCATCGACTATGACCCACTGGACAAGTTCATCTACTGGGTGGATGGGCG 3060
Db      3001 GAACGTCAAAGCCATCGACTATGACCCACTGGACAAGTTCATCTACTGGGTGGATGGGCG 3060
Qy      3061 CCAGAACATCAAGCGAGCCAAGGACGACGGGACCCAGCCCTTTGTTTTGACCTCTCTGAG 3120
Db      3061 CCAGAACATCAAGCGAGCCAAGGACGACGGGACCCAGCCCTTTGTTTTGACCTCTCTGAG 3120
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Db      3121 CCAAGGCCAAAACCCAGACAGGCAGCCCCACGACCTCAGCATCGACATCTACAGCCGGAC 3180
Qy      3181 ACTGTTCTGGACGTGCGAGGCCACCAATACCATCAACGTCCACAGGCTGAGCGGGGAAGC 3240
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Qy      3241 CATGGGGGTGGTGCTGCGTGGGGACCGCGACAAGCCCAGGGCCATCGTCGTCAACGCGGA 3300
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Qy      3421 GGTGGTGGACAACACACTGGGCAAGCTGTTCTGGGTGGACGCGGACCTGAAGCGCATTGA 3480
Db      3421 GGTGGTGGACAACACACTGGGCAAGCTGTTCTGGGTGGACGCGGACCTGAAGCGCATTGA 3480
Qy      3481 GAGCTGTGACCTGTCAGGGGCCAACCGCCTGACCCTGGAGGACGCCAACATCGTGCAGCC 3540
Db      3481 GAGCTGTGACCTGTCAGGGGCCAACCGCCTGACCCTGGAGGACGCCAACATCGTGCAGCC 3540
Qy      3541 TCTGGGCCTGACCATCCTTGGCAAGCATCTCTACTGGATCGACCGCCAGCAGCAGATGAT 3600
Db      3541 TCTGGGCCTGACCATCCTTGGCAAGCATCTCTACTGGATCGACCGCCAGCAGCAGATGAT 3600
Qy      3601 CGAGCGTGTGGAGAAGACCACCGGGGACAAGCGGACTCGCATCCAGGGCCGTGTCGCCCA 3660
Db      3601 CGAGCGTGTGGAGAAGACCACCGGGGACAAGCGGACTCGCATCCAGGGCCGTGTCGCCCA 3660
Qy      3661 CCTCACTGGCATCCATGCAGTGGAGGAAGTCAGCCTGGAGGAGTTCTCAGCCCACCCATG 3720
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Qy      3721 TGCCCGTGACAATGGTGGCTGCTCCCACATCTGTATTGCCAAGGGTGATGGGACACCACG 3780
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Qy      3781 GTGCTCATGCCCAGTCCACCTCGTGCTCCTGCAGAACCTGCTGACCTGTGGAGAGCCGCC 3840
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Qy      3901 CTGGCGCTGTGACGGCTTTCCCGAGTGCGATGACCAGAGCGACGAGGAGGGCTGCCCCGT 3960
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Qy      4081 GCCCAACCAGTTCCGGTGTGCGAGCGGCCAGTGTGTCCTCATCAAACAGCAGTGCGACTC 4140
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Qy      4201 AGACGACAGCCCGGCCCACAGCAGTGCCATCGGGCCCGTCATTGGCATCATCCTCTCTCT 4260
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Qy      4261 CTTCGTCATGGGTGGTGTCTATTTTGTGTGCCAGCGCGTGGTGTGCCAGCGCTATGCGGG 4320
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Qy      4321 GGCCAACGGGCCCTTCCCGCACGAGTATGTCAGCGGGACCCCGCACGTGCCCCTCAATTT 4380
Db      4321 GGCCAACGGGCCCTTCCCGCACGAGTATGTCAGCGGGACCCCGCACGTGCCCCTCAATTT 4380
Qy      4381 CATAGCCCCGGGCGGTTCCCAGCATGGCCCCTTCACAGGCATCGCATGCGGAAAGTCCAT 4440
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Db       4441 GATGAGCTCCGTGAGCCTGATGGGGGGCCGGGGCGGGGTGCCCCTCTACGACCGGAACCA 4500

Qy       4501 CGTCACAGGGGCCTCGTCCAGCAGCTCGTCCAGCACGAAGGCCACGCTGTACCCGCCGAT 4560
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Qy       4561 CCTGAACCCGCCGCCCTCCCCGGCCACGGACCCCTCCCTGTACAACATGGACATGTTCTA 4620
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Db       4561 CCTGAACCCGCCGCCCTCCCCGGCCACGGACCCCTCCCTGTACAACATGGACATGTTCTA 4620

Qy       4621 CTCTTCAAACATTCCGGCCACTGCGAGACCGTACAGGCCCTACATCATTCGAGGAATGGC 4680
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Qy       4681 GCCCCCGACGACGCCCTGCAGCACCGACGTGTGTGACAGCGACTACAGCGCCAGCCGCTG 4740
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Qy       4741 GAAGGCCAGCAAGTACTACCTGGATTTGAACTCGGACTCAGACCCCTATCCACCCCCACC 4800
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Qy       4981 AAAAAATATATTTTATGATTTAAAAAATAAATATAATTGGGATTTTAAAAACATGAGAAA 5040
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Qy       5041 TGTGAACTGTGATGGGGTGGGCAGGGCTGGGAGAACTTTGTACAGTGGAGAAATATTTAT 5100
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Qy       5101 AAACTTAATTTTGTAAAACA 5120
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Db       5101 AAACTTAATTTTGTAAAACA 5120
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RESULT 4
AR567475
LOCUS       AR567475               5120 bp    DNA     linear   PAT 08-OCT-2004
DEFINITION  Sequence 1 from patent US 6780609.
ACCESSION   AR567475
VERSION     AR567475.1  GI:53985257
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 5120)
  AUTHORS   Carulli,J.P., Little,R.D., Recker,R.R. and Johnson,M.L.
  TITLE     High bone mass gene of 1.1q13.3
  JOURNAL   Patent: US 6780609-A 1 24-AUG-2004;
FEATURES             Location/Qualifiers
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ORIGIN

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Qy         61 GCCGGACAACATGGAGGCAGCGCCGCCCGGGCCGCCGTGGCCGCTGCTGCTGCTGCTGCT 120
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Qy        121 GCTGCTGCTGGCGCTGTGCGGCTGCCCGGCCCCCGCCGCGGCCTCGCCGCTCCTGCTATT 180
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Qy        181 TGCCAACCGCCGGGACGTACGGCTGGTGGACGCCGGCGGAGTCAAGCTGGAGTCCACCAT 240
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Qy        241 CGTGGTCAGCGGCCTGGAGGATGCGGCCGCAGTGGACTTCCAGTTTTCCAAGGGAGCCGT 300
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Qy        301 GTACTGGACAGACGTGAGCGAGGAGGCCATCAAGCAGACCTACCTGAACCAGACGGGGGC 360
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Qy        361 CGCCGTGCAGAACGTGGTCATCTCCGGCCTGGTCTCTCCCGACGGCCTCGCCTGCGACTG 420
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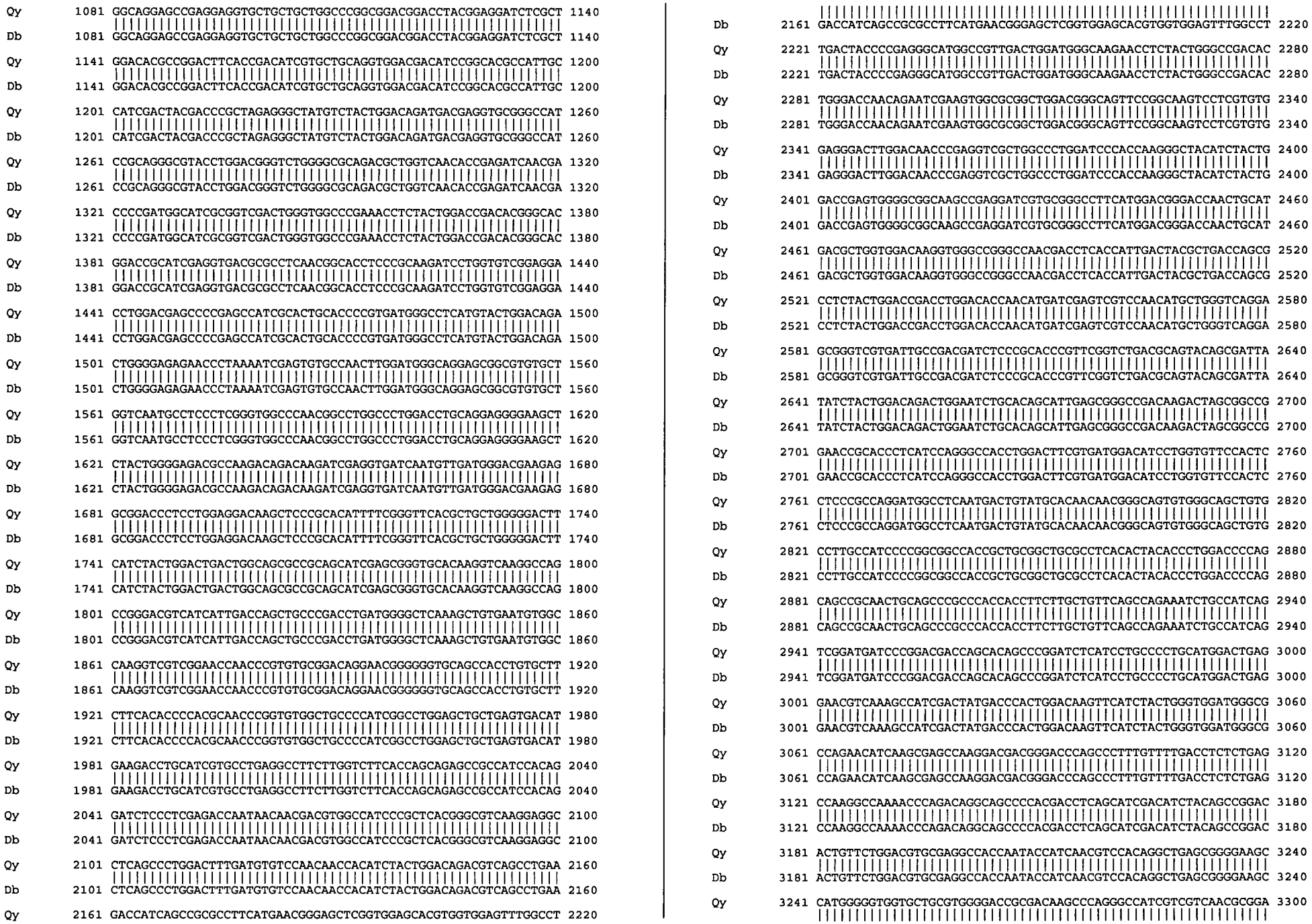
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Qy        901 CCTCTACTCACCCATGGACATCCAGGTGCTGAGCCAGGAGCGGCAGCCTTTCTTCCACAC 960
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RESULT 5
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DEFINITION Sequence 1 from Patent WO0177327.
ACCESSION AX277522
VERSION AX277522.1 GI:16604715
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Carulli,J.P., Little,R.D., Recker,R.R. and Johnson,M.L.
TITLE The high bone mass gene of 11q13.3
JOURNAL Patent: WO 0177327-A 1 18-OCT-2001;
Genome Therapeutics Corporation (US)
FEATURES Location/Qualifiers
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ORIGIN

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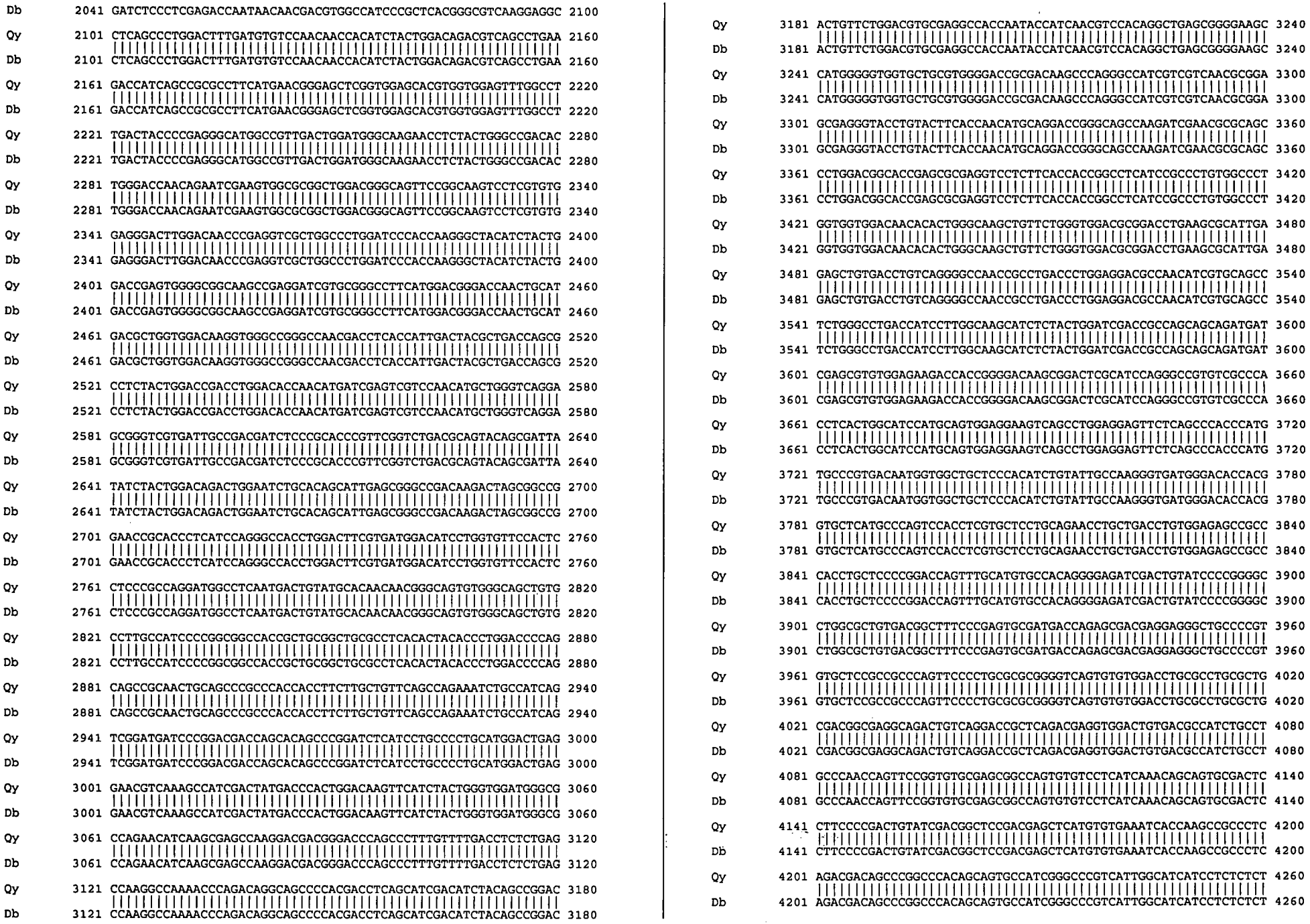
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DEFINITION  Sequence 1 from Patent WO0192891.
ACCESSION   AX418086
VERSION     AX418086.1  GI:21523100
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Carulli,J.P., Little,R.D., Recker,R.R. and Johnson,M.L.
  TITLE     Regulating lipid levels via the Zmax1 or HBM gene
  JOURNAL   Patent: WO 0192891-A 1 06-DEC-2001;
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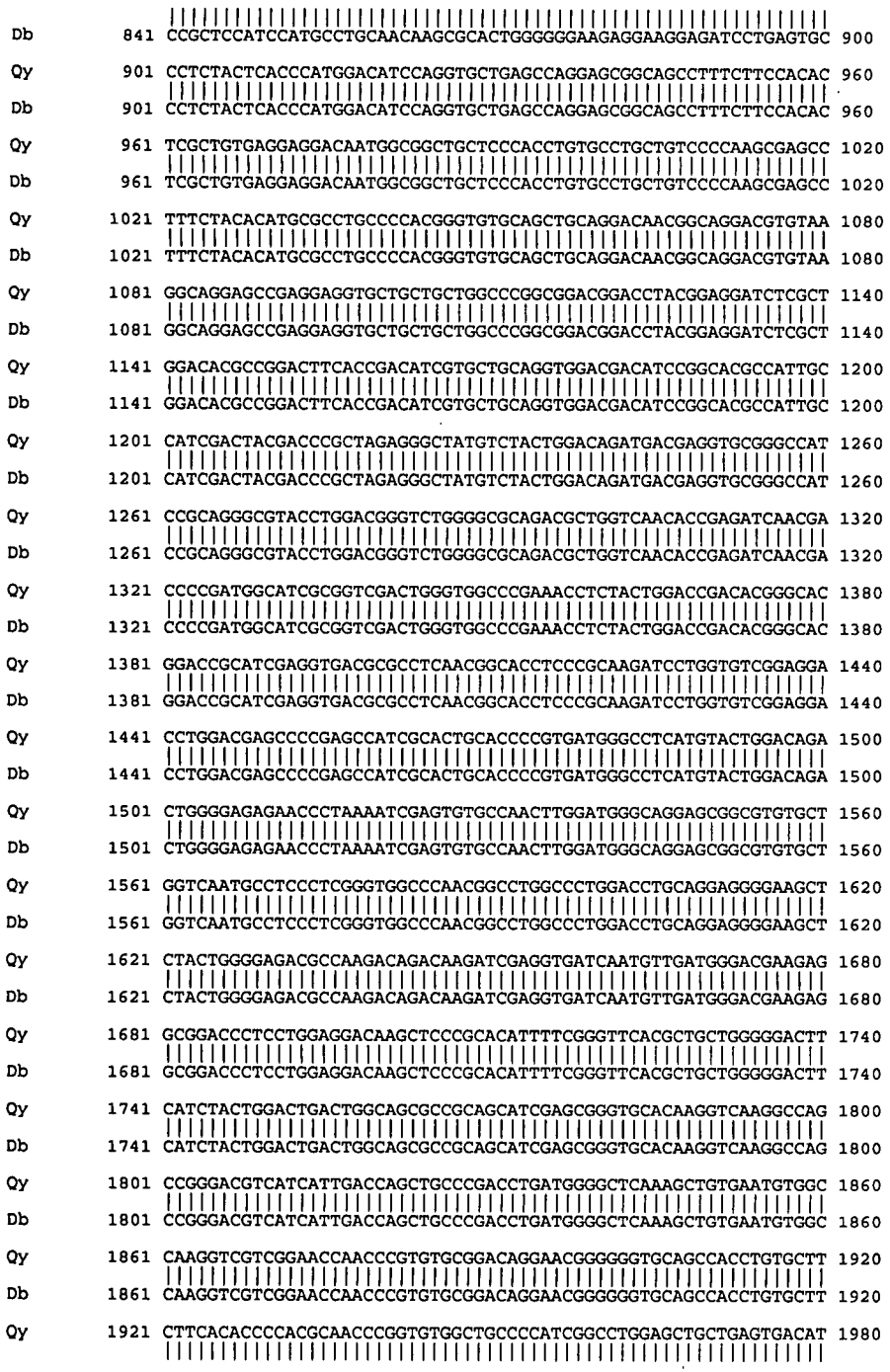
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RESULT 7
CQ870240
LOCUS CQ870240 5099 bp DNA linear PAT 13-SEP-2004
DEFINITION Sequence 661 from Patent WO2004074320.

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VERSION     CQ870240.1  GI:51999859
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE   1
  AUTHORS   Morris,D.W., Morris,D.W. and Malandro,M.S.
  TITLE     Novel therapeutic targets in cancer
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FEATURES             Location/Qualifiers
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ORIGIN
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Query Match 99.5%; Score 5094.8; DB 6; Length 5099;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5096; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy         83 CCGCCCGGGCCGCCGTGGCCGCTGCTGCTGCTGCTGCTGCTGGCGCTGTGCGGC 142
Db         61 CCGCCCGGGCCGCCGTGGCCGCTGCTGCTGCTGCTGCTGCTGCTGGCGCTGTGCGGC 120

Qy        143 TGCCCGGCCCCCGCCGCGGCCTCGCCGCTCCTGCTATTTGCCAACCGCCGGGACGTACGG 202
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Qy        263 GCGGCCGCAGTGGACTTCCAGTTTTCCAAGGGAGCCGTGTACTGGACAGACGTGAGCGAG 322
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Qy      1883 TGTGCGGACAGGAACGGGGGGTGCAGCCACCTGTGCTTCTTCACACCCCACGCAACCCGG 1942
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Qy      2243 GTTGACTGGATGGGCAAGAACCTCTACTGGGCCGACACTGGGACCAACAGAATCGAAGTG 2302
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RESULT 8

AX658229
LOCUS       AX658229                5135 bp    DNA     linear   PAT 22-MAR-2003
DEFINITION  Sequence 145 from Patent WO03000928.
ACCESSION   AX658229
VERSION     AX658229.1  GI:29160770
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Poulsen,H.S., Pedersen,N., Mortensen,S., Sorensen,S.B.,
            Petersen,M.W. and Elsner,H.I.
  TITLE     Methods for identification of cancer cell surface molecules and
            cancer specific promoters, and therapeutic uses thereof
  JOURNAL   Patent: WO 03000928-A 145 03-JAN-2003;
            Odin Medical A/S (DK)
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ORIGIN

  Query Match           99.4%;  Score 5091.6;  DB 6;  Length 5135;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 5094;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

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Qy       3668 GGCATCCATGCAGTGGAGGAAGTCAGCCTGGAGGAGTTCTCAGCCCACCCATGTGCCCGT 3727
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RESULT 9
AF077820
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DEFINITION  Homo sapiens LDL receptor member LR3 mRNA, complete cds.
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VERSION     AF077820.1  GI:3831747
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
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REFERENCE   1  (bases 1 to 5135)
  AUTHORS   Dong,Y., Lathrop,W., Weaver,D., Qiu,Q., Cini,J., Bertolini,D. and
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  TITLE     Molecular cloning and characterization of LR3, a novel LDL receptor
            family protein with mitogenic activity
  JOURNAL   Biochem. Biophys. Res. Commun. 251 (3), 784-790 (1998)
  MEDLINE   99008902
   PUBMED   9790987
REFERENCE   2  (bases 1 to 5135)
  AUTHORS   Dong,Y., Lathrop,W., Weaver,D., Qiu,Q., Cini,J., Bertolini,D. and
            Chen,D.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-JUL-1998) Bayer Pharmaceuticals, 400 Morgan Lane,
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Matches 5094;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

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Qy        848 ATCCATGCCTGCAACAAGCGCACTGGGGGGAAGAGGAAGGAGATCCTGAGTGCCCTCTAC 907
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Qy      3068 ATCAAGCGAGCCAAGGACGACGGGACCCAGCCCTTTGTTTTGACCTCTCTGAGCCAAGGC 3127
Db      3086 ATCAAGCGAGCCAAGGACGACGGGACCCAGCCCTTTGTTTTGACCTCTCTGAGCCAAGGC 3145
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Db      3146 CAAAACCCAGACAGGCAGCCCCACGACCTCAGCATCGACATCTACAGCCGGACACTGTTC 3205
Qy      3188 TGGACGTGCGAGGCCACCAATACCATCAACGTCCACAGGCTGAGCGGGGAAGCCATGGGG 3247
Db      3206 TGGACGTGCGAGGCCACCAATACCATCAACGTCCACAGGCTGAGCGGGGAAGCCATGGGG 3265
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Qy       3308 TACCTGTACTTCACCAACATGCAGGACCGGGCAGCCAAGATCGAACGCGCAGCCCTGGAC 3367
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Qy       3428 GACAACACACTGGGCAAGCTGTTCTGGGTGGACGCGGACCTGAAGCGCATTGAGAGCTGT 3487
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Qy       4028 GAGGCAGACTGTCAGGACCGCTCAGACGAGGTGGACTGTGACGCCATCTGCCTGCCCAAC 4087
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Qy       4688 ACGACGCCCTGCAGCACCGACGTGTGTGACAGCGACTACAGCGCCAGCCGCTGGAAGGCC 4747
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DEFINITION  Sequence 28 from Patent WO03068961.
ACCESSION   AX821900
VERSION     AX821900.1  GI:39725121
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE   1
  AUTHORS   Andrews,P.A., Walsh,J.A. and Gokhale,P.A.
  TITLE     Method to modify differentiation of pluripotential stem cells
  JOURNAL   Patent: WO 03068961-A 28 21-AUG-2003;
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ORIGIN

Query Match 99.2%; Score 5077.4; DB 6; Length 5100;
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Matches 5092; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

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Qy      23 ATGGAGCCCGAGTGAGCGCGGCGCGGGCCCGTCCGGCCGCCGGACAACATGGAGGCAGCG  82
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Qy      83 CCGCCCGGGCCGCCGTGGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGGCGCTGTGCGGC 142
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Qy     143 TGCCCGGCCCCCGCCGCGGCCTCGCCGCTCCTGCTATTTGCCAACCGCCGGGACGTACGG 202
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Qy     263 GCGGCCGCAGTGGACTTCCAGTTTTCCAAGGGAGCCGTGTACTGGACAGACGTGAGCGAG 322
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Qy     743 GACGGCTCGTTCCGGCAGAAGGTGGTGGAGGGCAGCCTGACGCACCCCTTCGCCCTGACG 802
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Qy    1103 CTGCTGGCCCGGCGGACGGACCTACGGAGGATCTCGCTGGACACGCCGGACTTCACCGAC 1162
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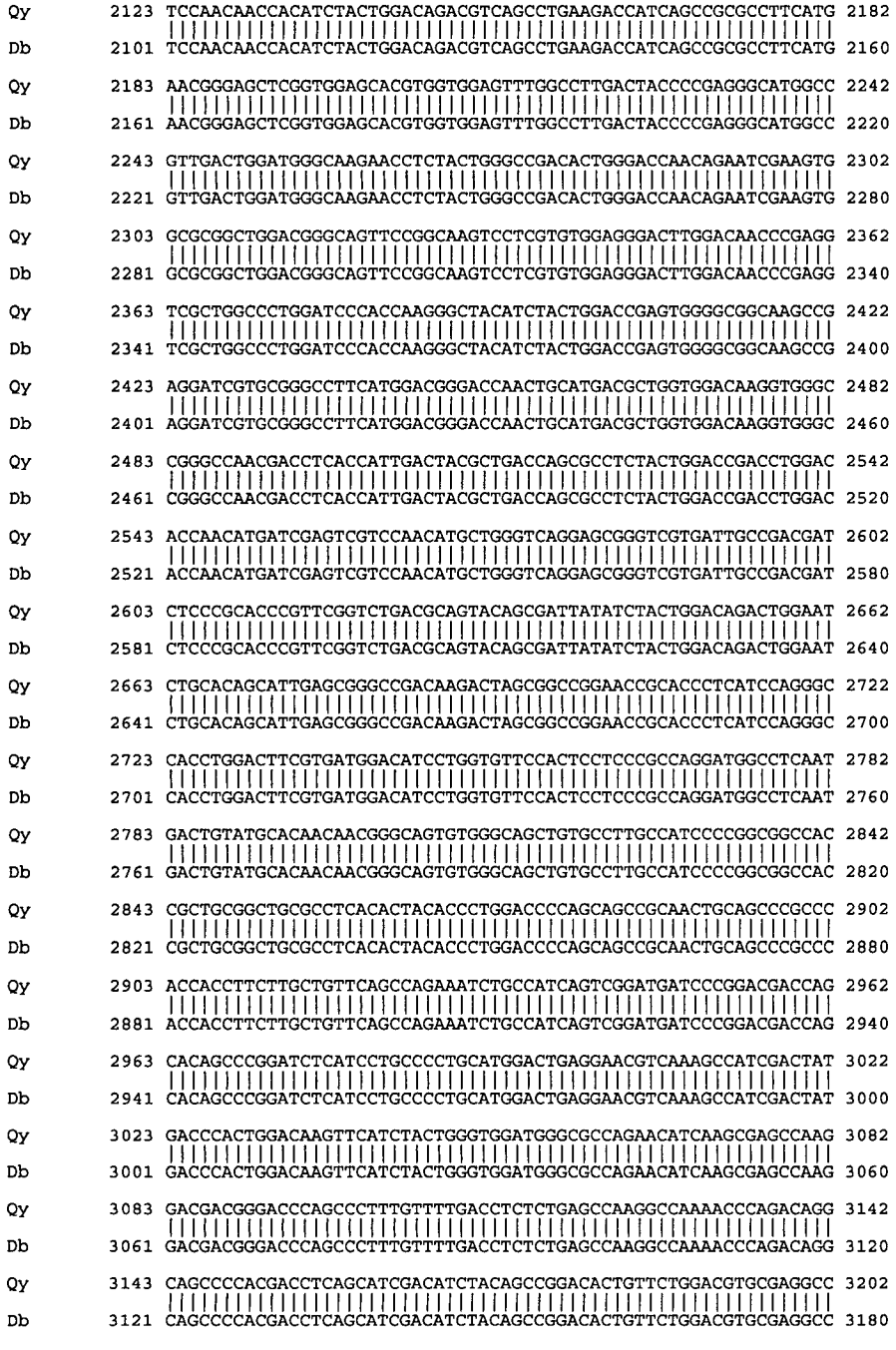
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VERSION     AF064548.1  GI:3641526
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
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REFERENCE   1  (bases 1 to 5100)
  AUTHORS   Hey,P.J., Twells,R.C., Phillips,M.S., Yusuke,Nakagawa., Brown,S.D.,
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            Metzker,M.L., Todd,J.A. and Hess,J.F.
  TITLE     Cloning of a novel member of the low-density lipoprotein receptor
            family
  JOURNAL   Gene 216 (1), 103-111 (1998)
  MEDLINE   98382578
   PUBMED   9714764
REFERENCE   2  (bases 1 to 5100)
  AUTHORS   Hey,P.J., Twells,R.C.J., Phillips,M.S., Nakagawa,Y., Brown,S.D.,
            Kawaguchi,Y., Cox,R., Xie,G., Dugan,V., Hammond,H., Metzker,M.L.,
            Todd,J.A. and Hess,J.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-MAY-1998) Human Genetics, Merck Research Lab,
            Sumneytown Pike, West Point, PA 19486, USA
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ORIGIN

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Db      2821 CGCTGCGGCTGCGCCTCACACTACACCCTGGACCCCAGCAGCCGCAACTGCAGCCCGCCC 2880
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RESULT 12
AR305075
LOCUS       AR305075               5098 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 1 from patent US 6545137.
ACCESSION   AR305075
VERSION     AR305075.1  GI:31694385
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 5098)
  AUTHORS   Todd,J.A., Hess,J.W., Caskey,C.T., Cox,R.D., Gerhold,D.,
            Hammond,H., Hey,P., Kawaguchi,Y., Merriman,T.R., Metzker,M.L.,
            Nakagawa,Y., Phillips,M.S. and Twells,R.C.J.
  TITLE     Receptor
  JOURNAL   Patent: US 6545137-A 1 08-APR-2003;
FEATURES             Location/Qualifiers
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                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             98.7%;  Score 5053.4;  DB 6;  Length 5098;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 5090;  Conservative    0;  Mismatches    6;  Indels    3;  Gaps    3;

Qy         23 ATGGAGCCCGAGTGAGCGCGGCGCGGGCCCGTCCGGCCGCCGGACAACATGGAGGCAGCG 82
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Db          1 ATGGAGCCCGAGTGAGCGCGGCGCGGGCCCGTCCGGCCGCCGGACAACATGGAGGCAGCG 60

Qy         83 CCGCCCGGGCCGCCGTGGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGGCGCTGTGCGGC 142
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CCGCCCGGGCCGCCGTGGCCGCTGCTGCTGCTGCTGCTGCTGCTGGCGCTGTGCGGC 120

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Db        241 GCGGCCGCAGTGGACTTCCAGTTTTCCAAGGGAGCCGTGTACTGGACAGACGTGAGCGAG 300

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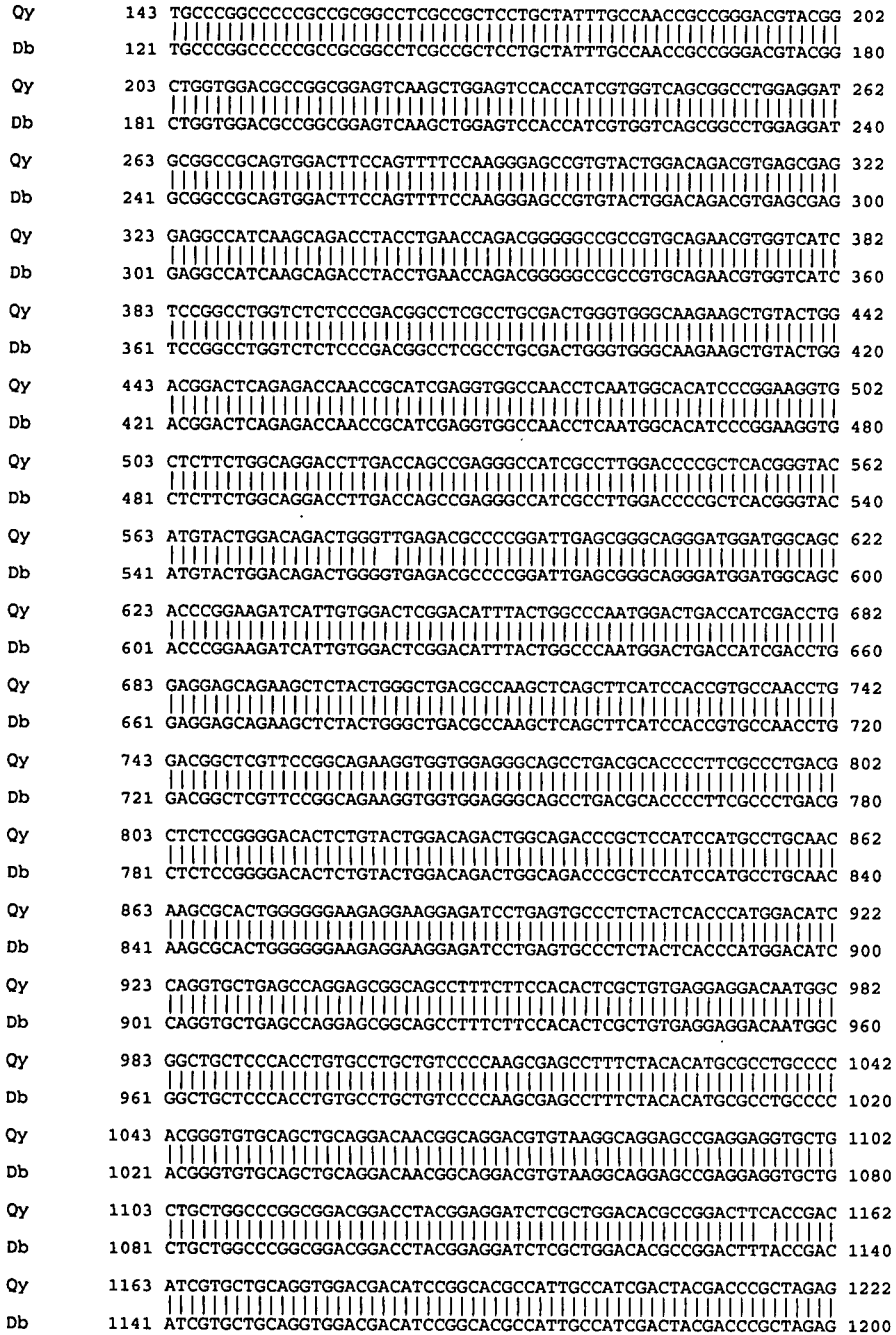
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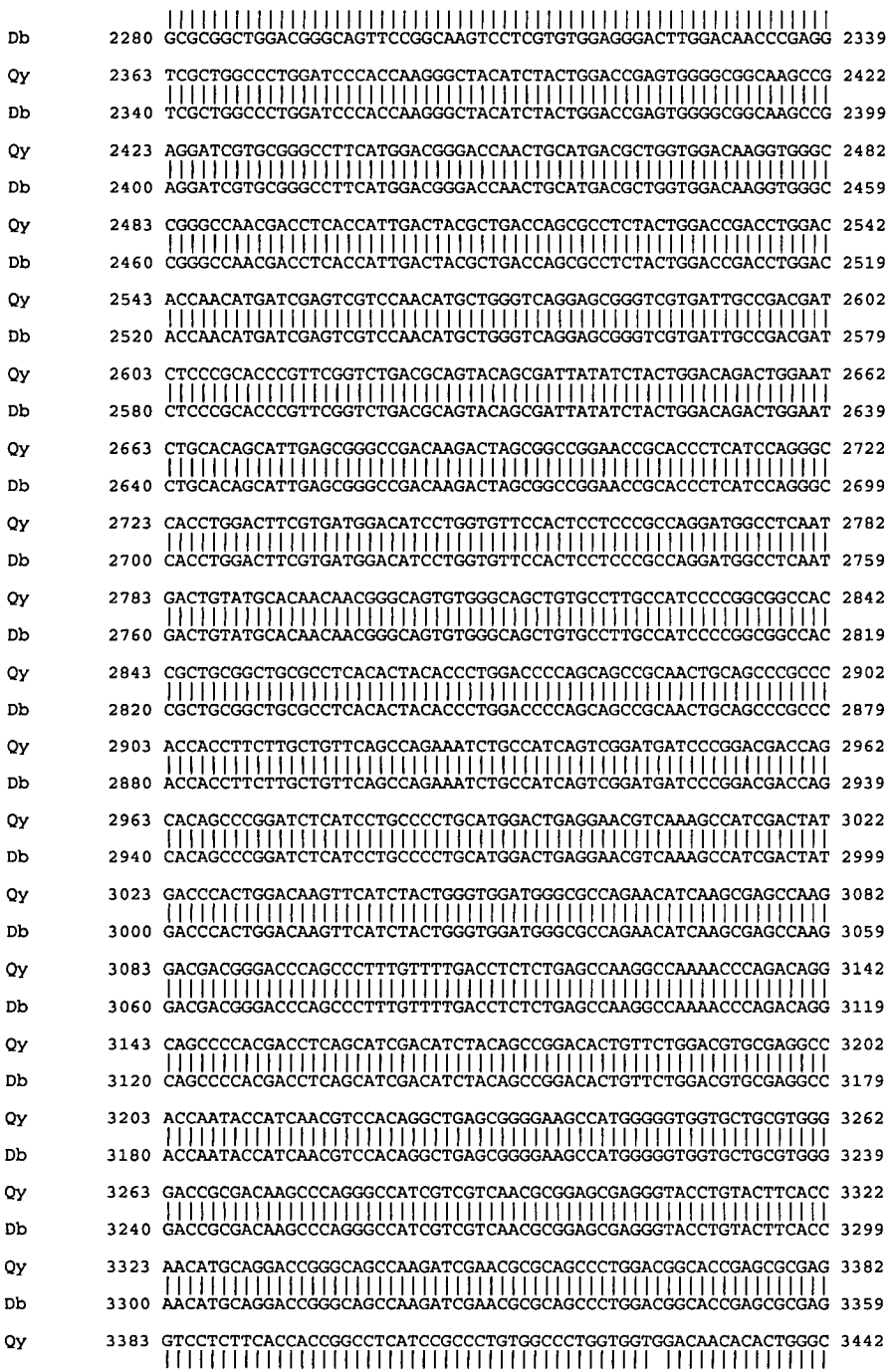
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VERSION     AR309179.1  GI:31701184
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
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REFERENCE   1  (bases 1 to 5098)
  AUTHORS   Todd,J.A., Hess,J.W., Caskey,C.T., Cox,R.D., Gerhold,D.,
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Qy 3863 GCATGTGCCACAGGGGAGATCGACTGTATCCCCGGGGCCTGGCGCTGTGACGGCTTTCCC 3922
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Qy 3923 GAGTGCGATGACCAGAGCGACGAGGAGGGCTGCCCCGTGTGCTCCGCCGCCCAGTTCCCC 3982
Db 3900 GAGTGCGATGACCAGAGCGACGAGGAGGGCTGCCCCGTGTGCTCCGCCGCCCAGTTCCCC 3959
Qy 3983 TGCGCGCGGGGTCAGTGTGTGGACCTGCGCCTGCGCTGCGACGGCGAGGCAGACTGTCAG 4042
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Qy       4523 AGCTCGTCCAGCACGAAGGCCACGCTGTACCCGCCGATCCTGAACCCGCCGCCCTCCCCG 4582
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Qy       4823 TCGGCGGAGGACAGCTGCCCGCCCTCGCCCGCCACCGAGAGGAGCTACTTCCATCTCTTC 4882
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RESULT 14
BD105986

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LOCUS       BD105986                5098 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Novel LDL-receptor.
ACCESSION   BD105986
VERSION     BD105986.1  GI:23200804
KEYWORDS    JP 2002501376-A/1.
SOURCE      Chlamydia sp.
  ORGANISM  Chlamydia sp.
            Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
REFERENCE   1  (bases 1 to 5098)
  AUTHORS   Todd,J.A., Hess,J.W., Caskey,C.T., Cox,R.D., Gerhold,D., Hammond,H.
            and Hey,P.
  TITLE     Novel LDL-receptor
  JOURNAL   Patent: JP 2002501376-A 1 15-JAN-2002;
            THE WELLCOME TRUST LTD AS TRUSTEE TO THE WELLCOME TRUST, MERCK & CO
            INC
COMMENT     PN   JP 2002501376-A/1
            PD   15-JAN-2002
            PF   15-APR-1998 JP 1998543635
            PR   15-APR-1997 US    60/043553,05-JUN-1997 US    60/048740 PI
            JOHN ANDREW TODD,JOHN WILFRED HESS,CHARLES
            THOMAS CASKEY,ROGER
            PI   DAVID COX,
            PI   DAVID GERHOLD,HOLLY HAMMOND,PATRICIA HEY
            PC   C12N15/12,C12N15/11,C12Q1/68,C07K14/705,C07K16/28,A61K38/17,
            PC   A61K39/395,
            PC   A61K48/00
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            CC   Topology: Linear;
            FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:35827"
ORIGIN
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Query Match 98.7%; Score 5053.4; DB 6; Length 5098;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 5090; Conservative 0; Mismatches 6; Indels 3; Gaps 3;

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Qy         23 ATGGAGCCCGAGTGAGCGCGGCGCGGGCCCGTCCGGCCGCCGGACAACATGGAGGCAGCG 82
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGAGCCCGAGTGAGCGCGGCGCGGGCCCGTCCGGCCGCCGGACAACATGGAGGCAGCG 60

Qy         83 CCGCCCGGGCCGCCGTGGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGGCGCTGTGCGGC 142
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CCGCCCGGGCCGCCGTGGCCGCTGCTGCTGCTGCTGCTGCTGCTGGCGCTGTGCGGC 120

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Db        121 TGCCCGGCCCCCGCCGCGGCCTCGCCGCTCCTGCTATTTGCCAACCGCCGGGACGTACGG 180

Qy        203 CTGGTGGACGCCGGCGGAGTCAAGCTGGAGTCCACCATCGTGGTCAGCGGCCTGGAGGAT 262
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Qy        263 GCGGCCGCAGTGGACTTCCAGTTTTCCAAGGGAGCCGTGTACTGGACAGACGTGAGCGAG 322
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Db        241 GCGGCCGCAGTGGACTTCCAGTTTTCCAAGGGAGCCGTGTACTGGACAGACGTGAGCGAG 300

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Db        301 GAGGCCATCAAGCAGACCTACCTGAACCAGACGGGGGCCGCCGTGCAGAACGTGGTCATC 360

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Qy        623 ACCCGGAAGATCATTGTGGACTCGGACATTTACTGGCCCAATGGACTGACCATCGACCTG 682
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Qy        683 GAGGAGCAGAAGCTCTACTGGGCTGACGCCAAGCTCAGCTTCATCCACCGTGCCAACCTG 742
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Qy        743 GACGGCTCGTTCCGGCAGAAGGTGGTGGAGGGCAGCCTGACGCACCCCTTCGCCCTGACG 802
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        863 AAGCGCACTGGGGGGAAGAGGAAGGAGATCCTGAGTGCCCTCTACTCACCCATGGACATC 922
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGCGCACTGGGGGGAAGAGGAAGGAGATCCTGAGTGCCCTCTACTCACCCATGGACATC 900

Qy        923 CAGGTGCTGAGCCAGGAGCGGCAGCCTTTCTTCCACACTCGCTGTGAGGAGGACAATGGC 982
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        901 CAGGTGCTGAGCCAGGAGCGGCAGCCTTTCTTCCACACTCGCTGTGAGGAGGACAATGGC 960
Qy        983 GGCTGCTCCCACCTGTGCCTGCTGTCCCCAAGCGAGCCTTTCTACACATGCGCCTGCCCC 1042
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Qy       1043 ACGGGTGTGCAGCTGCAGGACAACGGCAGGACGTGTAAGGCAGGAGCCGAGGAGGTGCTG 1102
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Qy       1463 GCACTGCACCCCGTGATGGGCCTCATGTACTGGACAGACTGGGGAGAGAACCCTAAAATC 1522
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             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       3563 AAGCATCTCTACTGGATCGACCGCCAGCAGCAGATGATCGAGCGTGTGGAGAAGACCACC 3622
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3540 AAGCATCTCTACTGGATCGACCGCCAGCAGCAGATGATCGAGCGTGTGGAGAAGACCACC 3599

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Qy       3743 TCCCACATCTGTATTGCCAAGGGTGATGGGACACCACGGTGCTCATGCCCAGTCCACCTC 3802
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Qy       3803 GTGCTCCTGCAGAACCTGCTGACCTGTGGAGAGCCGCCCACCTGCTCCCCGGACCAGTTT 3862
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Qy       4103 AGCGGCCAGTGTGTCCTCATCAAACAGCAGTGCGACTCCTTCCCCGACTGTATCGACGGC 4162
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Qy       4343 GAGTATGTCAGCGGGACCCCGCACGTGCCCCTCAATTTCATAGCCCCGGGCGGTTCCCAG 4402
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RESULT 15
CQ870242
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DEFINITION  Sequence 663 from Patent WO2004074320.
ACCESSION   CQ870242
VERSION     CQ870242.1  GI:51999860
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Morris,D.W., Morris,D.W. and Malandro,M.S.
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  TITLE     Novel therapeutic targets in cancer
  JOURNAL   Patent: WO 2004074320-A 663 02-SEP-2004;
            Sagres Discovery, Inc. (US)
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match             98.6%;  Score 5048.8;  DB 6;  Length 5135;
  Best Local Similarity   99.3%;  Pred. No. 0;
  Matches 5096;  Conservative    0;  Mismatches    2;  Indels   36;  Gaps    1;

Qy         23 ATGGAGCCCGAGTGAGCGCGGCGCGGGCCCGTCCGGCCGCCGGACAACATGGAGGCAGCG 82
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Db          1 ATGGAGCCCGAGTGAGCGCGGCGCGGGCCCGTCCGGCCGCCGGACAACATGGAGGCAGCG 60

Qy         83 CCGCCCGGGCCGCCGTGGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGGCGCTGTGCGGC 142
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Qy        203 CTGGTGGACGCCGGCGGAGTCAAGCTGGAGTCCACCATCGTGGTCAGCGGCCTGGAGGAT 262
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Qy        263 GCGGCCGCAGTGGACTTCCAGTTTTCCAAGGGAGCCGTGTACTGGACAGACGTGAGCGAG 322
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Qy        323 GAGGCCATCAAGCAGACCTACCTGAACCAGACGGGGGCCGCCGTGCAGAACGTGGTCATC 382
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Qy        383 TCCGGCCTGGTCTCTCCCGACGGCCTCGCCTGCGACTGGGTGGGCAAGAAGCTGTACTGG 442
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Qy        563 ATGTACTGGACAGACTGGGTTGAGACGCCCCGGATTGAGCGGGCAGGGATGGATGGCAGC 622
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Qy        803 CTCTCCGGGGACACTCTGTACTGGACAGACTGGCAGACCCGCTCCATCCATGCCTGCAAC 862
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Qy       1103 CTGCTGGCCCGGCGGACGGACCTACGGAGGATCTCGCTGGACACGCCGGACTTCACCGAC 1162
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Qy       1223 GGCTATGTCTACTGGACAGATGACGAGGTGCGGGCCATCCGCAGGGCGTACCTGGACGGG 1282
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Qy       1283 TCTGGGGCGCAGACGCTGGTCAACACCGAGATCAACGACCCCGATGGCATCGCGGTCGAC 1342
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Qy       1943 TGTGGCTGCCCCATCGGCCTGGAGCTGCTGAGTGACATGAAGACCTGCATCGTGCCTGAG 2002
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Qy       2003 GCCTTCTTGGTCTTCACCAGCAGAGCCGCCATCCACAGGATCTCCCTCGAGACCAATAAC 2062
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Qy       2903 ACCACCTTCTTGCTGTTCAGCCAGAAATCTGCCATCAGTCGGATGATCCCGGACGACCAG 2962
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Db       2881 ACCACCTTCTTGCTGTTCAGCCAGAAATCTGCCATCAGTCGGATGATCCCGGACGACCAG 2940

Qy       2963 CACAGCCCGGATCTCATCCTGCCCCTGCATGGACTGAGGAACGTCAAAGCCATCGACTAT 3022
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2941 CACAGCCCGGATCTCATCCTGCCCCTGCATGGACTGAGGAACGTCAAAGCCATCGACTAT 3000

Qy       3023 GACCCACTGGACAAGTTCATCTACTGGGTGGATGGGCGCCAGAACATCAAGCGAGCCAAG 3082
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Db       3001 GACCCACTGGACAAGTTCATCTACTGGGTGGATGGGCGCCAGAACATCAAGCGAGCCAAG 3060

Qy       3083 GACGACGGGACC----------------------------------CAGCCCTTTGTT 3106
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                  ||||||||||                                ||||||||||||
Db       3061 GACGACGGGACCCAGGCAGTGCTCAGGAGTCTTGGTTTCTTTGTCTTACAGCCCTTTGTT 3120

Qy       3107 TTGACCTCTCTGAGCCAAGGCCAAAACCCAGACAGGCAGCCCCACGACCTCAGCATCGAC 3166
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3121 TTGACCTCTCTGAGCCAAGGCCAAAACCCAGACAGGCAGCCCCACGACCTCAGCATCGAC 3180

Qy       3167 ATCTACAGCCGGACACTGTTCTGGACGTGCGAGGCCACCAATACCATCAACGTCCACAGG 3226
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Db       3181 ATCTACAGCCGGACACTGTTCTGGACGTGCGAGGCCACCAATACCATCAACGTCCACAGG 3240

Qy       3227 CTGAGCGGGGAAGCCATGGGGGTGGTGCTGCGTGGGGACCGCGACAAGCCCAGGGCCATC 3286
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Db       3241 CTGAGCGGGGAAGCCATGGGGGTGGTGCTGCGTGGGGACCGCGACAAGCCCAGGGCCATC 3300

Qy       3287 GTCGTCAACGCGGAGCGAGGGTACCTGTACTTCACCAACATGCAGGACCGGGCAGCCAAG 3346
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Db       3301 GTCGTCAACGCGGAGCGAGGGTACCTGTACTTCACCAACATGCAGGACCGGGCAGCCAAG 3360

Qy       3347 ATCGAACGCGCAGCCCTGGACGGCACCGAGCGCGAGGTCCTCTTCACCACCGGCCTCATC 3406
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Db       3361 ATCGAACGCGCAGCCCTGGACGGCACCGAGCGCGAGGTCCTCTTCACCACCGGCCTCATC 3420

Qy       3407 CGCCCTGTGGCCCTGGTGGTGGACAACACACTGGGCAAGCTGTTCTGGGTGGACGCGGAC 3466
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Db       3421 CGCCCTGTGGCCCTGGTGGTGGACAACACACTGGGCAAGCTGTTCTGGGTGGACGCGGAC 3480

Qy       3467 CTGAAGCGCATTGAGAGCTGTGACCTGTCAGGGGCCAACCGCCTGACCCTGGAGGACGCC 3526
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Db       3481 CTGAAGCGCATTGAGAGCTGTGACCTGTCAGGGGCCAACCGCCTGACCCTGGAGGACGCC 3540

Qy       3527 AACATCGTGCAGCCTCTGGGCCTGACCATCCTTGGCAAGCATCTCTACTGGATCGACCGC 3586
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Qy       3587 CAGCAGCAGATGATCGAGCGTGTGGAGAAGACCACCGGGGACAAGCGGACTCGCATCCAG 3646
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Qy       3647 GGCCGTGTCGCCCACCTCACTGGCATCCATGCAGTGGAGGAAGTCAGCCTGGAGGAGTTC 3706
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Db       3661 GGCCGTGTCGCCCACCTCACTGGCATCCATGCAGTGGAGGAAGTCAGCCTGGAGGAGTTC 3720

Qy       3707 TCAGCCCACCCATGTGCCCGTGACAATGGTGGCTGCTCCCACATCTGTATTGCCAAGGGT 3766
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Qy       3767 GATGGGACACCACGGTGCTCATGCCCAGTCCACCTCGTGCTCCTGCAGAACCTGCTGACC 3826
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Qy       3887 TGTATCCCCGGGGCCTGGCGCTGTGACGGCTTTCCCGAGTGCGATGACCAGAGCGACGAG 3946
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Db       3901 TGTATCCCCGGGGCCTGGCGCTGTGACGGCTTTCCCGAGTGCGATGACCAGAGCGACGAG 3960

Qy       3947 GAGGGCTGCCCCGTGTGCTCCGCCGCCCAGTTCCCCTGCGCGCGGGGTCAGTGTGTGGAC 4006
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Qy       4007 CTGCGCCTGCGCTGCGACGGCGAGGCAGACTGTCAGGACCGCTCAGACGAGGTGGACTGT 4066
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Qy       4067 GACGCCATCTGCCTGCCCAACCAGTTCCGGTGTGCGAGCGGCCAGTGTGTCCTCATCAAA 4126
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Qy       4127 CAGCAGTGCGACTCCTTCCCCGACTGTATCGACGGCTCCGACGAGCTCATGTGTGAAATC 4186
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Db       4141 CAGCAGTGCGACTCCTTCCCCGACTGTATCGACGGCTCCGACGAGCTCATGTGTGAAATC 4200

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Qy       4247 ATCATCCTCTCTCTCTTCGTCATGGGTGGTGTCTATTTTGTGTGCCAGCGCGTGGTGTGC 4306
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Qy       4307 CAGCGCTATGCGGGGGCCAACGGGCCCTTCCCGCACGAGTATGTCAGCGGGACCCCGCAC 4366
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Db       4321 CAGCGCTATGCGGGGGCCAACGGGCCCTTCCCGCACGAGTATGTCAGCGGGACCCCGCAC 4380

Qy       4367 GTGCCCCTCAATTTCATAGCCCCGGGCGGTTCCCAGCATGGCCCCTTCACAGGCATCGCA 4426
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Db       4381 GTGCCCCTCAATTTCATAGCCCCGGGCGGTTCCCAGCATGGCCCCTTCACAGGCATCGCA 4440

Qy       4427 TGCGGAAAGTCCATGATGAGCTCCGTGAGCCTGATGGGGGGCCGGGGCGGGGTGCCCCTC 4486
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Db       4441 TGCGGAAAGTCCATGATGAGCTCCGTGAGCCTGATGGGGGGCCGGGGCGGGGTGCCCCTC 4500

Qy       4487 TACGACCGGAACCACGTCACAGGGGCCTCGTCCAGCAGCTCGTCCAGCACGAAGGCCACG 4546
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Qy       4547 CTGTACCCGCCGATCCTGAACCCGCCGCCCTCCCCGGCCACGGACCCCTCCCTGTACAAC 4606
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Db       4561 CTGTACCCGCCGATCCTGAACCCGCCGCCCTCCCCGGCCACGGACCCCTCCCTGTACAAC 4620

Qy       4607 ATGGACATGTTCTACTCTTCAAACATTCCGGCCACTGCGAGACCGTACAGGCCCTACATC 4666
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Db       4621 ATGGACATGTTCTACTCTTCAAACATTCCGGCCACTGCGAGACCGTACAGGCCCTACATC 4680

Qy       4667 ATTCGAGGAATGGCGCCCCCGACGACGCCCTGCAGCACCGACGTGTGTGACAGCGACTAC 4726
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Qy       4727 AGCGCCAGCCGCTGGAAGGCCAGCAAGTACTACCTGGATTTGAACTCGGACTCAGACCCC 4786
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Qy       4787 TATCCACCCCCACCCACGCCCCACAGCCAGTACCTGTCGGCGGAGGACAGCTGCCCGCCC 4846
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Qy       4847 TCGCCCGCCACCGAGAGGAGCTACTTCCATCTCTTCCCGCCCCCTCCGTCCCCCTGCACG 4906
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Qy       4907 GACTCATCCTGACCTCGGCCGGGCCACTCTGGCTTCTCTGTGCCCCTGTAAATAGTTTTA 4966
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Db       4921 GACTCATCCTGACCTCGGCCGGGCCACTCTGGCTTCTCTGTGCCCCTGTAAATAGTTTTA 4980

Qy       4967 AATATGAACAAAGAAAAAAATATATTTTATGATTTAAAAAATAAATATAATTGGGATTTT 5026
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Db       4981 AATATGAACAAAGAAAAAAATATATTTTATGATTTAAAAAATAAATATAATTGGGATTTT 5040

Qy       5027 AAAAACATGAGAAATGTGAACTGTGATGGGGTGGGCAGGGCTGGGAGAACTTTGTACAGT 5086
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Db       5101 GGAGAAATATTTATAAACTTAATTTTGTAAAACA 5134


Search completed: May 19, 2005, 09:34:12
Job time : 21165 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 13, 2005, 07:17:04 ; Search time 2455 Seconds
(without alignments)
12345.856 Million cell updates/sec

Title: US-10-680-287A-2
Perfect score: 5120
Sequence: 1 actaaagcgccgccgccgcg.....aaacttaatttgtaaaaca 5120

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	5120	100.0	5120	6	ABK22777	Abk22777 Human hig
2	5120	100.0	5120	8	ACC45359	Acc45359 Human LRP
3	5120	100.0	5120	10	ADB99039	Adb99039 LRP5 vari
4	5120	100.0	5120	10	ADE82640	Ade82640 Human HBM
5	5120	100.0	5120	13	ADR16920	Adr16920 Human hig
6	5118.4	100.0	5120	5	ABA82617	Aba82617 Human Zma
7	5118.4	100.0	5120	5	ABA82618	Aba82618 Human HBM
8	5118.4	100.0	5120	8	ACC45358	Acc45358 Human wil
9	5118.4	100.0	5120	10	ADB99038	Adb99038 Human LRP
10	5118.4	100.0	5120	10	ADE82639	Ade82639 Human Zma
11	5118.4	100.0	5120	13	ADR16919	Adr16919 Human hig
12	5116.8	99.9	5278	8	ACC46078	Acc46078 Mouse HBM
13	5116.8	99.9	5278	10	ADB98796	Adb98796 Mouse HBM
14	5115.2	99.9	5278	8	ACC46079	Acc46079 Human ZMA
15	5115.2	99.9	5278	10	ADB98797	Adb98797 Human ZMA
16	5096	99.5	5112	13	ADR47571	Adr47571 Human hig
17	5094.8	99.5	5099	13	ABD32937	Abd32937 Human can
18	5093.2	99.5	5099	13	ADQ86437	Adq86437 Human tum
19	5093.2	99.5	5099	13	ADQ83350	Adq83350 Human tum
20	5078.4	99.2	5115	13	ADR47570	Adr47570 Human hig
21	5077.4	99.2	5100	10	ADK66938	Adk66938 Gene #28
22	5077.4	99.2	5100	13	ADR73481	Adr73481 Human low
23	5056.6	98.8	5063	6	AAD34322	Aad34322 Human bon
24	5055	98.7	5063	6	AAD34405	Aad34405 Human BSM
25	5055	98.7	5063	6	AAD34401	Aad34401 Human BSM
26	5055	98.7	5063	6	AAD34404	Aad34404 Human BSM
27	5053.4	98.7	5098	2	AAV70396	Aav70396 LRP5 isof
28	5048.8	98.6	5135	11	ACN44787	Acn44787 Human mRN
29	5048.8	98.6	5135	13	ABD32938	Abd32938 Human can
30	5043.6	98.5	5066	6	AAD34403	Aad34403 Human BSM
31	5014.2	97.9	5059	12	ADQ20523	Adq20523 Human sof
32	4990	97.5	5599	12	ADQ24509	Adq24509 Human sof
33	4927.4	96.2	5022	2	AAV85549	Aav85549 LRP5 isof
34	4919.8	96.1	5263	2	AAV70400	Aav70400 LRP5 isof
35	4916	96.0	5125	2	AAV86019	Aav86019 Lrp5 isof
36	4915	96.0	5162	2	AAV85550	Aav85550 LRP5 isof
37	4906.4	95.8	5166	2	AAV85551	Aav85551 LRP5 isof
38	4840	94.5	4848	12	ADI27199	Adi27199 Human LRP
39	4813	94.0	4843	2	AAV70395	Aav70395 LRP5 cDNA
40	4723.6	92.3	4915	2	AAV70398	Aav70398 LRP5 isof
41	4625.4	90.3	4736	6	ABK22776	Abk22776 Human Zma
42	4321	84.4	4351	2	AAV70397	Aav70397 LRP5 isof
43	3932.4	76.8	5119	6	ABA94317	Aba94317 LPR5 poly
44	3919	76.5	5018	13	ABD32935	Abd32935 Mouse can
45	3911.6	76.4	5117	2	AAV86018	Aav86018 Mouse Lrp

ALIGNMENTS

RESULT 1
ABK22777
ID ABK22777 standard; cDNA; 5120 BP.
XX
AC ABK22777;
XX
DT 09-APR-2002 (first entry)
XX
DE Human high bone mass (HBM) polynucleotide.
XX
KW Human; mouse; Zmax1; HBM; high bone mass gene; lipid regulation; stroke;
KW lipid-associated condition; arteriosclerosis; cardiovascular disease; ss;
KW osteoporosis; atherosclerosis; diabetic atherosclerosis; plaque build-up;
KW neurovascular condition; wound healing; gene therapy; PCR primer; probe;
KW bone development disorder; antiarteriosclerotic; cardiovascular;
KW osteopathic; cerebroprotective.
XX
OS Homo sapiens.
XX
PN WO200192891-A2.
XX
PD 06-DEC-2001.
XX
PF 25-MAY-2001; 2001WO-US016946.
XX
PR 26-MAY-2000; 2000US-00578900.
XX
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (UYCR-) UNIV CREIGHTON SCHOOL MEDICINE.
XX
PI Carulli JP, Little RD, Recker RR, Johnson ML;
XX
DR WPI; 2002-097784/13.
DR P-PSDB; AAU80880.
XX
PT Identifying molecules involved in lipid regulation, useful for
PT diagnosing, treating or preventing e.g., arteriosclerosis, comprises
PT identifying a molecule that binds to high bone mass gene or its
PT corresponding wild type gene.
XX
PS Claim 6; Page 181-195; 409pp; English.
XX
CC The invention relates to a method for identifying a molecule involved in

CC lipid regulation comprising identifying a molecule that binds to or
CC inhibits binding of a molecule to high bone mass (HBM) or its wild type
CC gene, Zmax1. Compounds identified by the method are useful for treating,
CC diagnosing, preventing or screening for normal and abnormal lipid-
CC associated conditions, including arteriosclerosis, cardiovascular
CC disease, stroke, and osteoporosis. The compounds may also be used in the
CC treatment or prevention of diabetic atherosclerosis, neurovascular
CC conditions caused by plaque build-up, poor circulation due to plaque
CC build-up and associated poor wound healing. The methods may be used in
CC gene therapy, pharmaceutical development, and diagnostic assays for bone
CC development disorders. Molecules identified by comparison of Zmax1 and
CC HBM systems can be used as surrogate markers in pharmaceutical
CC development, in diagnosis of human or animal bone disease, and in the
CC treatment of bone diseases. Sequences ABK22776-ABK23411 represent cDNA
CC molecules encoding human Zmax1 and HBM, and PCR primers, probes, linkers
CC and adapters of the invention
XX
SQ Sequence 5120 BP; 1037 A; 1657 C; 1548 G; 878 T; 0 U; 0 Other;

Query Match 100.0%; Score 5120; DB 6; Length 5120;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ACTAAAGCGCCGCCGCCGCGCCATGGAGCCCGAGTGAGCGCGGCGCGGGCCCGTCCGGCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ACTAAAGCGCCGCCGCCGCGCCATGGAGCCCGAGTGAGCGCGGCGCGGGCCCGTCCGGCC 60

Qy         61 GCCGGACAACATGGAGGCAGCGCCGCCCGGGCCGCCGTGGCCGCTGCTGCTGCTGCTGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCCGGACAACATGGAGGCAGCGCCGCCCGGGCCGCCGTGGCCGCTGCTGCTGCTGCTGCT 120

Qy        121 GCTGCTGCTGGCGCTGTGCGGCTGCCCGGCCCCCGCCGCGGCCTCGCCGCTCCTGCTATT 180
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Qy        181 TGCCAACCGCCGGGACGTACGGCTGGTGGACGCCGGCGGAGTCAAGCTGGAGTCCACCAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TGCCAACCGCCGGGACGTACGGCTGGTGGACGCCGGCGGAGTCAAGCTGGAGTCCACCAT 240

Qy        241 CGTGGTCAGCGGCCTGGAGGATGCGGCCGCAGTGGACTTCCAGTTTTCCAAGGGAGCCGT 300
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Db        241 CGTGGTCAGCGGCCTGGAGGATGCGGCCGCAGTGGACTTCCAGTTTTCCAAGGGAGCCGT 300

Qy        301 GTACTGGACAGACGTGAGCGAGGAGGCCATCAAGCAGACCTACCTGAACCAGACGGGGGC 360
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Db        301 GTACTGGACAGACGTGAGCGAGGAGGCCATCAAGCAGACCTACCTGAACCAGACGGGGGC 360

Qy        361 CGCCGTGCAGAACGTGGTCATCTCCGGCCTGGTCTCTCCCGACGGCCTCGCCTGCGACTG 420
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Db        361 CGCCGTGCAGAACGTGGTCATCTCCGGCCTGGTCTCTCCCGACGGCCTCGCCTGCGACTG 420

Qy        421 GGTGGGCAAGAAGCTGTACTGGACGGACTCAGAGACCAACCGCATCGAGGTGGCCAACCT 480
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Db        421 GGTGGGCAAGAAGCTGTACTGGACGGACTCAGAGACCAACCGCATCGAGGTGGCCAACCT 480

Qy        481 CAATGGCACATCCCGGAAGGTGCTCTTCTGGCAGGACCTTGACCAGCCGAGGGCCATCGC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CAATGGCACATCCCGGAAGGTGCTCTTCTGGCAGGACCTTGACCAGCCGAGGGCCATCGC 540

Qy        541 CTTGGACCCCGCTCACGGGTACATGTACTGGACAGACTGGGTTGAGACGCCCCGGATTGA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CTTGGACCCCGCTCACGGGTACATGTACTGGACAGACTGGGTTGAGACGCCCCGGATTGA 600

Qy        601 GCGGGCAGGGATGGATGGCAGCACCCGGAAGATCATTGTGGACTCGGACATTTACTGGCC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GCGGGCAGGGATGGATGGCAGCACCCGGAAGATCATTGTGGACTCGGACATTTACTGGCC 660

Qy        661 CAATGGACTGACCATCGACCTGGAGGAGCAGAAGCTCTACTGGGCTGACGCCAAGCTCAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAATGGACTGACCATCGACCTGGAGGAGCAGAAGCTCTACTGGGCTGACGCCAAGCTCAG 720

Qy        721 CTTCATCCACCGTGCCAACCTGGACGGCTCGTTCCGGCAGAAGGTGGTGGAGGGCAGCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        721 CTTCATCCACCGTGCCAACCTGGACGGCTCGTTCCGGCAGAAGGTGGTGGAGGGCAGCCT 780

Qy        781 GACGCACCCCTTCGCCCTGACGCTCTCCGGGGACACTCTGTACTGGACAGACTGGCAGAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACGCACCCCTTCGCCCTGACGCTCTCCGGGGACACTCTGTACTGGACAGACTGGCAGAC 840

Qy        841 CCGCTCCATCCATGCCTGCAACAAGCGCACTGGGGGGAAGAGGAAGGAGATCCTGAGTGC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CCGCTCCATCCATGCCTGCAACAAGCGCACTGGGGGGAAGAGGAAGGAGATCCTGAGTGC 900

Qy        901 CCTCTACTCACCCATGGACATCCAGGTGCTGAGCCAGGAGCGGCAGCCTTTCTTCCACAC 960
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Db        901 CCTCTACTCACCCATGGACATCCAGGTGCTGAGCCAGGAGCGGCAGCCTTTCTTCCACAC 960

Qy        961 TCGCTGTGAGGAGGACAATGGCGGCTGCTCCCACCTGTGCCTGCTGTCCCCAAGCGAGCC 1020
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Qy       1021 TTTCTACACATGCGCCTGCCCCACGGGTGTGCAGCTGCAGGACAACGGCAGGACGTGTAA 1080
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Qy       1081 GGCAGGAGCCGAGGAGGTGCTGCTGCTGGCCCGGCGGACGGACCTACGGAGGATCTCGCT 1140
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Qy       1321 CCCCGATGGCATCGCGGTCGACTGGGTGGCCCGAAACCTCTACTGGACCGACACGGGCAC 1380
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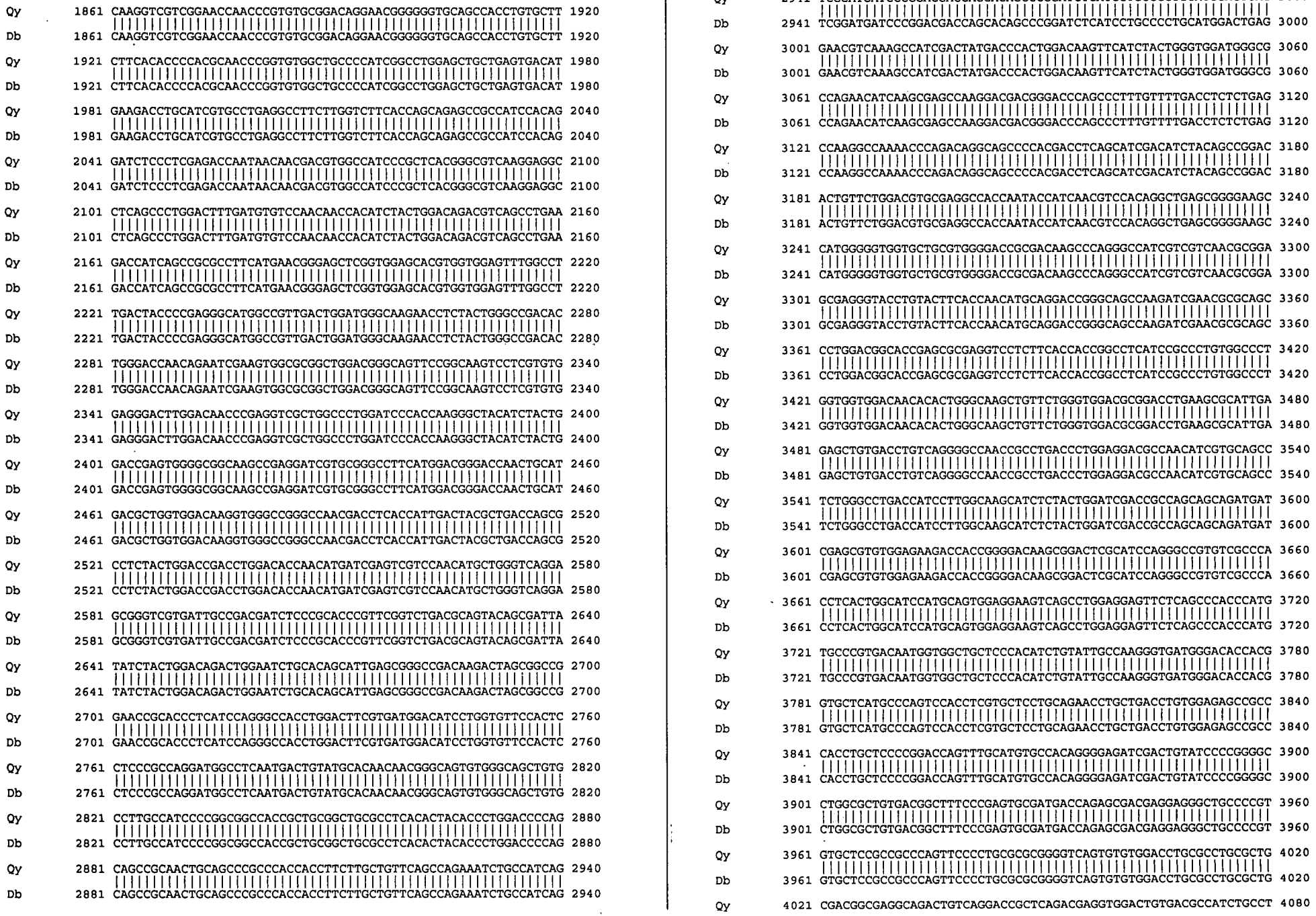
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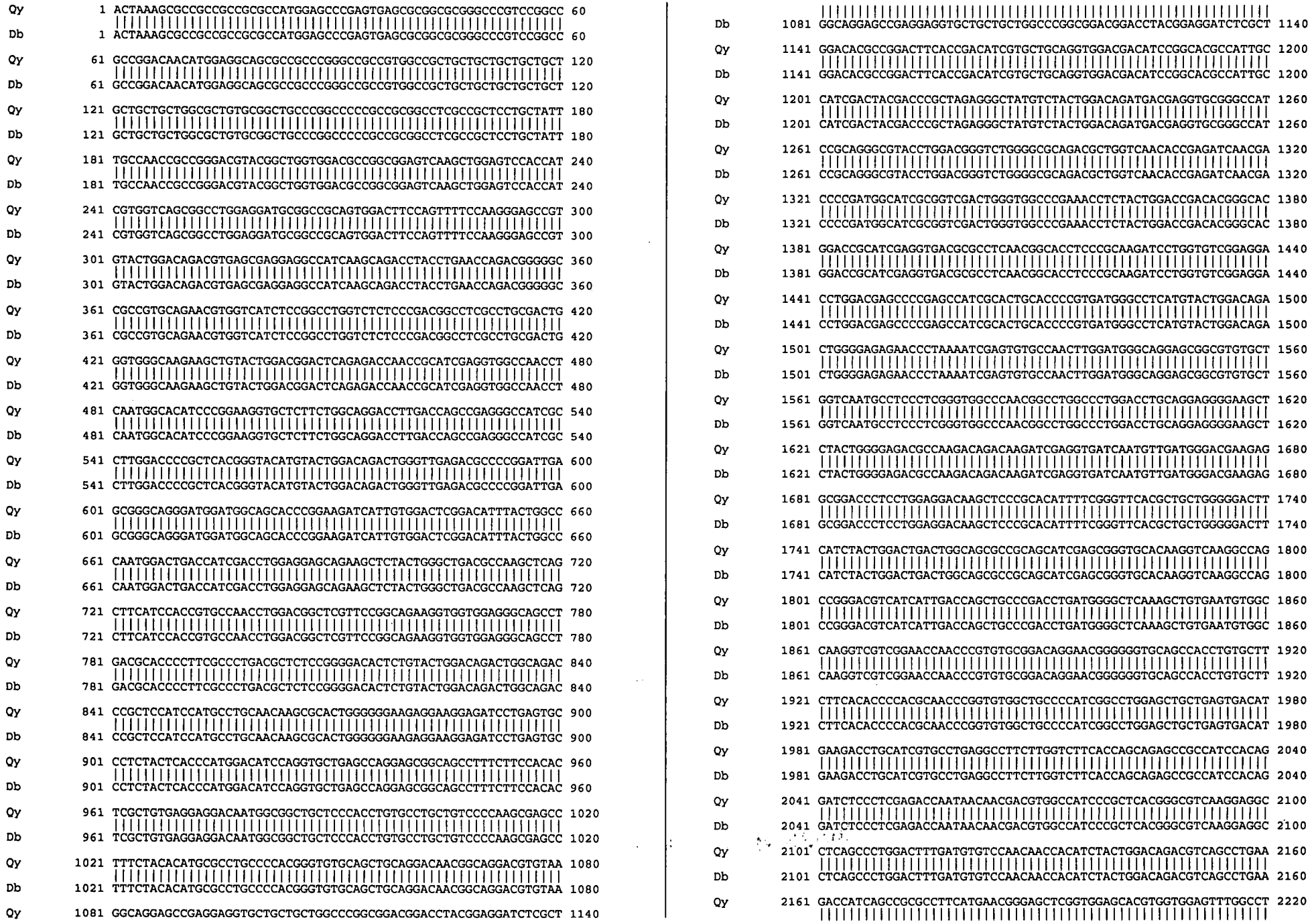
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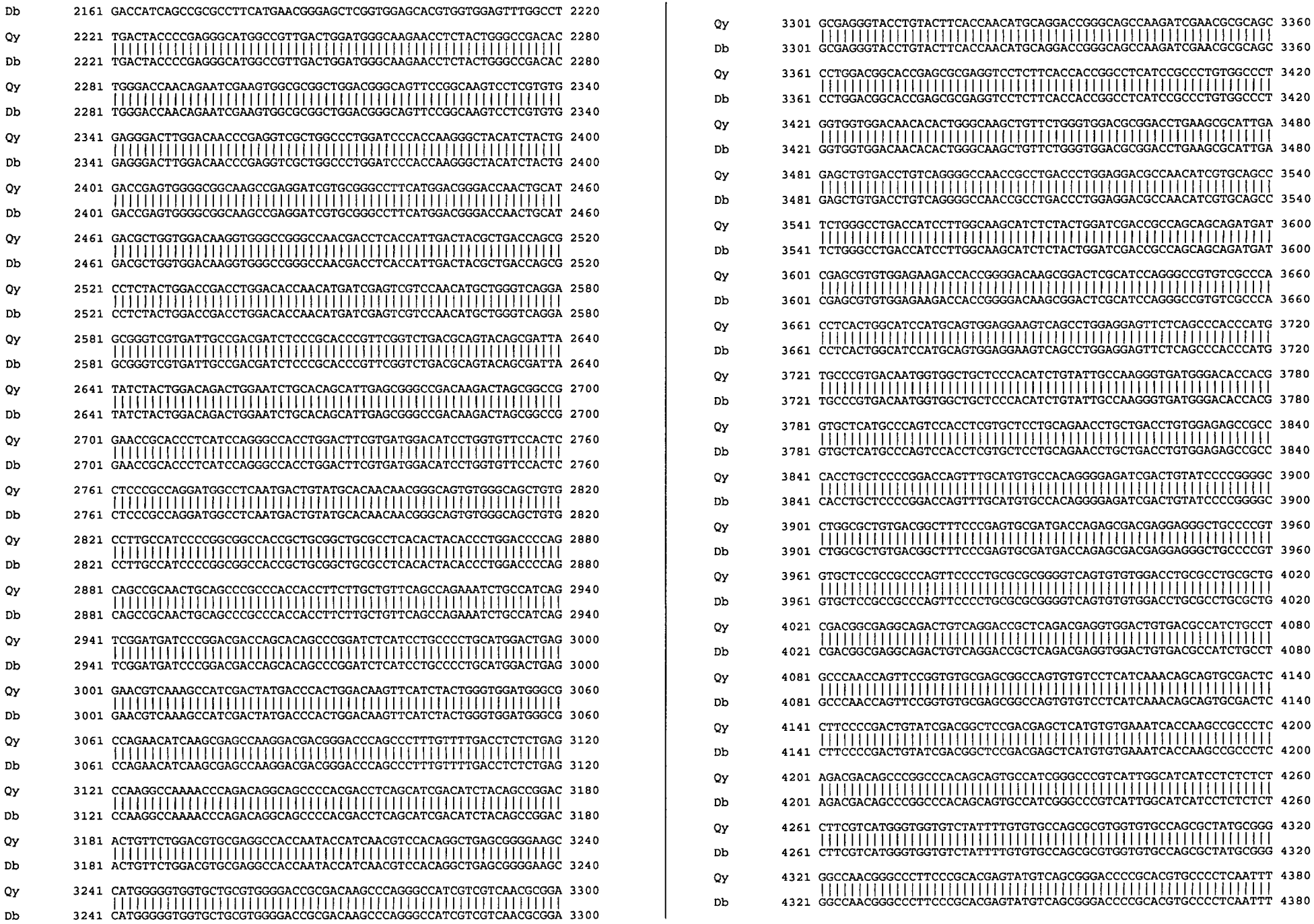
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RESULT 2
ACC45359
ID ACC45359 standard; DNA; 5120 BP.
XX
AC ACC45359;
XX
DT 02-JUN-2003 (first entry)
XX
DE Human LRP5 allelic variant HBM gene.
XX
KW Human; high bone mass; HBM; LRP5; LRP6; transgenic; bone mass modulation;
KW gene therapy; bone density modulation; bone strength; trabecular number;
KW bone size; bone tissue connectivity; bone disease; osteoporosis;
KW osteomalacia; rickets; Paget's disease; neoplasm of the bone; gene; ds.
XX
OS Homo sapiens.
XX
PN WO200292764-A2.
XX
PD 21-NOV-2002.
XX
PF 13-MAY-2002; 2002WO-US014876.
XX
PR 11-MAY-2001; 2001US-0290071P.
PR 17-MAY-2001; 2001US-0291311P.
PR 01-FEB-2002; 2002US-0353058P.
PR 04-MAR-2002; 2002US-0361293P.
XX
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (AMHP) WYETH.
XX
PI Babij P, Bex FJ, Yaworsky PJ, Bodine PV;
XX
DR WPI; 2003-129278/12.
DR P-PSDB; ABR41094.
XX
PT New transgenic animals (e.g. mice), useful as models for studying bone
PT density modulation, developing drugs for treating or preventing bone
PT diseases (e.g. osteoporosis), or diagnosing diseases characterized by
PT reduced bone density.
XX
PS Claim 1; Page 288-294; 603pp; English.
XX
CC The invention relates to novel transgenic animals expressing the high
CC bone mass (HBM) gene, expressing the corresponding wild type HBM gene,
CC comprising an alteration of the gene encoding LRP5 or LRP6, or expressing
CC an LRP5 that is modulated by an altered gene control sequence introduced
CC by homologous or non-homologous recombination. The transgenic animals are
CC for the study of bone density modulation or bone mass modulation. The
CC invention has osteopathic and cytostatic activity. The polynucleotides of
CC the invention may have a use in gene therapy. The transgenic animals and
CC nucleic acids are for the study of bone density modulation, where the
CC bone mass is modulated relative to non-transgenic animals of the same
CC species in more than one parameter selected from bone density, bone
CC strength, trabecular number, bone size, or bone tissue connectivity. The
CC transgenic animals, nucleic acids and methods are useful for identifying
CC molecules involved in bone development, and for developing pharmaceutical
CC compositions, which may be employed for treating or preventing bone
CC diseases, e.g. osteoporosis, osteomalacia, rickets, Paget's disease, or
CC neoplasms of the bone. The transgenic animals and nucleic acids are also
CC useful in methods for diagnosing diseases involved in bone development,
CC or characterised by reduced bone density or mass. The present sequence is
CC used in the exemplification of the invention
XX
SQ Sequence 5120 BP; 1037 A; 1657 C; 1548 G; 878 T; 0 U; 0 Other;

  Query Match   100.0%; Score 5120; DB 8; Length 5120;
  Best Local Similarity 100.0%; Pred. No. 0;
  Matches 5120; Conservative   0; Mismatches   0; Indels   0; Gaps   0;




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Db 2941 TCGGATGATCCCGGACGACCAGCACAGCCCGGATCTCATCCTGCCCCTGCATGGACTGAG 3000
Qy 3001 GAACGTCAAAGCCATCGACTATGACCCACTGGACAAGTTCATCTACTGGGTGGATGGGCG 3060
Db 3001 GAACGTCAAAGCCATCGACTATGACCCACTGGACAAGTTCATCTACTGGGTGGATGGGCG 3060
Qy 3061 CCAGAACATCAAGCGAGCCAAGGACGACGGGACCCAGCCCTTTGTTTTGACCTCTCTGAG 3120
Db 3061 CCAGAACATCAAGCGAGCCAAGGACGACGGGACCCAGCCCTTTGTTTTGACCTCTCTGAG 3120
Qy 3121 CCAAGGCCAAAACCCAGACAGGCAGCCCCACGACCTCAGCATCGACATCTACAGCCGGAC 3180
Db 3121 CCAAGGCCAAAACCCAGACAGGCAGCCCCACGACCTCAGCATCGACATCTACAGCCGGAC 3180
Qy 3181 ACTGTTCTGGACGTGCGAGGCCACCAATACCATCAACGTCCACAGGCTGAGCGGGGAAGC 3240
Db 3181 ACTGTTCTGGACGTGCGAGGCCACCAATACCATCAACGTCCACAGGCTGAGCGGGGAAGC 3240
Qy 3241 CATGGGGGTGGTGCTGCGTGGGGACCGCGACAAGCCCAGGGCCATCGTCGTCAACGCGGA 3300
Db 3241 CATGGGGGTGGTGCTGCGTGGGGACCGCGACAAGCCCAGGGCCATCGTCGTCAACGCGGA 3300
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Db 3301 GCGAGGGTACCTGTACTTCACCAACATGCAGGACCGGGCAGCCAAGATCGAACGCGCAGC 3360
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Db 3361 CCTGGACGGCACCGAGCGCGAGGTCCTCTTCACCACCGGCCTCATCCGCCCTGTGGCCCT 3420
Qy 3421 GGTGGTGGACAACACACTGGGCAAGCTGTTCTGGGTGGACGCGGACCTGAAGCGCATTGA 3480
Db 3421 GGTGGTGGACAACACACTGGGCAAGCTGTTCTGGGTGGACGCGGACCTGAAGCGCATTGA 3480
Qy 3481 GAGCTGTGACCTGTCAGGGGCCAACCGCCTGACCCTGGAGGACGCCAACATCGTGCAGCC 3540
Db 3481 GAGCTGTGACCTGTCAGGGGCCAACCGCCTGACCCTGGAGGACGCCAACATCGTGCAGCC 3540
Qy 3541 TCTGGGCCTGACCATCCTTGGCAAGCATCTCTACTGGATCGACCGCCAGCAGCAGATGAT 3600
Db 3541 TCTGGGCCTGACCATCCTTGGCAAGCATCTCTACTGGATCGACCGCCAGCAGCAGATGAT 3600
Qy 3601 CGAGCGTGTGGAGAAGACCACCGGGGACAAGCGGACTCGCATCCAGGGCCGTGTCGCCCA 3660
Db 3601 CGAGCGTGTGGAGAAGACCACCGGGGACAAGCGGACTCGCATCCAGGGCCGTGTCGCCCA 3660
Qy 3661 CCTCACTGGCATCCATGCAGTGGAGGAAGTCAGCCTGGAGGAGTTCTCAGCCCACCCATG 3720
Db 3661 CCTCACTGGCATCCATGCAGTGGAGGAAGTCAGCCTGGAGGAGTTCTCAGCCCACCCATG 3720
Qy 3721 TGCCCGTGACAATGGTGGCTGCTCCCACATCTGTATTGCCAAGGGTGATGGGACACCACG 3780
Db 3721 TGCCCGTGACAATGGTGGCTGCTCCCACATCTGTATTGCCAAGGGTGATGGGACACCACG 3780
Qy 3781 GTGCTCATGCCCAGTCCACCTCGTGCTCCTGCAGAACCTGCTGACCTGTGGAGAGCCGCC 3840
Db 3781 GTGCTCATGCCCAGTCCACCTCGTGCTCCTGCAGAACCTGCTGACCTGTGGAGAGCCGCC 3840
Qy 3841 CACCTGCTCCCCGGACCAGTTTGCATGTGCCACAGGGGAGATCGACTGTATCCCCGGGGC 3900
Db 3841 CACCTGCTCCCCGGACCAGTTTGCATGTGCCACAGGGGAGATCGACTGTATCCCCGGGGC 3900
Qy 3901 CTGGCGCTGTGACGGCTTTCCCGAGTGCGATGACCAGAGCGACGAGGAGGGCTGCCCCGT 3960
Db 3901 CTGGCGCTGTGACGGCTTTCCCGAGTGCGATGACCAGAGCGACGAGGAGGGCTGCCCCGT 3960
Qy 3961 GTGCTCCGCCGCCCAGTTCCCCTGCGCGCGGGGTCAGTGTGTGGACCTGCGCCTGCGCTG 4020
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Qy 4081 GCCCAACCAGTTCCGGTGTGCGAGCGGCCAGTGTGTCCTCATCAAACAGCAGTGCGACTC 4140
Db 4081 GCCCAACCAGTTCCGGTGTGCGAGCGGCCAGTGTGTCCTCATCAAACAGCAGTGCGACTC 4140
Qy 4141 CTTCCCCGACTGTATCGACGGCTCCGACGAGCTCATGTGTGAAATCACCAAGCCGCCCTC 4200
Db 4141 CTTCCCCGACTGTATCGACGGCTCCGACGAGCTCATGTGTGAAATCACCAAGCCGCCCTC 4200
Qy 4201 AGACGACAGCCCGGCCCACAGCAGTGCCATCGGGCCCGTCATTGGCATCATCCTCTCTCT 4260
Db 4201 AGACGACAGCCCGGCCCACAGCAGTGCCATCGGGCCCGTCATTGGCATCATCCTCTCTCT 4260
Qy 4261 CTTCGTCATGGGTGGTGTCTATTTTGTGTGCCAGCGCGTGGTGTGCCAGCGCTATGCGGG 4320
Db 4261 CTTCGTCATGGGTGGTGTCTATTTTGTGTGCCAGCGCGTGGTGTGCCAGCGCTATGCGGG 4320
Qy 4321 GGCCAACGGGCCCTTCCCGCACGAGTATGTCAGCGGGACCCCGCACGTGCCCCTCAATTT 4380
Db 4321 GGCCAACGGGCCCTTCCCGCACGAGTATGTCAGCGGGACCCCGCACGTGCCCCTCAATTT 4380

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Qy       4381 CATAGCCCCGGGCGGTTCCCAGCATGGCCCCTTCACAGGCATCGCATGCGGAAAGTCCAT 4440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4381 CATAGCCCCGGGCGGTTCCCAGCATGGCCCCTTCACAGGCATCGCATGCGGAAAGTCCAT 4440

Qy       4441 GATGAGCTCCGTGAGCCTGATGGGGGGCCGGGGCGGGGTGCCCCTCTACGACCGGAACCA 4500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4441 GATGAGCTCCGTGAGCCTGATGGGGGGCCGGGGCGGGGTGCCCCTCTACGACCGGAACCA 4500

Qy       4501 CGTCACAGGGGCCTCGTCCAGCAGCTCGTCCAGCACGAAGGCCACGCTGTACCCGCCGAT 4560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       4561 CCTGAACCCGCCGCCCTCCCCGGCCACGGACCCCTCCCTGTACAACATGGACATGTTCTA 4620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4561 CCTGAACCCGCCGCCCTCCCCGGCCACGGACCCCTCCCTGTACAACATGGACATGTTCTA 4620

Qy       4621 CTCTTCAAACATTCCGGCCACTGCGAGACCGTACAGGCCCTACATCATTCGAGGAATGGC 4680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4621 CTCTTCAAACATTCCGGCCACTGCGAGACCGTACAGGCCCTACATCATTCGAGGAATGGC 4680

Qy       4681 GCCCCCGACGACGCCCTGCAGCACCGACGTGTGTGACAGCGACTACAGCGCCAGCCGCTG 4740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4681 GCCCCCGACGACGCCCTGCAGCACCGACGTGTGTGACAGCGACTACAGCGCCAGCCGCTG 4740

Qy       4741 GAAGGCCAGCAAGTACTACCTGGATTTGAACTCGGACTCAGACCCCTATCCACCCCCACC 4800
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4741 GAAGGCCAGCAAGTACTACCTGGATTTGAACTCGGACTCAGACCCCTATCCACCCCCACC 4800

Qy       4801 CACGCCCCACAGCCAGTACCTGTCGGCGGAGGACAGCTGCCCGCCCTCGCCCGCCACCGA 4860
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4801 CACGCCCCACAGCCAGTACCTGTCGGCGGAGGACAGCTGCCCGCCCTCGCCCGCCACCGA 4860

Qy       4861 GAGGAGCTACTTCCATCTCTTCCCGCCCCCTCCGTCCCCCTGCACGGACTCATCCTGACC 4920
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4861 GAGGAGCTACTTCCATCTCTTCCCGCCCCCTCCGTCCCCCTGCACGGACTCATCCTGACC 4920

Qy       4921 TCGGCCGGGCCACTCTGGCTTCTCTGTGCCCCTGTAAATAGTTTTAAATATGAACAAAGA 4980
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       4981 AAAAAATATATTTTATGATTTAAAAAATAAATATAATTGGGATTTTAAAAACATGAGAAA 5040
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Qy       5041 TGTGAACTGTGATGGGGTGGGCAGGGCTGGGAGAACTTTGTACAGTGGAGAAATATTTAT 5100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5041 TGTGAACTGTGATGGGGTGGGCAGGGCTGGGAGAACTTTGTACAGTGGAGAAATATTTAT 5100

Qy       5101 AAACTTAATTTTGTAAAACA 5120
             ||||||||||||||||||||
Db       5101 AAACTTAATTTTGTAAAACA 5120
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RESULT 3
ADB99039
ID ADB99039 standard; DNA; 5120 BP.
XX
AC ADB99039;
XX
DT 04-DEC-2003 (first entry)
XX
DE LRP5 variant coding sequence.
XX
KW Osteopathic; Gene therapy; High Bone Mass; HBM; LRP5; Zmax1; LRP6;
KW bone mass modulation; osteoporosis; gene; mutein; mutant; ds.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO200292000-A2.
XX
PD 21-NOV-2002.
XX
PF 13-MAY-2002; 2002WO-US014877.
XX
PR 11-MAY-2001; 2001US-0290071P.
PR 17-MAY-2001; 2001US-0291311P.
PR 01-FEB-2002; 2002US-0353058P.
PR 04-MAR-2002; 2002US-0361293P.
XX
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (AMHP) WYETH.
XX
PI Allen K, Anisowicz A, Graham JR, Morales A, Yaworsky PJ, Liu W;
XX
DR WPI; 2003-129214/12.
DR P-PSDB; ADB98059.
XX
PT New nucleic acid comprising a mutation in LRP5 or LRP6, useful for
PT diagnosing a HBM-like phenotype in a subject and for preparing a
PT composition for modulating bone mass and/or lipid levels in a subject
PT suffering from e.g. osteoporosis.
XX
PS Disclosure; SEQ ID NO 2; 629pp; English.
XX
CC The present invention relates to High Bone Mass (HBM), LRP5 (Zmax1) and
CC LRP6 mutants, which results in a HBM-like phenotype when expressed in a
CC cell. The HBM-like phenotype results in bone mass modulation and/or lipid
CC level modulation. The invention is useful for diagnosing a HBM-like
CC phenotype in a subject and for preparing a composition for modulating
CC bone mass and/or lipid levels in a subject suffering from e.g.
CC osteoporosis. The present sequence is the coding sequence for a LRP5
CC mutein.
XX
SQ Sequence 5120 BP; 1037 A; 1657 C; 1548 G; 878 T; 0 U; 0 Other;

Query Match 100.0%; Score 5120; DB 10; Length 5120;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ACTAAAGCGCCGCCGCCGCGCCATGGAGCCCGAGTGAGCGCGGCGCGGGCCCGTCCGGCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ACTAAAGCGCCGCCGCCGCGCCATGGAGCCCGAGTGAGCGCGGCGCGGGCCCGTCCGGCC 60

Qy         61 GCCGGACAACATGGAGGCAGCGCCGCCCGGGCCGCCGTGGCCGCTGCTGCTGCTGCTGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCCGGACAACATGGAGGCAGCGCCGCCCGGGCCGCCGTGGCCGCTGCTGCTGCTGCT 120

Qy        121 GCTGCTGCTGGCGCTGTGCGGCTGCCCGGCCCCCGCCGCGGCCTCGCCGCTCCTGCTATT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCTGCTGCTGGCGCTGTGCGGCTGCCCGGCCCCCGCCGCGGCCTCGCCGCTCCTGCTATT 180

Qy        181 TGCCAACCGCCGGGACGTACGGCTGGTGGACGCCGGCGGAGTCAAGCTGGAGTCCACCAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TGCCAACCGCCGGGACGTACGGCTGGTGGACGCCGGCGGAGTCAAGCTGGAGTCCACCAT 240

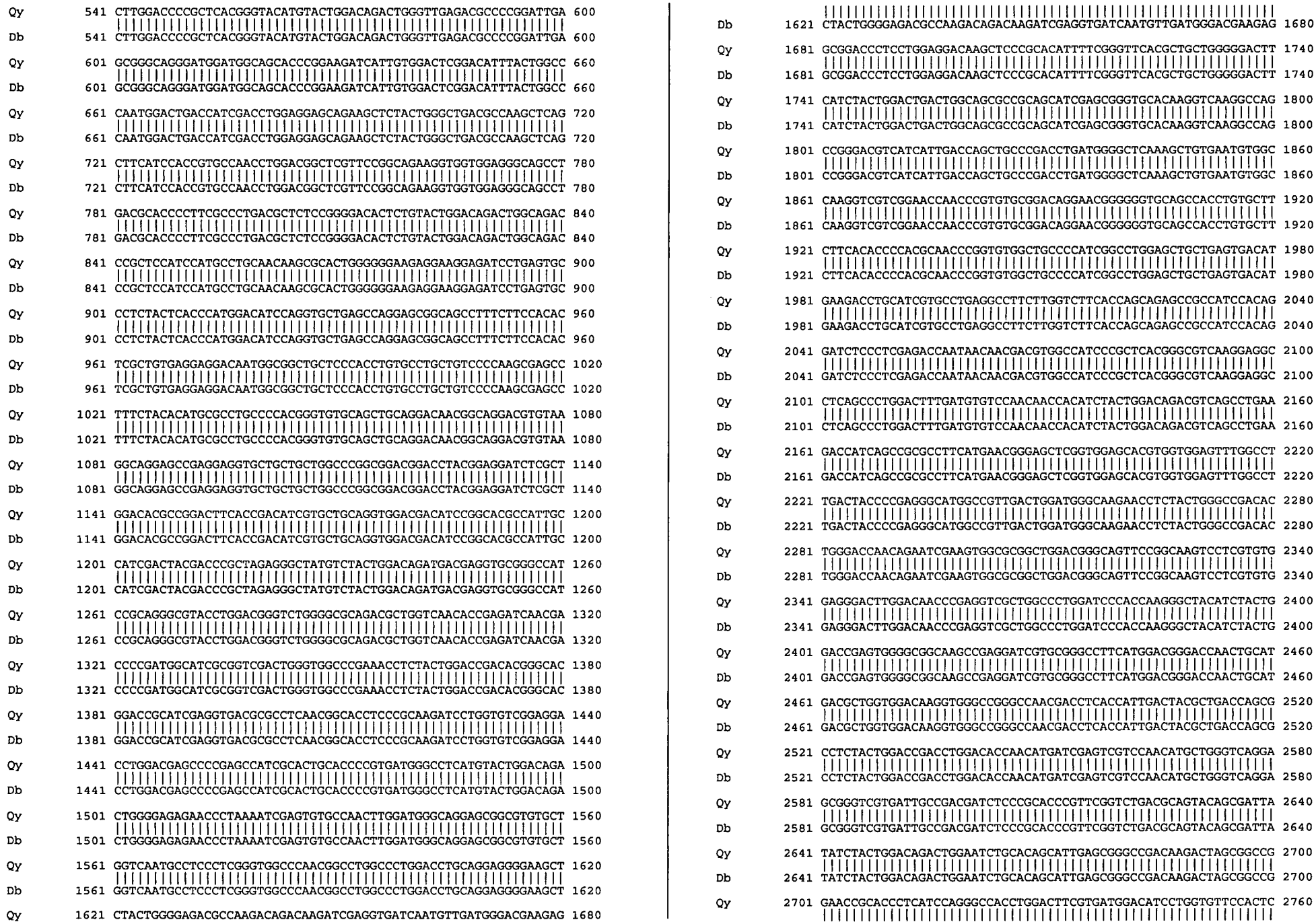
Qy        241 CGTGGTCAGCGGCCTGGAGGATGCGGCCGCAGTGGACTTCCAGTTTTCCAAGGGAGCCGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CGTGGTCAGCGGCCTGGAGGATGCGGCCGCAGTGGACTTCCAGTTTTCCAAGGGAGCCGT 300

Qy        301 GTACTGGACAGACGTGAGCGAGGAGGCCATCAAGCAGACCTACCTGAACCAGACGGGGGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GTACTGGACAGACGTGAGCGAGGAGGCCATCAAGCAGACCTACCTGAACCAGACGGGGGC 360

Qy        361 CGCCGTGCAGAACGTGGTCATCTCCGGCCTGGTCTCTCCCGACGGCCTCGCCTGCGACTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CGCCGTGCAGAACGTGGTCATCTCCGGCCTGGTCTCTCCCGACGGCCTCGCCTGCGACTG 420

Qy        421 GGTGGGCAAGAAGCTGTACTGGACGGACTCAGAGACCAACCGCATCGAGGTGGCCAACCT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GGTGGGCAAGAAGCTGTACTGGACGGACTCAGAGACCAACCGCATCGAGGTGGCCAACCT 480

Qy        481 CAATGGCACATCCCGGAAGGTGCTCTTCTGGCAGGACCTTGACCAGCCGAGGGCCATCGC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CAATGGCACATCCCGGAAGGTGCTCTTCTGGCAGGACCTTGACCAGCCGAGGGCCATCGC 540
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Qy 541 CTTGGACCCCGCTCACGGGTACATGTACTGGACAGACTGGGTTGAGACGCCCCGGATTGA 600
Db 541 CTTGGACCCCGCTCACGGGTACATGTACTGGACAGACTGGGTTGAGACGCCCCGGATTGA 600
Qy 601 GCGGGCAGGGATGGATGGCAGCACCCGGAAGATCATTGTGGACTCGGACATTTACTGGCC 660
Db 601 GCGGGCAGGGATGGATGGCAGCACCCGGAAGATCATTGTGGACTCGGACATTTACTGGCC 660
Qy 661 CAATGGACTGACCATCGACCTGGAGGAGCAGAAGCTCTACTGGGCTGACGCCAAGCTCAG 720
Db 661 CAATGGACTGACCATCGACCTGGAGGAGCAGAAGCTCTACTGGGCTGACGCCAAGCTCAG 720
Qy 721 CTTCATCCACCGTGCCAACCTGGACGGCTCGTTCCGGCAGAAGGTGGTGGAGGGCAGCCT 780
Db 721 CTTCATCCACCGTGCCAACCTGGACGGCTCGTTCCGGCAGAAGGTGGTGGAGGGCAGCCT 780
Qy 781 GACGCACCCCTTCGCCCTGACGCTCTCCGGGGACACTCTGTACTGGACAGACTGGCAGAC 840
Db 781 GACGCACCCCTTCGCCCTGACGCTCTCCGGGGACACTCTGTACTGGACAGACTGGCAGAC 840
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Db 901 CCTCTACTCACCCATGGACATCCAGGTGCTGAGCCAGGAGCGGCAGCCTTTCTTCCACAC 960
Qy 961 TCGCTGTGAGGAGGACAATGGCGGCTGCTCCCACCTGTGCCTGCTGTCCCCAAGCGAGCC 1020
Db 961 TCGCTGTGAGGAGGACAATGGCGGCTGCTCCCACCTGTGCCTGCTGTCCCCAAGCGAGCC 1020
Qy 1021 TTTCTACACATGCGCCTGCCCCACGGGTGTGCAGCTGCAGGACAACGGCAGGACGTGTAA 1080
Db 1021 TTTCTACACATGCGCCTGCCCCACGGGTGTGCAGCTGCAGGACAACGGCAGGACGTGTAA 1080
Qy 1081 GGCAGGAGCCGAGGAGGTGCTGCTGCTGGCCCGGCGGACGGACCTACGGAGGATCTCGCT 1140
Db 1081 GGCAGGAGCCGAGGAGGTGCTGCTGCTGGCCCGGCGGACGGACCTACGGAGGATCTCGCT 1140
Qy 1141 GGACACGCCGGACTTCACCGACATCGTGCTGCAGGTGGACGACATCCGGCACGCCATTGC 1200
Db 1141 GGACACGCCGGACTTCACCGACATCGTGCTGCAGGTGGACGACATCCGGCACGCCATTGC 1200
Qy 1201 CATCGACTACGACCCGCTAGAGGGCTATGTCTACTGGACAGATGACGAGGTGCGGGCCAT 1260
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Qy 1261 CCGCAGGGCGTACCTGGACGGGTCTGGGGCGCAGACGCTGGTCAACACCGAGATCAACGA 1320
Db 1261 CCGCAGGGCGTACCTGGACGGGTCTGGGGCGCAGACGCTGGTCAACACCGAGATCAACGA 1320
Qy 1321 CCCCGATGGCATCGCGGTCGACTGGGTGGCCCGAAACCTCTACTGGACCGACACGGGCAC 1380
Db 1321 CCCCGATGGCATCGCGGTCGACTGGGTGGCCCGAAACCTCTACTGGACCGACACGGGCAC 1380
Qy 1381 GGACCGCATCGAGGTGACGCGCCTCAACGGCACCTCCCGCAAGATCCTGGTGTCGGAGGA 1440
Db 1381 GGACCGCATCGAGGTGACGCGCCTCAACGGCACCTCCCGCAAGATCCTGGTGTCGGAGGA 1440
Qy 1441 CCTGGACGAGCCCCGAGCCATCGCACTGCACCCCGTGATGGGCCTCATGTACTGGACAGA 1500
Db 1441 CCTGGACGAGCCCCGAGCCATCGCACTGCACCCCGTGATGGGCCTCATGTACTGGACAGA 1500
Qy 1501 CTGGGGAGAGAACCCTAAAATCGAGTGTGCCAACTTGGATGGGCAGGAGCGGCGTGTGCT 1560
Db 1501 CTGGGGAGAGAACCCTAAAATCGAGTGTGCCAACTTGGATGGGCAGGAGCGGCGTGTGCT 1560
Qy 1561 GGTCAATGCCTCCCTCGGGTGGCCCAACGGCCTGGCCCTGGACCTGCAGGAGGGGAAGCT 1620
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Qy 1621 CTACTGGGGAGACGCCAAGACAGACAAGATCGAGGTGATCAATGTTGATGGGACGAAGAG 1680
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Qy 1681 GCGGACCCTCCTGGAGGACAAGCTCCCGCACATTTTCGGGTTCACGCTGCTGGGGGACTT 1740
Db 1681 GCGGACCCTCCTGGAGGACAAGCTCCCGCACATTTTCGGGTTCACGCTGCTGGGGGACTT 1740
Qy 1741 CATCTACTGGACTGACTGGCAGCGCCGCAGCATCGAGCGGGTGCACAAGGTCAAGGCCAG 1800
Db 1741 CATCTACTGGACTGACTGGCAGCGCCGCAGCATCGAGCGGGTGCACAAGGTCAAGGCCAG 1800
Qy 1801 CCGGGACGTCATCATTGACCAGCTGCCCGACCTGATGGGGCTCAAAGCTGTGAATGTGGC 1860
Db 1801 CCGGGACGTCATCATTGACCAGCTGCCCGACCTGATGGGGCTCAAAGCTGTGAATGTGGC 1860
Qy 1861 CAAGGTCGTCGGAACCAACCCGTGTGCGGACAGGAACGGGGGGTGCAGCCACCTGTGCTT 1920
Db 1861 CAAGGTCGTCGGAACCAACCCGTGTGCGGACAGGAACGGGGGGTGCAGCCACCTGTGCTT 1920
Qy 1921 CTTCACACCCCACGCAACCCGGTGTGGCTGCCCCATCGGCCTGGAGCTGCTGAGTGACAT 1980
Db 1921 CTTCACACCCCACGCAACCCGGTGTGGCTGCCCCATCGGCCTGGAGCTGCTGAGTGACAT 1980
Qy 1981 GAAGACCTGCATCGTGCCTGAGGCCTTCTTGGTCTTCACCAGCAGAGCCGCCATCCACAG 2040
Db 1981 GAAGACCTGCATCGTGCCTGAGGCCTTCTTGGTCTTCACCAGCAGAGCCGCCATCCACAG 2040
Qy 2041 GATCTCCCTCGAGACCAATAACAACGACGTGGCCATCCCGCTCACGGGCGTCAAGGAGGC 2100
Db 2041 GATCTCCCTCGAGACCAATAACAACGACGTGGCCATCCCGCTCACGGGCGTCAAGGAGGC 2100
Qy 2101 CTCAGCCCTGGACTTTGATGTGTCCAACAACCACATCTACTGGACAGACGTCAGCCTGAA 2160
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Db       2941 TCGGATGATCCCGGACGACCAGCACAGCCCGGATCTCATCCTGCCCCTGCATGGACTGAG 3000
Qy       3001 GAACGTCAAAGCCATCGACTATGACCCACTGGACAAGTTCATCTACTGGGTGGATGGGCG 3060
Db       3001 GAACGTCAAAGCCATCGACTATGACCCACTGGACAAGTTCATCTACTGGGTGGATGGGCG 3060
Qy       3061 CCAGAACATCAAGCGAGCCAAGGACGACGGGACCCAGCCCTTTGTTTTGACCTCTCTGAG 3120
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Qy       3121 CCAAGGCCAAAACCCAGACAGGCAGCCCCACGACCTCAGCATCGACATCTACAGCCGGAC 3180
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Db       3301 GCGAGGGTACCTGTACTTCACCAACATGCAGGACCGGGCAGCCAAGATCGAACGCGCAGC 3360
Qy       3361 CCTGGACGGCACCGAGCGCGAGGTCCTCTTCACCACCGGCCTCATCCGCCCTGTGGCCCT 3420
Db       3361 CCTGGACGGCACCGAGCGCGAGGTCCTCTTCACCACCGGCCTCATCCGCCCTGTGGCCCT 3420
Qy       3421 GGTGGTGGACAACACACTGGGCAAGCTGTTCTGGGTGGACGCGGACCTGAAGCGCATTGA 3480
Db       3421 GGTGGTGGACAACACACTGGGCAAGCTGTTCTGGGTGGACGCGGACCTGAAGCGCATTGA 3480
Qy       3481 GAGCTGTGACCTGTCAGGGGCCAACCGCCTGACCCTGGAGGACGCCAACATCGTGCAGCC 3540
Db       3481 GAGCTGTGACCTGTCAGGGGCCAACCGCCTGACCCTGGAGGACGCCAACATCGTGCAGCC 3540
Qy       3541 TCTGGGCCTGACCATCCTTGGCAAGCATCTCTACTGGATCGACCGCCAGCAGCAGATGAT 3600
Db       3541 TCTGGGCCTGACCATCCTTGGCAAGCATCTCTACTGGATCGACCGCCAGCAGCAGATGAT 3600
Qy       3601 CGAGCGTGTGGAGAAGACCACCGGGGACAAGCGGACTCGCATCCAGGGCCGTGTCGCCCA 3660
Db       3601 CGAGCGTGTGGAGAAGACCACCGGGGACAAGCGGACTCGCATCCAGGGCCGTGTCGCCCA 3660
Qy       3661 CCTCACTGGCATCCATGCAGTGGAGGAAGTCAGCCTGGAGGAGTTCTCAGCCCACCCATG 3720
Db       3661 CCTCACTGGCATCCATGCAGTGGAGGAAGTCAGCCTGGAGGAGTTCTCAGCCCACCCATG 3720
Qy       3721 TGCCCGTGACAATGGTGGCTGCTCCCACATCTGTATTGCCAAGGGTGATGGGACACCACG 3780
Db       3721 TGCCCGTGACAATGGTGGCTGCTCCCACATCTGTATTGCCAAGGGTGATGGGACACCACG 3780
Qy       3781 GTGCTCATGCCCAGTCCACCTCGTGCTCCTGCAGAACCTGCTGACCTGTGGAGAGCCGCC 3840
Db       3781 GTGCTCATGCCCAGTCCACCTCGTGCTCCTGCAGAACCTGCTGACCTGTGGAGAGCCGCC 3840

Qy       3841 CACCTGCTCCCCGGACCAGTTTGCATGTGCCACAGGGGAGATCGACTGTATCCCCGGGGC 3900
Db       3841 CACCTGCTCCCCGGACCAGTTTGCATGTGCCACAGGGGAGATCGACTGTATCCCCGGGGC 3900
Qy       3901 CTGGCGCTGTGACGGCTTTCCCGAGTGCGATGACCAGAGCGACGAGGAGGGCTGCCCCGT 3960
Db       3901 CTGGCGCTGTGACGGCTTTCCCGAGTGCGATGACCAGAGCGACGAGGAGGGCTGCCCCGT 3960
Qy       3961 GTGCTCCGCCGCCCAGTTCCCCTGCGCGCGGGGTCAGTGTGTGGACCTGCGCCTGCGCTG 4020
Db       3961 GTGCTCCGCCGCCCAGTTCCCCTGCGCGCGGGGTCAGTGTGTGGACCTGCGCCTGCGCTG 4020
Qy       4021 CGACGGCGAGGCAGACTGTCAGGACCGCTCAGACGAGGTGGACTGTGACGCCATCTGCCT 4080
Db       4021 CGACGGCGAGGCAGACTGTCAGGACCGCTCAGACGAGGTGGACTGTGACGCCATCTGCCT 4080
Qy       4081 GCCCAACCAGTTCCGGTGTGCGAGCGGCCAGTGTGTCCTCATCAAACAGCAGTGCGACTC 4140
Db       4081 GCCCAACCAGTTCCGGTGTGCGAGCGGCCAGTGTGTCCTCATCAAACAGCAGTGCGACTC 4140
Qy       4141 CTTCCCCGACTGTATCGACGGCTCCGACGAGCTCATGTGTGAAATCACCAAGCCGCCCTC 4200
Db       4141 CTTCCCCGACTGTATCGACGGCTCCGACGAGCTCATGTGTGAAATCACCAAGCCGCCCTC 4200
Qy       4201 AGACGACAGCCCGGCCCACAGCAGTGCCATCGGGCCCGTCATTGGCATCATCCTCTCTCT 4260
Db       4201 AGACGACAGCCCGGCCCACAGCAGTGCCATCGGGCCCGTCATTGGCATCATCCTCTCTCT 4260
Qy       4261 CTTCGTCATGGGTGGTGTCTATTTTGTGTGCCAGCGCGTGGTGTGCCAGCGCTATGCGGG 4320
Db       4261 CTTCGTCATGGGTGGTGTCTATTTTGTGTGCCAGCGCGTGGTGTGCCAGCGCTATGCGGG 4320
Qy       4321 GGCCAACGGGCCCTTCCCGCACGAGTATGTCAGCGGGACCCCGCACGTGCCCCTCAATTT 4380
Db       4321 GGCCAACGGGCCCTTCCCGCACGAGTATGTCAGCGGGACCCCGCACGTGCCCCTCAATTT 4380
Qy       4381 CATAGCCCCGGGCGGTTCCCAGCATGGCCCCTTCACAGGCATCGCATGCGGAAAGTCCAT 4440
Db       4381 CATAGCCCCGGGCGGTTCCCAGCATGGCCCCTTCACAGGCATCGCATGCGGAAAGTCCAT 4440
Qy       4441 GATGAGCTCCGTGAGCCTGATGGGGGGCCGGGGCGGGGTGCCCCTCTACGACCGGAACCA 4500
Db       4441 GATGAGCTCCGTGAGCCTGATGGGGGGCCGGGGCGGGGTGCCCCTCTACGACCGGAACCA 4500
Qy       4501 CGTCACAGGGGCCTCGTCCAGCAGCTCGTCCAGCACGAAGGCCACGCTGTACCCGCCGAT 4560
Db       4501 CGTCACAGGGGCCTCGTCCAGCAGCTCGTCCAGCACGAAGGCCACGCTGTACCCGCCGAT 4560
Qy       4561 CCTGAACCCGCCGCCCTCCCCGGCCACGGACCCCTCCCTGTACAACATGGACATGTTCTA 4620
Db       4561 CCTGAACCCGCCGCCCTCCCCGGCCACGGACCCCTCCCTGTACAACATGGACATGTTCTA 4620
Qy       4621 CTCTTCAAACATTCCGGCCACTGCGAGACCGTACAGGCCCTACATCATTCGAGGAATGGC 4680
Db       4621 CTCTTCAAACATTCCGGCCACTGCGAGACCGTACAGGCCCTACATCATTCGAGGAATGGC 4680
Qy       4681 GCCCCCGACGACGCCCTGCAGCACCGACGTGTGTGACAGCGACTACAGCGCCAGCCGCTG 4740
Db       4681 GCCCCCGACGACGCCCTGCAGCACCGACGTGTGTGACAGCGACTACAGCGCCAGCCGCTG 4740
Qy       4741 GAAGGCCAGCAAGTACTACCTGGATTTGAACTCGGACTCAGACCCCTATCCACCCCCACC 4800
Db       4741 GAAGGCCAGCAAGTACTACCTGGATTTGAACTCGGACTCAGACCCCTATCCACCCCCACC 4800
Qy       4801 CACGCCCCACAGCCAGTACCTGTCGGCGGAGGACAGCTGCCCGCCCTCGCCCGCCACCGA 4860
Db       4801 CACGCCCCACAGCCAGTACCTGTCGGCGGAGGACAGCTGCCCGCCCTCGCCCGCCACCGA 4860
Qy       4861 GAGGAGCTACTTCCATCTCTTCCCGCCCCCTCCGTCCCCCTGCACGGACTCATCCTGACC 4920
Db       4861 GAGGAGCTACTTCCATCTCTTCCCGCCCCCTCCGTCCCCCTGCACGGACTCATCCTGACC 4920
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Qy       4921 TCGGCCGGGCCACTCTGGCTTCTCTGTGCCCCTGTAAATAGTTTTAAATATGAACAAAGA 4980
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4921 TCGGCCGGGCCACTCTGGCTTCTCTGTGCCCCTGTAAATAGTTTTAAATATGAACAAAGA 4980

Qy       4981 AAAAAATATATTTTATGATTTAAAAAATAAATATAATTGGGATTTTAAAAACATGAGAAA 5040
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4981 AAAAAATATATTTTATGATTTAAAAAATAAATATAATTGGGATTTTAAAAACATGAGAAA 5040

Qy       5041 TGTGAACTGTGATGGGGTGGGCAGGGCTGGGAGAACTTTGTACAGTGGAGAAATATTTAT 5100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5041 TGTGAACTGTGATGGGGTGGGCAGGGCTGGGAGAACTTTGTACAGTGGAGAAATATTTAT 5100

Qy       5101 AAACTTAATTTTGTAAAACA 5120
             ||||||||||||||||||||
Db       5101 AAACTTAATTTTGTAAAACA 5120
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RESULT 4
ADE82640
ID ADE82640 standard; DNA; 5120 BP.
XX
AC ADE82640;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human HBM gene encoding sequence.
XX
KW LRP5; LRP6; HBM; Dkk activity; Osteopathic; Antiinflammatory;
KW Antiarthritic; bone mass disorders; osteoporosis; hypercalcaemia;
KW hyperostosis; osteogenesis; Wnt signaling; ds.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT CDS   71. .4915
FT   /*tag= a
XX
PN WO200292015-A2.
XX
PD 21-NOV-2002.
XX
PF 17-MAY-2002; 2002WO-US015982.
XX
PR 17-MAY-2001; 2001US-0291311P.
PR 01-FEB-2002; 2002US-0353058P.
PR 04-MAR-2002; 2002US-0361293P.
XX
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (AMHP) WYETH.
XX
PI Allen K, Anisowicz A, Bhat BM, Damagnez V, Robinson JA;
PI Yaworsky PJ;
XX
DR WPI; 2003-129219/12.
DR P-PSDB; ADE82428.
XX
PT Regulating LRP5, LRP6 or HBM activity in a subject, useful for modulating
PT lipid levels and/or bone mass, and for in treating bone mass disorders,
PT e.g. osteoporosis, comprises administering a composition which modulates
PT a Dkk activity.
XX
PS Disclosure; SEQ ID NO 2; 173pp; English.
XX
CC The present invention relates to regulating LRP5, LRP6 or HBM activity in
CC a subject comprising administering a composition which modulates a Dkk
CC activity. The method is useful for modulating lipid levels and/or bone
CC mass, and is useful in treating or diagnosing abnormal lipid levels and
CC bone mass disorders, such as osteoporosis, bond fracture, age-related
CC loss of bone, a chondrodystrophy, drug-induced bone disorder, high bone
CC turnover, hypercalcaemia, hyperostosis, osteogenesis, imperfecta,
CC osteomalacia, osteomyelitis, Paget's disease, osteoarthritis, and
CC rickets. Modulators of Dkk activity are useful for as reagents in
CC studying bone mass and lipid level modulation, in modulating Wnt
CC signaling, or treating Dkk-mediated disorders. The present sequence
CC represents human HBM gene encoding sequence.
XX
SQ Sequence 5120 BP; 1037 A; 1657 C; 1548 G; 878 T; 0 U; 0 Other;

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  Query Match            100.0%;  Score 5120;  DB 10;  Length 5120;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 5120;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ACTAAAGCGCCGCCGCCGCGCCATGGAGCCCGAGTGAGCGCGGCGCGGGCCCGTCCGGCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ACTAAAGCGCCGCCGCCGCGCCATGGAGCCCGAGTGAGCGCGGCGCGGGCCCGTCCGGCC 60

Qy         61 GCCGGACAACATGGAGGCAGCGCCGCCCGGGCCGCCGTGGCCGCTGCTGCTGCTGCTGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCCGGACAACATGGAGGCAGCGCCGCCCGGGCCGCCGTGGCCGCTGCTGCTGCTGCTGCT 120

Qy        121 GCTGCTGCTGGCGCTGTGCGGCTGCCCGGCCCCCGCCGCGGCCTCGCCGCTCCTGCTATT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCTGCTGCTGGCGCTGTGCGGCTGCCCGGCCCCCGCCGCGGCCTCGCCGCTCCTGCTATT 180

Qy        181 TGCCAACCGCCGGGACGTACGGCTGGTGGACGCCGGCGGAGTCAAGCTGGAGTCCACCAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TGCCAACCGCCGGGACGTACGGCTGGTGGACGCCGGCGGAGTCAAGCTGGAGTCCACCAT 240

Qy        241 CGTGGTCAGCGGCCTGGAGGATGCGGCCGCAGTGGACTTCCAGTTTTCCAAGGGAGCCGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CGTGGTCAGCGGCCTGGAGGATGCGGCCGCAGTGGACTTCCAGTTTTCCAAGGGAGCCGT 300

Qy        301 GTACTGGACAGACGTGAGCGAGGAGGCCATCAAGCAGACCTACCTGAACCAGACGGGGGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GTACTGGACAGACGTGAGCGAGGAGGCCATCAAGCAGACCTACCTGAACCAGACGGGGGC 360

Qy        361 CGCCGTGCAGAACGTGGTCATCTCCGGCCTGGTCTCTCCCGACGGCCTCGCCTGCGACTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CGCCGTGCAGAACGTGGTCATCTCCGGCCTGGTCTCTCCCGACGGCCTCGCCTGCGACTG 420

Qy        421 GGTGGGCAAGAAGCTGTACTGGACGGACTCAGAGACCAACCGCATCGAGGTGGCCAACCT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GGTGGGCAAGAAGCTGTACTGGACGGACTCAGAGACCAACCGCATCGAGGTGGCCAACCT 480

Qy        481 CAATGGCACATCCCGGAAGGTGCTCTTCTGGCAGGACCTTGACCAGCCGAGGGCCATCGC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CAATGGCACATCCCGGAAGGTGCTCTTCTGGCAGGACCTTGACCAGCCGAGGGCCATCGC 540

Qy        541 CTTGGACCCCGCTCACGGGTACATGTACTGGACAGACTGGGTTGAGACGCCCCGGATTGA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CTTGGACCCCGCTCACGGGTACATGTACTGGACAGACTGGGTTGAGACGCCCCGGATTGA 600

Qy        601 GCGGGCAGGGATGGATGGCAGCACCCGGAAGATCATTGTGGACTCGGACATTTACTGGCC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GCGGGCAGGGATGGATGGCAGCACCCGGAAGATCATTGTGGACTCGGACATTTACTGGCC 660

Qy        661 CAATGGACTGACCATCGACCTGGAGGAGCAGAAGCTCTACTGGGCTGACGCCAAGCTCAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAATGGACTGACCATCGACCTGGAGGAGCAGAAGCTCTACTGGGCTGACGCCAAGCTCAG 720

Qy        721 CTTCATCCACCGTGCCAACCTGGACGGCTCGTTCCGGCAGAAGGTGGTGGAGGGCAGCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CTTCATCCACCGTGCCAACCTGGACGGCTCGTTCCGGCAGAAGGTGGTGGAGGGCAGCCT 780

Qy        781 GACGCACCCCTTCGCCCTGACGCTCTCCGGGGACACTCTGTACTGGACAGACTGGCAGAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACGCACCCCTTCGCCCTGACGCTCTCCGGGGACACTCTGTACTGGACAGACTGGCAGAC 840

Qy        841 CCGCTCCATCCATGCCTGCAACAAGCGCACTGGGGGGAAGAGGAAGGAGATCCTGAGTGC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CCGCTCCATCCATGCCTGCAACAAGCGCACTGGGGGGAAGAGGAAGGAGATCCTGAGTGC 900

Qy        901 CCTCTACTCACCCATGGACATCCAGGTGCTGAGCCAGGAGCGGCAGCCTTTCTTCCACAC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CCTCTACTCACCCATGGACATCCAGGTGCTGAGCCAGGAGCGGCAGCCTTTCTTCCACAC 960
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Qy       961 TCGCTGTGAGGAGGACAATGGCGGCTGCTCCCACCTGTGCCTGCTGTCCCCAAGCGAGCC 1020
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       961 TCGCTGTGAGGAGGACAATGGCGGCTGCTCCCACCTGTGCCTGCTGTCCCCAAGCGAGCC 1020

Qy      1021 TTTCTACACATGCGCCTGCCCCACGGGTGTGCAGCTGCAGGACAACGGCAGGACGTGTAA 1080
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1021 TTTCTACACATGCGCCTGCCCCACGGGTGTGCAGCTGCAGGACAACGGCAGGACGTGTAA 1080

Qy      1081 GGCAGGAGCCGAGGAGGTGCTGCTGCTGGCCCGGCGGACGGACCTACGGAGGATCTCGCT 1140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1081 GGCAGGAGCCGAGGAGGTGCTGCTGCTGGCCCGGCGGACGGACCTACGGAGGATCTCGCT 1140

Qy      1141 GGACACGCCGGACTTCACCGACATCGTGCTGCAGGTGGACGACATCCGGCACGCCATTGC 1200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1141 GGACACGCCGGACTTCACCGACATCGTGCTGCAGGTGGACGACATCCGGCACGCCATTGC 1200

Qy      1201 CATCGACTACGACCCGCTAGAGGGCTATGTCTACTGGACAGATGACGAGGTGCGGGCCAT 1260
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1201 CATCGACTACGACCCGCTAGAGGGCTATGTCTACTGGACAGATGACGAGGTGCGGGCCAT 1260

Qy      1261 CCGCAGGGCGTACCTGGACGGGTCTGGGGCGCAGACGCTGGTCAACACCGAGATCAACGA 1320
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1261 CCGCAGGGCGTACCTGGACGGGTCTGGGGCGCAGACGCTGGTCAACACCGAGATCAACGA 1320

Qy      1321 CCCCGATGGCATCGCGGTCGACTGGGTGGCCCGAAACCTCTACTGGACCGACACGGGCAC 1380
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1321 CCCCGATGGCATCGCGGTCGACTGGGTGGCCCGAAACCTCTACTGGACCGACACGGGCAC 1380

Qy      1381 GGACCGCATCGAGGTGACGCGCCTCAACGGCACCTCCCGCAAGATCCTGGTGTCGGAGGA 1440
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1381 GGACCGCATCGAGGTGACGCGCCTCAACGGCACCTCCCGCAAGATCCTGGTGTCGGAGGA 1440

Qy      1441 CCTGGACGAGCCCCGAGCCATCGCACTGCACCCCGTGATGGGCCTCATGTACTGGACAGA 1500
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1441 CCTGGACGAGCCCCGAGCCATCGCACTGCACCCCGTGATGGGCCTCATGTACTGGACAGA 1500

Qy      1501 CTGGGGAGAGAACCCTAAAATCGAGTGTGCCAACTTGGATGGGCAGGAGCGGCGTGTGCT 1560
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1501 CTGGGGAGAGAACCCTAAAATCGAGTGTGCCAACTTGGATGGGCAGGAGCGGCGTGTGCT 1560

Qy      1561 GGTCAATGCCTCCCTCGGGTGGCCCAACGGCCTGGCCCTGGACCTGCAGGAGGGGAAGCT 1620
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1561 GGTCAATGCCTCCCTCGGGTGGCCCAACGGCCTGGCCCTGGACCTGCAGGAGGGGAAGCT 1620

Qy      1621 CTACTGGGGAGACGCCAAGACAGACAAGATCGAGGTGATCAATGTTGATGGGACGAAGAG 1680
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1621 CTACTGGGGAGACGCCAAGACAGACAAGATCGAGGTGATCAATGTTGATGGGACGAAGAG 1680

Qy      1681 GCGGACCCTCCTGGAGGACAAGCTCCCGCACATTTTCGGGTTCACGCTGCTGGGGGACTT 1740
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1681 GCGGACCCTCCTGGAGGACAAGCTCCCGCACATTTTCGGGTTCACGCTGCTGGGGGACTT 1740

Qy      1741 CATCTACTGGACTGACTGGCAGCGCCGCAGCATCGAGCGGGTGCACAAGGTCAAGGCCAG 1800
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1741 CATCTACTGGACTGACTGGCAGCGCCGCAGCATCGAGCGGGTGCACAAGGTCAAGGCCAG 1800

Qy      1801 CCGGGACGTCATCATTGACCAGCTGCCCGACCTGATGGGGCTCAAAGCTGTGAATGTGGC 1860
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1801 CCGGGACGTCATCATTGACCAGCTGCCCGACCTGATGGGGCTCAAAGCTGTGAATGTGGC 1860

Qy      1861 CAAGGTCGTCGGAACCAACCCGTGTGCGGACAGGAACGGGGGGGTGCAGCCACCTGTGCTT 1920
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1861 CAAGGTCGTCGGAACCAACCCGTGTGCGGACAGGAACGGGGGGGTGCAGCCACCTGTGCTT 1920

Qy      1921 CTTCACACCCCACGCAACCCGGTGTGGCTGCCCCATCGGCCTGGAGCTGCTGAGTGACAT 1980
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1921 CTTCACACCCCACGCAACCCGGTGTGGCTGCCCCATCGGCCTGGAGCTGCTGAGTGACAT 1980

Qy      1981 GAAGACCTGCATCGTGCCTGAGGCCTTCTTGGTCTTCACCAGCAGAGCCGCCATCCACAG 2040
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1981 GAAGACCTGCATCGTGCCTGAGGCCTTCTTGGTCTTCACCAGCAGAGCCGCCATCCACAG 2040

Qy      2041 GATCTCCCTCGAGACCAATAACAACGACGTGGCCATCCCGCTCACGGGCGTCAAGGAGGC 2100
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            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2041 GATCTCCCTCGAGACCAATAACAACGACGTGGCCATCCCGCTCACGGGCGTCAAGGAGGC 2100

Qy      2101 CTCAGCCCTGGACTTTGATGTGTCCAACAACCACATCTACTGGACAGACGTCAGCCTGAA 2160
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2101 CTCAGCCCTGGACTTTGATGTGTCCAACAACCACATCTACTGGACAGACGTCAGCCTGAA 2160

Qy      2161 GACCATCAGCCGCGCCTTCATGAACGGGAGCTCGGTGGAGCACGTGGTGGAGTTTGGCCT 2220
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2161 GACCATCAGCCGCGCCTTCATGAACGGGAGCTCGGTGGAGCACGTGGTGGAGTTTGGCCT 2220

Qy      2221 TGACTACCCCGAGGGCATGGCCGTTGACTGGATGGGCAAGAACCTCTACTGGGCCGACAC 2280
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2221 TGACTACCCCGAGGGCATGGCCGTTGACTGGATGGGCAAGAACCTCTACTGGGCCGACAC 2280

Qy      2281 TGGGACCAACAGAATCGAAGTGGCGCGGCTGGACGGGCAGTTCCGGCAAGTCCTCGTGTG 2340
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2281 TGGGACCAACAGAATCGAAGTGGCGCGGCTGGACGGGCAGTTCCGGCAAGTCCTCGTGTG 2340

Qy      2341 GAGGGACTTGGACAACCCGAGGTCGCTGGCCCTGGATCCCACCAAGGGCTACATCTACTG 2400
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2341 GAGGGACTTGGACAACCCGAGGTCGCTGGCCCTGGATCCCACCAAGGGCTACATCTACTG 2400

Qy      2401 GACCGAGTGGGGCGGCAAGCCGAGGATCGTGCGGGCCTTCATGGACGGGACCAACTGCAT 2460
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2401 GACCGAGTGGGGCGGCAAGCCGAGGATCGTGCGGGCCTTCATGGACGGGACCAACTGCAT 2460

Qy      2461 GACGCTGGTGGACAAGGTGGGCCGGGCCAACGACCTCACCATTGACTACGCTGACCAGCG 2520
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2461 GACGCTGGTGGACAAGGTGGGCCGGGCCAACGACCTCACCATTGACTACGCTGACCAGCG 2520

Qy      2521 CCTCTACTGGACCGACCTGGACACCAACATGATCGAGTCGTCCAACATGCTGGGTCAGGA 2580
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2521 CCTCTACTGGACCGACCTGGACACCAACATGATCGAGTCGTCCAACATGCTGGGTCAGGA 2580

Qy      2581 GCGGGTCGTGATTGCCGACGATCTCCCGCACCCGTTCGGTCTGACGCAGTACAGCGATTA 2640
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2581 GCGGGTCGTGATTGCCGACGATCTCCCGCACCCGTTCGGTCTGACGCAGTACAGCGATTA 2640

Qy      2641 TATCTACTGGACAGACTGGAATCTGCACAGCATTGAGCGGGCCGACAAGACTAGCGGCCG 2700
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2641 TATCTACTGGACAGACTGGAATCTGCACAGCATTGAGCGGGCCGACAAGACTAGCGGCCG 2700

Qy      2701 GAACCGCACCCTCATCCAGGGCCACCTGGACTTCGTGATGGACATCCTGGTGTTCCACTC 2760
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2701 GAACCGCACCCTCATCCAGGGCCACCTGGACTTCGTGATGGACATCCTGGTGTTCCACTC 2760

Qy      2761 CTCCCGCCAGGATGGCCTCAATGACTGTATGCACAACAACGGGCAGTGTGGGCAGCTGTG 2820
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2761 CTCCCGCCAGGATGGCCTCAATGACTGTATGCACAACAACGGGCAGTGTGGGCAGCTGTG 2820

Qy      2821 CCTTGCCATCCCCGGCGGCCACCGCTGCGGCTGCGCCTCACACTACACCCTGGACCCCAG 2880
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2821 CCTTGCCATCCCCGGCGGCCACCGCTGCGGCTGCGCCTCACACTACACCCTGGACCCCAG 2880

Qy      2881 CAGCCGCAACTGCAGCCCGCCCACCACCTTCTTGCTGTTCAGCCAGAAATCTGCCATCAG 2940
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2881 CAGCCGCAACTGCAGCCCGCCCACCACCTTCTTGCTGTTCAGCCAGAAATCTGCCATCAG 2940

Qy      2941 TCGGATGATCCCGGACGACCAGCACAGCCCGGATCTCATCCTGCCCCTGCATGGACTGAG 3000
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2941 TCGGATGATCCCGGACGACCAGCACAGCCCGGATCTCATCCTGCCCCTGCATGGACTGAG 3000

Qy      3001 GAACGTCAAAGCCATCGACTATGACCCACTGGACAAGTTCATCTACTGGGTGGATGGGCG 3060
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Db      3001 GAACGTCAAAGCCATCGACTATGACCCACTGGACAAGTTCATCTACTGGGTGGATGGGCG 3060

Qy      3061 CCAGAACATCAAGCGAGCCAAGGACGACGGGACCCAGCCCTTTGTTTTGACCTCTCTGAG 3120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3061 CCAGAACATCAAGCGAGCCAAGGACGACGGGACCCAGCCCTTTGTTTTGACCTCTCTGAG 3120

Qy      3121 CCAAGGCCAAAACCCAGACAGGCAGCCCCACGACCTCAGCATCGACATCTACAGCCGGAC 3180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       3121 CCAAGGCCAAAACCCAGACAGGCAGCCCCACGACCTCAGCATCGACATCTACAGCCGGAC 3180

Qy       3181 ACTGTTCTGGACGTGCGAGGCCACCAATACCATCAACGTCCACAGGCTGAGCGGGGAAGC 3240
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3181 ACTGTTCTGGACGTGCGAGGCCACCAATACCATCAACGTCCACAGGCTGAGCGGGGAAGC 3240

Qy       3241 CATGGGGGTGGTGCTGCGTGGGGACCGCGACAAGCCCAGGGCCATCGTCGTCAACGCGGA 3300
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Db       3241 CATGGGGGTGGTGCTGCGTGGGGACCGCGACAAGCCCAGGGCCATCGTCGTCAACGCGGA 3300

Qy       3301 GCGAGGGTACCTGTACTTCACCAACATGCAGGACCGGGCAGCCAAGATCGAACGCGCAGC 3360
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3301 GCGAGGGTACCTGTACTTCACCAACATGCAGGACCGGGCAGCCAAGATCGAACGCGCAGC 3360

Qy       3361 CCTGGACGGCACCGAGCGCGAGGTCCTCTTCACCACCGGCCTCATCCGCCCTGTGGCCCT 3420
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3361 CCTGGACGGCACCGAGCGCGAGGTCCTCTTCACCACCGGCCTCATCCGCCCTGTGGCCCT 3420

Qy       3421 GGTGGTGGACAACACACTGGGCAAGCTGTTCTGGGTGGACGCGGACCTGAAGCGCATTGA 3480
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3421 GGTGGTGGACAACACACTGGGCAAGCTGTTCTGGGTGGACGCGGACCTGAAGCGCATTGA 3480

Qy       3481 GAGCTGTGACCTGTCAGGGGCCAACCGCCTGACCCTGGAGGACGCCAACATCGTGCAGCC 3540
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3481 GAGCTGTGACCTGTCAGGGGCCAACCGCCTGACCCTGGAGGACGCCAACATCGTGCAGCC 3540

Qy       3541 TCTGGGCCTGACCATCCTTGGCAAGCATCTCTACTGGATCGACCGCCAGCAGCAGATGAT 3600
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Db       3541 TCTGGGCCTGACCATCCTTGGCAAGCATCTCTACTGGATCGACCGCCAGCAGCAGATGAT 3600

Qy       3601 CGAGCGTGTGGAGAAGACCACCGGGGACAAGCGGACTCGCATCCAGGGCCGTGTCGCCCA 3660
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Db       3601 CGAGCGTGTGGAGAAGACCACCGGGGACAAGCGGACTCGCATCCAGGGCCGTGTCGCCCA 3660

Qy       3661 CCTCACTGGCATCCATGCAGTGGAGGAAGTCAGCCTGGAGGAGTTCTCAGCCCACCCATG 3720
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Db       3661 CCTCACTGGCATCCATGCAGTGGAGGAAGTCAGCCTGGAGGAGTTCTCAGCCCACCCATG 3720

Qy       3721 TGCCCGTGACAATGGTGGCTGCTCCCACATCTGTATTGCCAAGGGTGATGGGACACCACG 3780
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       3781 GTGCTCATGCCCAGTCCACCTCGTGCTCCTGCAGAACCTGCTGACCTGTGGAGAGCCGCC 3840
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3781 GTGCTCATGCCCAGTCCACCTCGTGCTCCTGCAGAACCTGCTGACCTGTGGAGAGCCGCC 3840

Qy       3841 CACCTGCTCCCCGGACCAGTTTGCATGTGCCACAGGGGAGATCGACTGTATCCCCGGGGC 3900
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Qy       3901 CTGGCGCTGTGACGGCTTTCCCGAGTGCGATGACCAGAGCGACGAGGAGGGCTGCCCCGT 3960
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Qy       3961 GTGCTCCGCCGCCCAGTTCCCCTGCGCGCGGGGTCAGTGTGTGGACCTGCGCCTGCGCTG 4020
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Qy       4021 CGACGGCGAGGCAGACTGTCAGGACCGCTCAGACGAGGTGGACTGTGACGCCATCTGCCT 4080
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Qy       4081 GCCCAACCAGTTCCGGTGTGCGAGCGGCCAGTGTGTCCTCATCAAACAGCAGTGCGACTC 4140
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Qy       4141 CTTCCCCGACTGTATCGACGGCTCCGACGAGCTCATGTGTGAAATCACCAAGCCGCCCTC 4200
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Db       4141 CTTCCCCGACTGTATCGACGGCTCCGACGAGCTCATGTGTGAAATCACCAAGCCGCCCTC 4200

Qy       4201 AGACGACAGCCCGGCCCACAGCAGTGCCATCGGGCCCGTCATTGGCATCATCCTCTCTCT 4260
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       4261 CTTCGTCATGGGTGGTGTCTATTTTGTGTGCCAGCGCGTGGTGTGCCAGCGCTATGCGGG 4320
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       4321 GGCCAACGGGCCCTTCCCGCACGAGTATGTCAGCGGGACCCCGCACGTGCCCCTCAATTT 4380
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4321 GGCCAACGGGCCCTTCCCGCACGAGTATGTCAGCGGGACCCCGCACGTGCCCCTCAATTT 4380

Qy       4381 CATAGCCCCGGGCGGTTCCCAGCATGGCCCCTTCACAGGCATCGCATGCGGAAAGTCCAT 4440
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Qy       4441 GATGAGCTCCGTGAGCCTGATGGGGGGCCGGGGCGGGGTGCCCCTCTACGACCGGAACCA 4500
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Qy       4501 CGTCACAGGGGCCTCGTCCAGCAGCTCGTCCAGCACGAAGGCCACGCTGTACCCGCCGAT 4560
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Qy       4561 CCTGAACCCGCCGCCCTCCCCGGCCACGGACCCCTCCCTGTACAACATGGACATGTTCTA 4620
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Qy       4621 CTCTTCAAACATTCCGGCCACTGCGAGACCGTACAGGCCCTACATCATTCGAGGAATGGC 4680
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       4681 GCCCCCGACGACGCCCTGCAGCACCGACGTGTGTGACAGCGACTACAGCGCCAGCCGCTG 4740
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Qy       4741 GAAGGCCAGCAAGTACTACCTGGATTTGAACTCGGACTCAGACCCCTATCCACCCCCACC 4800
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Db       4741 GAAGGCCAGCAAGTACTACCTGGATTTGAACTCGGACTCAGACCCCTATCCACCCCCACC 4800

Qy       4801 CACGCCCCACAGCCAGTACCTGTCGGCGGAGGACAGCTGCCCGCCCTCGCCCGCCACCGA 4860
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Db       4801 CACGCCCCACAGCCAGTACCTGTCGGCGGAGGACAGCTGCCCGCCCTCGCCCGCCACCGA 4860

Qy       4861 GAGGAGCTACTTCCATCTCTTCCCGCCCCCTCCGTCCCCCTGCACGGACTCATCCTGACC 4920
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Qy       4921 TCGGCCGGGCCACTCTGGCTTCTCTGTGCCCCTGTAAATAGTTTTAAATATGAACAAAGA 4980
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Qy       4981 AAAAAATATATTTTATGATTTAAAAAATAAATATAATTGGGATTTTAAAAACATGAGAAA 5040
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Db       4981 AAAAAATATATTTTATGATTTAAAAAATAAATATAATTGGGATTTTAAAAACATGAGAAA 5040

Qy       5041 TGTGAACTGTGATGGGGTGGGCAGGGCTGGGAGAACTTTGTACAGTGGAGAAATATTTAT 5100
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Db       5041 TGTGAACTGTGATGGGGTGGGCAGGGCTGGGAGAACTTTGTACAGTGGAGAAATATTTAT 5100

Qy       5101 AAACTTAATTTTGTAAAACA 5120
             ||||||||||||||||||||
Db       5101 AAACTTAATTTTGTAAAACA 5120
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RESULT 5
ADR16920
ID ADR16920 standard; DNA; 5120 BP.
XX
AC ADR16920;
XX
DT 04-NOV-2004 (first entry)
XX
DE Human high bone mass gene, HBM allele DNA.
XX
KW Human; high bone mass; Zmax1; ds; gene; HBM; osteoporosis;

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KW   chromosome 11q13.3; osteopathic; LDL receptor; bone development;
KW   metabolic bone disease; SNP; single nucleotide polymorphism.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             71. .4918
FT                   /*tag=  a
FT                   /product= "HBM protein"
FT                   /transl_except= (pos:530. .532,aa:Lys)
FT                   /note= "Applies to SEQ ID 4 only"
FT                   /transl_except= (pos:986. .988,aa:Trp)
FT                   /note= "Applies to SEQ ID 4 only"
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FT                   /note= "Applies to SEQ ID 4 only"
FT   allele          replace(582,G)
FT                   /*tag=  b
FT                   /standard_name= "Single nucleotide polymorphism"
XX
PN   US6780609-B1.
XX
PD   24-AUG-2004.
XX
PF   05-APR-2000; 2000US-00543771.
XX
PR   13-JAN-1998;   98US-0071449P.
PR   23-OCT-1998;   98US-0105511P.
PR   13-JAN-1999;   99US-00229319.
XX
PA   (GENO-) GENOME THERAPEUTICS CORP.
XX
PI   Carulli JP,  Little RD,  Recker RR,  Johnson ML;
XX
DR   WPI; 2004-623529/60.
DR   P-PSDB; ADR16922, ADR17561.
XX
PT   New high bone mass gene of chromosome 1.1Q13.3, encoding protein useful
PT   for treating, diagnosing, preventing, or screening for normal and
PT   abnormal conditions of bone, including metabolic bone diseases, e.g.
PT   osteoporosis.
XX
PS   Disclosure; SEQ ID NO 2; 284pp; English.
XX
CC   The invention relates to an isolated amino acid protein sequence selected
CC   from an amino acid sequence appearing as ADR16922 or an amino acid
CC   sequence comprising or consisting of the extracellular domain of
CC   ADR16922(amino acids 23-1385). ADR16922 is encoded by the HBM (high bone
CC   mass) allele of the human Zmax1 gene and has sequence similarity to LDL
CC   receptors. Also disclosed are nucleic acids, proteins, cloning vectors,
CC   expression vectors, transformed hosts, methods of developing
CC   pharmaceutical compositions, methods of identifying molecules involved in
CC   bone development, and methods of diagnosing and treating diseases
CC   involved in bone development. Specifically disclosed is the Zmax1 gene
CC   and the high bone mass (HBM) allele on chromosome 11q13.3 encoding
CC   ADR16922. The protein is useful for treating, diagnosing, preventing, or
CC   screening for normal and abnormal conditions of bone, including metabolic
CC   bone diseases, e.g. osteoporosis. The present sequence is the high bone
CC   mass phenotype-causing allele of the human Zmax1 gene, HBM (probably a
CC   cDNA since 23 exons are disclosed yet this sequence is uninterrupted by
CC   introns).
XX
SQ   Sequence 5120 BP; 1037 A; 1657 C; 1548 G; 878 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 5120;  DB 13;  Length 5120;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 5120;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ACTAAAGCGCCGCCGCCGCGCCATGGAGCCCGAGTGAGCGCGGCGCGGGCCCGTCCGGCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ACTAAAGCGCCGCCGCCGCGCCATGGAGCCCGAGTGAGCGCGGCGCGGGCCCGTCCGGCC 60

Qy         61 GCCGGACAACATGGAGGCAGCGCCGCCCGGGCCGCCGTGGCCGCTGCTGCTGCTGCTGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCCGGACAACATGGAGGCAGCGCCGCCCGGGCCGCCGTGGCCGCTGCTGCTGCTGCTGCT 120

Qy        121 GCTGCTGCTGGCGCTGTGCGGCTGCCCGGCCCCCGCCGCGGCCTCGCCGCTCCTGCTATT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        181 TGCCAACCGCCGGGACGTACGGCTGGTGGACGCCGGCGGAGTCAAGCTGGAGTCCACCAT 240
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Db        181 TGCCAACCGCCGGGACGTACGGCTGGTGGACGCCGGCGGAGTCAAGCTGGAGTCCACCAT 240

Qy        241 CGTGGTCAGCGGCCTGGAGGATGCGGCCGCAGTGGACTTCCAGTTTTCCAAGGGAGCCGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CGTGGTCAGCGGCCTGGAGGATGCGGCCGCAGTGGACTTCCAGTTTTCCAAGGGAGCCGT 300

Qy        301 GTACTGGACAGACGTGAGCGAGGAGGCCATCAAGCAGACCTACCTGAACCAGACGGGGGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GTACTGGACAGACGTGAGCGAGGAGGCCATCAAGCAGACCTACCTGAACCAGACGGGGGC 360

Qy        361 CGCCGTGCAGAACGTGGTCATCTCCGGCCTGGTCTCTCCCGACGGCCTCGCCTGCGACTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CGCCGTGCAGAACGTGGTCATCTCCGGCCTGGTCTCTCCCGACGGCCTCGCCTGCGACTG 420

Qy        421 GGTGGGCAAGAAGCTGTACTGGACGGACTCAGAGACCAACCGCATCGAGGTGGCCAACCT 480
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Qy        481 CAATGGCACATCCCGGAAGGTGCTCTTCTGGCAGGACCTTGACCAGCCGAGGGCCATCGC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CAATGGCACATCCCGGAAGGTGCTCTTCTGGCAGGACCTTGACCAGCCGAGGGCCATCGC 540

Qy        541 CTTGGACCCCGCTCACGGGTACATGTACTGGACAGACTGGGTTGAGACGCCCCGGATTGA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CTTGGACCCCGCTCACGGGTACATGTACTGGACAGACTGGGTTGAGACGCCCCGGATTGA 600

Qy        601 GCGGGCAGGGATGGATGGCAGCACCCGGAAGATCATTGTGGACTCGGACATTTACTGGCC 660
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Db        601 GCGGGCAGGGATGGATGGCAGCACCCGGAAGATCATTGTGGACTCGGACATTTACTGGCC 660

Qy        661 CAATGGACTGACCATCGACCTGGAGGAGCAGAAGCTCTACTGGGCTGACGCCAAGCTCAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAATGGACTGACCATCGACCTGGAGGAGCAGAAGCTCTACTGGGCTGACGCCAAGCTCAG 720

Qy        721 CTTCATCCACCGTGCCAACCTGGACGGCTCGTTCCGGCAGAAGGTGGTGGAGGGCAGCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        781 GACGCACCCCTTCGCCCTGACGCTCTCCGGGGACACTCTGTACTGGACAGACTGGCAGAC 840
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Qy        841 CCGCTCCATCCATGCCTGCAACAAGCGCACTGGGGGGAAGAGGAAGGAGATCCTGAGTGC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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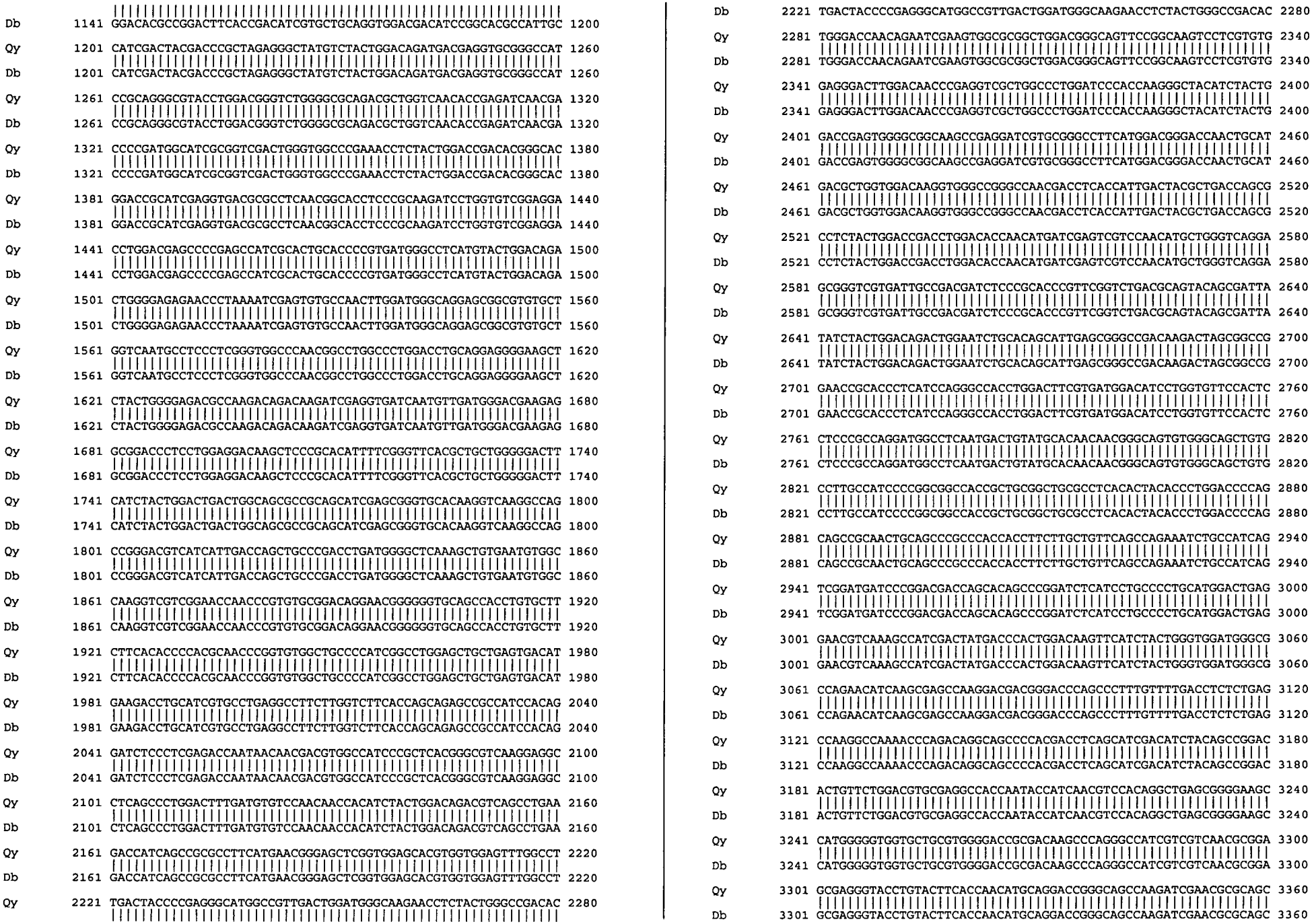
Qy        901 CCTCTACTCACCCATGGACATCCAGGTGCTGAGCCAGGAGCGGCAGCCTTTCTTCCACAC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CCTCTACTCACCCATGGACATCCAGGTGCTGAGCCAGGAGCGGCAGCCTTTCTTCCACAC 960

Qy        961 TCGCTGTGAGGAGGACAATGGCGGCTGCTCCCACCTGTGCCTGCTGTCCCCAAGCGAGCC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TCGCTGTGAGGAGGACAATGGCGGCTGCTCCCACCTGTGCCTGCTGTCCCCAAGCGAGCC 1020

Qy       1021 TTTCTACACATGCGCCTGCCCCACGGGTGTGCAGCTGCAGGACAACGGCAGGACGTGTAA 1080
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Db       1021 TTTCTACACATGCGCCTGCCCCACGGGTGTGCAGCTGCAGGACAACGGCAGGACGTGTAA 1080

Qy       1081 GGCAGGAGCCGAGGAGGTGCTGCTGCTGGCCCGGCGGACGGACCTACGGAGGATCTCGCT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 GGCAGGAGCCGAGGAGGTGCTGCTGCTGGCCCGGCGGACGGACCTACGGAGGATCTCGCT 1140

Qy       1141 GGACACGCCGGACTTCACCGACATCGTGCTGCAGGTGGACGACATCCGGCACGCCATTGC 1200
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Db 1141 GGACACGCCGGACTTCACCGACATCGTGCTGCAGGTGGACGACATCCGGCACGCCATTGC 1200
Qy 1201 CATCGACTACGACCCGCTAGAGGGCTATGTCTACTGGACAGATGACGAGGTGCGGGCCAT 1260
Db 1201 CATCGACTACGACCCGCTAGAGGGCTATGTCTACTGGACAGATGACGAGGTGCGGGCCAT 1260
Qy 1261 CCGCAGGGCGTACCTGGACGGGTCTGGGGCGCAGACGCTGGTCAACACCGAGATCAACGA 1320
Db 1261 CCGCAGGGCGTACCTGGACGGGTCTGGGGCGCAGACGCTGGTCAACACCGAGATCAACGA 1320
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Qy 2041 GATCTCCCTCGAGACCAATAACAACGACGTGGCCATCCCGCTCACGGGCGTCAAGGAGGC 2100
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Qy 2101 CTCAGCCCTGGACTTTGATGTGTCCAACAACCACATCTACTGGACAGACGTCAGCCTGAA 2160
Db 2101 CTCAGCCCTGGACTTTGATGTGTCCAACAACCACATCTACTGGACAGACGTCAGCCTGAA 2160
Qy 2161 GACCATCAGCCGCGCCTTCATGAACGGGAGCTCGGTGGAGCACGTGGTGGAGTTTGGCCT 2220
Db 2161 GACCATCAGCCGCGCCTTCATGAACGGGAGCTCGGTGGAGCACGTGGTGGAGTTTGGCCT 2220
Qy 2221 TGACTACCCCGAGGGCATGGCCGTTGACTGGATGGGCAAGAACCTCTACTGGGCCGACAC 2280
Db 2221 TGACTACCCCGAGGGCATGGCCGTTGACTGGATGGGCAAGAACCTCTACTGGGCCGACAC 2280
Qy 2281 TGGGACCAACAGAATCGAAGTGGCGCGGCTGGACGGGCAGTTCCGGCAAGTCCTCGTGTG 2340
Db 2281 TGGGACCAACAGAATCGAAGTGGCGCGGCTGGACGGGCAGTTCCGGCAAGTCCTCGTGTG 2340
Qy 2341 GAGGGACTTGGACAACCCGAGGTCGCTGGCCCTGGATCCCACCAAGGGCTACATCTACTG 2400
Db 2341 GAGGGACTTGGACAACCCGAGGTCGCTGGCCCTGGATCCCACCAAGGGCTACATCTACTG 2400
Qy 2401 GACCGAGTGGGGCGGCAAGCCGAGGATCGTGCGGGCCTTCATGGACGGGACCAACTGCAT 2460
Db 2401 GACCGAGTGGGGCGGCAAGCCGAGGATCGTGCGGGCCTTCATGGACGGGACCAACTGCAT 2460
Qy 2461 GACGCTGGTGGACAAGGTGGGCCGGGCCAACGACCTCACCATTGACTACGCTGACCAGCG 2520
Db 2461 GACGCTGGTGGACAAGGTGGGCCGGGCCAACGACCTCACCATTGACTACGCTGACCAGCG 2520
Qy 2521 CCTCTACTGGACCGACCTGGACACCAACATGATCGAGTCGTCCAACATGCTGGGTCAGGA 2580
Db 2521 CCTCTACTGGACCGACCTGGACACCAACATGATCGAGTCGTCCAACATGCTGGGTCAGGA 2580
Qy 2581 GCGGGTCGTGATTGCCGACGATCTCCCGCACCCGTTCGGTCTGACGCAGTACAGCGATTA 2640
Db 2581 GCGGGTCGTGATTGCCGACGATCTCCCGCACCCGTTCGGTCTGACGCAGTACAGCGATTA 2640
Qy 2641 TATCTACTGGACAGACTGGAATCTGCACAGCATTGAGCGGGCCGACAAGACTAGCGGCCG 2700
Db 2641 TATCTACTGGACAGACTGGAATCTGCACAGCATTGAGCGGGCCGACAAGACTAGCGGCCG 2700
Qy 2701 GAACCGCACCCTCATCCAGGGCCACCTGGACTTCGTGATGGACATCCTGGTGTTCCACTC 2760
Db 2701 GAACCGCACCCTCATCCAGGGCCACCTGGACTTCGTGATGGACATCCTGGTGTTCCACTC 2760
Qy 2761 CTCCCGCCAGGATGGCCTCAATGACTGTATGCACAACAACGGGCAGTGTGGGCAGCTGTG 2820
Db 2761 CTCCCGCCAGGATGGCCTCAATGACTGTATGCACAACAACGGGCAGTGTGGGCAGCTGTG 2820
Qy 2821 CCTTGCCATCCCCGGCGGCCACCGCTGCGGCTGCGCCTCACACTACACCCTGGACCCCAG 2880
Db 2821 CCTTGCCATCCCCGGCGGCCACCGCTGCGGCTGCGCCTCACACTACACCCTGGACCCCAG 2880
Qy 2881 CAGCCGCAACTGCAGCCCGCCCACCACCTTCTTGCTGTTCAGCCAGAAATCTGCCATCAG 2940
Db 2881 CAGCCGCAACTGCAGCCCGCCCACCACCTTCTTGCTGTTCAGCCAGAAATCTGCCATCAG 2940
Qy 2941 TCGGATGATCCCCGGACGACCAGCACAGCCCGGATCTCATCCTGCCCCTGCATGGACTGAG 3000
Db 2941 TCGGATGATCCCCGGACGACCAGCACAGCCCGGATCTCATCCTGCCCCTGCATGGACTGAG 3000
Qy 3001 GAACGTCAAAGCCATCGACTATGACCCACTGGACAAGTTCATCTACTGGGTGGATGGGCG 3060
Db 3001 GAACGTCAAAGCCATCGACTATGACCCACTGGACAAGTTCATCTACTGGGTGGATGGGCG 3060
Qy 3061 CCAGAACATCAAGCGAGCCAAGGACGACGGGACCCAGCCCTTTGTTTTGACCTCTCTGAG 3120
Db 3061 CCAGAACATCAAGCGAGCCAAGGACGACGGGACCCAGCCCTTTGTTTTGACCTCTCTGAG 3120
Qy 3121 CCAAGGCCAAAACCCAGACAGGCAGCCCCACGACCTCAGCATCGACATCTACAGCCGGAC 3180
Db 3121 CCAAGGCCAAAACCCAGACAGGCAGCCCCACGACCTCAGCATCGACATCTACAGCCGGAC 3180
Qy 3181 ACTGTTCTGGACGTGCGAGGCCACCAATACCATCAACGTCCACAGGCTGAGCGGGGAAGC 3240
Db 3181 ACTGTTCTGGACGTGCGAGGCCACCAATACCATCAACGTCCACAGGCTGAGCGGGGAAGC 3240
Qy 3241 CATGGGGGTGGTGCTGCGTGGGGACCGCGACAAGCCCAGGGCCATCGTCGTCAACGCGGA 3300
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Qy 3301 GCGAGGGTACCTGTACTTCACCAACATGCAGGACCGGGCAGCCAAGATCGAACGCGCAGC 3360
Db 3301 GCGAGGGTACCTGTACTTCACCAACATGCAGGACCGGGCAGCCAAGATCGAACGCGCAGC 3360

```
Qy       3361 CCTGGACGGCACCGAGCGCGAGGTCCTCTTCACCACCGGCCTCATCCGCCCTGTGGCCCT 3420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3361 CCTGGACGGCACCGAGCGCGAGGTCCTCTTCACCACCGGCCTCATCCGCCCTGTGGCCCT 3420

Qy       3421 GGTGGTGGACAACACACTGGGCAAGCTGTTCTGGGTGGACGCGGACCTGAAGCGCATTGA 3480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3421 GGTGGTGGACAACACACTGGGCAAGCTGTTCTGGGTGGACGCGGACCTGAAGCGCATTGA 3480

Qy       3481 GAGCTGTGACCTGTCAGGGGCCAACCGCCTGACCCTGGAGGACGCCAACATCGTGCAGCC 3540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3481 GAGCTGTGACCTGTCAGGGGCCAACCGCCTGACCCTGGAGGACGCCAACATCGTGCAGCC 3540

Qy       3541 TCTGGGCCTGACCATCCTTGGCAAGCATCTCTACTGGATCGACCGCCAGCAGCAGATGAT 3600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3541 TCTGGGCCTGACCATCCTTGGCAAGCATCTCTACTGGATCGACCGCCAGCAGCAGATGAT 3600

Qy       3601 CGAGCGTGTGGAGAAGACCACCGGGGACAAGCGGACTCGCATCCAGGGCCGTGTCGCCCA 3660
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Db       3601 CGAGCGTGTGGAGAAGACCACCGGGGACAAGCGGACTCGCATCCAGGGCCGTGTCGCCCA 3660

Qy       3661 CCTCACTGGCATCCATGCAGTGGAGGAAGTCAGCCTGGAGGAGTTCTCAGCCCACCCATG 3720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3661 CCTCACTGGCATCCATGCAGTGGAGGAAGTCAGCCTGGAGGAGTTCTCAGCCCACCCATG 3720

Qy       3721 TGCCCGTGACAATGGTGGCTGCTCCCACATCTGTATTGCCAAGGGTGATGGGACACCACG 3780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3721 TGCCCGTGACAATGGTGGCTGCTCCCACATCTGTATTGCCAAGGGTGATGGGACACCACG 3780

Qy       3781 GTGCTCATGCCCAGTCCACCTCGTGCTCCTGCAGAACCTGCTGACCTGTGGAGAGCCGCC 3840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3781 GTGCTCATGCCCAGTCCACCTCGTGCTCCTGCAGAACCTGCTGACCTGTGGAGAGCCGCC 3840

Qy       3841 CACCTGCTCCCCGGACCAGTTTGCATGTGCCACAGGGGAGATCGACTGTATCCCCGGGGC 3900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3841 CACCTGCTCCCCGGACCAGTTTGCATGTGCCACAGGGGAGATCGACTGTATCCCCGGGGC 3900

Qy       3901 CTGGCGCTGTGACGGCTTTCCCGAGTGCGATGACCAGAGCGACGAGGAGGGCTGCCCCGT 3960
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Db       3901 CTGGCGCTGTGACGGCTTTCCCGAGTGCGATGACCAGAGCGACGAGGAGGGCTGCCCCGT 3960

Qy       3961 GTGCTCCGCCGCCCAGTTCCCCTGCGCGCGGGGTCAGTGTGTGGACCTGCGCCTGCGCTG 4020
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Db       3961 GTGCTCCGCCGCCCAGTTCCCCTGCGCGCGGGGTCAGTGTGTGGACCTGCGCCTGCGCTG 4020

Qy       4021 CGACGGCGAGGCAGACTGTCAGGACCGCTCAGACGAGGTGGACTGTGACGCCATCTGCCT 4080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4021 CGACGGCGAGGCAGACTGTCAGGACCGCTCAGACGAGGTGGACTGTGACGCCATCTGCCT 4080

Qy       4081 GCCCAACCAGTTCCGGTGTGCGAGCGGCCAGTGTGTCCTCATCAAACAGCAGTGCGACTC 4140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4081 GCCCAACCAGTTCCGGTGTGCGAGCGGCCAGTGTGTCCTCATCAAACAGCAGTGCGACTC 4140

Qy       4141 CTTCCCCGACTGTATCGACGGCTCCGACGAGCTCATGTGTGAAATCACCAAGCCGCCCTC 4200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4141 CTTCCCCGACTGTATCGACGGCTCCGACGAGCTCATGTGTGAAATCACCAAGCCGCCCTC 4200

Qy       4201 AGACGACAGCCCGGCCCACAGCAGTGCCATCGGGCCCGTCATTGGCATCATCCTCTCTCT 4260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4201 AGACGACAGCCCGGCCCACAGCAGTGCCATCGGGCCCGTCATTGGCATCATCCTCTCTCT 4260

Qy       4261 CTTCGTCATGGGTGGTGTCTATTTTGTGTGCCAGCGCGTGGTGTGCCAGCGCTATGCGGG 4320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4261 CTTCGTCATGGGTGGTGTCTATTTTGTGTGCCAGCGCGTGGTGTGCCAGCGCTATGCGGG 4320

Qy       4321 GGCCAACGGGCCCTTCCCGCACGAGTATGTCAGCGGGACCCCGCACGTGCCCCTCAATTT 4380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4321 GGCCAACGGGCCCTTCCCGCACGAGTATGTCAGCGGGACCCCGCACGTGCCCCTCAATTT 4380

Qy       4381 CATAGCCCCGGGCGGTTCCCAGCATGGCCCCTTCACAGGCATCGCATGCGGAAAGTCCAT 4440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4381 CATAGCCCCGGGCGGTTCCCAGCATGGCCCCTTCACAGGCATCGCATGCGGAAAGTCCAT 4440

Qy       4441 GATGAGCTCCGTGAGCCTGATGGGGGGCCGGGGCGGGGTGCCCCCTCTACGACCGGAACCA 4500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4441 GATGAGCTCCGTGAGCCTGATGGGGGGCCGGGGCGGGGTGCCCCCTCTACGACCGGAACCA 4500

Qy       4501 CGTCACAGGGGCCTCGTCCAGCAGCTCGTCCAGCACGAAGGCCACGCTGTACCCGCCGAT 4560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4501 CGTCACAGGGGCCTCGTCCAGCAGCTCGTCCAGCACGAAGGCCACGCTGTACCCGCCGAT 4560

Qy       4561 CCTGAACCCGCCGCCCTCCCCGGCCACGGACCCCTCCCTGTACAACATGGACATGTTCTA 4620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4561 CCTGAACCCGCCGCCCTCCCCGGCCACGGACCCCTCCCTGTACAACATGGACATGTTCTA 4620

Qy       4621 CTCTTCAAACATTCCGGCCACTGCGAGACCGTACAGGCCCTACATCATTCGAGGAATGGC 4680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4621 CTCTTCAAACATTCCGGCCACTGCGAGACCGTACAGGCCCTACATCATTCGAGGAATGGC 4680

Qy       4681 GCCCCCGACGACGCCCTGCAGCACCGACGTGTGTGACAGCGACTACAGCGCCAGCCGCTG 4740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4681 GCCCCCGACGACGCCCTGCAGCACCGACGTGTGTGACAGCGACTACAGCGCCAGCCGCTG 4740

Qy       4741 GAAGGCCAGCAAGTACTACCTGGATTTGAACTCGGACTCAGACCCCTATCCACCCCCACC 4800
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4741 GAAGGCCAGCAAGTACTACCTGGATTTGAACTCGGACTCAGACCCCTATCCACCCCCACC 4800

Qy       4801 CACGCCCCACAGCCAGTACCTGTCGGCGGAGGACAGCTGCCCGCCCTCGCCCGCCACCGA 4860
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4801 CACGCCCCACAGCCAGTACCTGTCGGCGGAGGACAGCTGCCCGCCCTCGCCCGCCACCGA 4860

Qy       4861 GAGGAGCTACTTCCATCTCTTCCCGCCCCCTCCGTCCCCCTGCACGGACTCATCCTGACC 4920
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4861 GAGGAGCTACTTCCATCTCTTCCCGCCCCCTCCGTCCCCCTGCACGGACTCATCCTGACC 4920

Qy       4921 TCGGCCGGGCCACTCTGGCTTCTCTGTGCCCCTGTAAATAGTTTTAAATATGAACAAAGA 4980
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4921 TCGGCCGGGCCACTCTGGCTTCTCTGTGCCCCTGTAAATAGTTTTAAATATGAACAAAGA 4980

Qy       4981 AAAAAATATATTTTATGATTTAAAAAATAAATATAATTGGGATTTTAAAAACATGAGAAA 5040
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4981 AAAAAATATATTTTATGATTTAAAAAATAAATATAATTGGGATTTTAAAAACATGAGAAA 5040

Qy       5041 TGTGAACTGTGATGGGGTGGGCAGGGCTGGGAGAACTTTGTACAGTGGAGAAATATTTAT 5100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5041 TGTGAACTGTGATGGGGTGGGCAGGGCTGGGAGAACTTTGTACAGTGGAGAAATATTTAT 5100

Qy       5101 AAACTTAATTTTGTAAAACA 5120
             ||||||||||||||||||||
Db       5101 AAACTTAATTTTGTAAAACA 5120
```

RESULT 6
ABA82617
ID ABA82617 standard; DNA; 5120 BP.
XX
AC ABA82617;
XX
DT 25-JAN-2002 (first entry)
XX
DE Human Zmax1 gene SEQ ID NO:1.
XX
KW Human; high bone mass; HBM gene; Zmax1 gene; chromosome 11; 11q13.3;
KW sequence tagged site; STS; osteoporosis; osteopathic; gene therapy;
KW antisense therapy; vaccine; bone disorder; Paget's disease; sclerostosis;
KW osteomalacia; fibrous dysplasia; ds.
XX
OS Homo sapiens.
XX
PN WO200177327-A1.
XX
PD 18-OCT-2001.
XX
PF 21-JUN-2000; 2000WO-US016951.
XX
PR 05-APR-2000; 2000US-00543771.

PR 05-APR-2000; 2000US-00544398.
XX
PA (GENO-) GENOME THERAPEUTICS CORP.
XX
PI Carulli JP, Little RD, Recker RR, Johnson ML;
XX
DR WPI; 2001-657171/75.
DR P-PSDB; AAG68169.
XX
PT New high bone mass (HBM) and Zmax1 genes and proteins useful for
PT modulating bone mass for the treatment of e.g. osteoporosis.
XX
PS Claim 22; Page 159-171; 443pp; English.
XX
CC The present invention describes the human Zmax1 gene and the high bone
CC mass (HBM) gene,which are found on chromosome 11q13.3. The Zmax1 and HBM
CC genes have osteopathic activities. The genes can be used in gene therapy,
CC antisense therapy and in the production of vaccines. They can be used in
CC the diagnosis and treatment of bone disorders including osteoporosis,
CC Paget's disease, sclerostosis, osteomalacia and fibrous dysplasia.
CC ABA82038 to ABA82700 and AAG68168 to AAG68193 represent sequences used in
CC the exemplification of the present invention
XX
SQ Sequence 5120 BP; 1037 A; 1657 C; 1549 G; 877 T; 0 U; 0 Other;

Query Match 100.0%; Score 5118.4; DB 5; Length 5120;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5119; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 ACTAAAGCGCCGCCGCCGCGCCATGGAGCCCGAGTGAGCGCGGCGCGGGCCCGTCCGGCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ACTAAAGCGCCGCCGCCGCGCCATGGAGCCCGAGTGAGCGCGGCGCGGGCCCGTCCGGCC 60

Qy         61 GCCGGACAACATGGAGGCAGCGCCGCCCGGGCCGCCGTGGCCGCTGCTGCTGCTGCTGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCCGGACAACATGGAGGCAGCGCCGCCCGGGCCGCCGTGGCCGCTGCTGCTGCTGCTGCT 120

Qy        121 GCTGCTGCTGGCGCTGTGCGGCTGCCCGGCCCCCGCCGCGGCCTCGCCGCTCCTGCTATT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCTGCTGCTGGCGCTGTGCGGCTGCCCGGCCCCCGCCGCGGCCTCGCCGCTCCTGCTATT 180

Qy        181 TGCCAACCGCCGGGACGTACGGCTGGTGGACGCCGGCGGAGTCAAGCTGGAGTCCACCAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TGCCAACCGCCGGGACGTACGGCTGGTGGACGCCGGCGGAGTCAAGCTGGAGTCCACCAT 240

Qy        241 CGTGGTCAGCGGCCTGGAGGATGCGGCCGCAGTGGACTTCCAGTTTTCCAAGGGAGCCGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CGTGGTCAGCGGCCTGGAGGATGCGGCCGCAGTGGACTTCCAGTTTTCCAAGGGAGCCGT 300

Qy        301 GTACTGGACAGACGTGAGCGAGGAGGCCATCAAGCAGACCTACCTGAACCAGACGGGGGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GTACTGGACAGACGTGAGCGAGGAGGCCATCAAGCAGACCTACCTGAACCAGACGGGGGC 360

Qy        361 CGCCGTGCAGAACGTGGTCATCTCCGGCCTGGTCTCTCCCGACGGCCTCGCCTGCGACTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CGCCGTGCAGAACGTGGTCATCTCCGGCCTGGTCTCTCCCGACGGCCTCGCCTGCGACTG 420

Qy        421 GGTGGGCAAGAAGCTGTACTGGACGGACTCAGAGACCAACCGCATCGAGGTGGCCAACCT 480
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Db        421 GGTGGGCAAGAAGCTGTACTGGACGGACTCAGAGACCAACCGCATCGAGGTGGCCAACCT 480

Qy        481 CAATGGCACATCCCGGAAGGTGCTCTTCTGGCAGGACCTTGACCAGCCGAGGGCCATCGC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CAATGGCACATCCCGGAAGGTGCTCTTCTGGCAGGACCTTGACCAGCCGAGGGCCATCGC 540

Qy        541 CTTGGACCCCGCTCACGGGTACATGTACTGGACAGACTGGGTTGAGACGCCCCGGATTGA 600
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db        541 CTTGGACCCCGCTCACGGGTACATGTACTGGACAGACTGGGGTGAGACGCCCCGGATTGA 600

Qy        601 GCGGGCAGGGATGGATGGCAGCACCCGGAAGATCATTGTGGACTCGGACATTTACTGGCC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GCGGGCAGGGATGGATGGCAGCACCCGGAAGATCATTGTGGACTCGGACATTTACTGGCC 660

Qy        661 CAATGGACTGACCATCGACCTGGAGGAGCAGAAGCTCTACTGGGCTGACGCCAAGCTCAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAATGGACTGACCATCGACCTGGAGGAGCAGAAGCTCTACTGGGCTGACGCCAAGCTCAG 720

Qy        721 CTTCATCCACCGTGCCAACCTGGACGGCTCGTTCCGGCAGAAGGTGGTGGAGGGCAGCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CTTCATCCACCGTGCCAACCTGGACGGCTCGTTCCGGCAGAAGGTGGTGGAGGGCAGCCT 780

Qy        781 GACGCACCCCTTCGCCCTGACGCTCTCCGGGGACACTCTGTACTGGACAGACTGGCAGAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACGCACCCCTTCGCCCTGACGCTCTCCGGGGACACTCTGTACTGGACAGACTGGCAGAC 840

Qy        841 CCGCTCCATCCATGCCTGCAACAAGCGCACTGGGGGGAAGAGGAAGGAGATCCTGAGTGC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CCGCTCCATCCATGCCTGCAACAAGCGCACTGGGGGGAAGAGGAAGGAGATCCTGAGTGC 900

Qy        901 CCTCTACTCACCCATGGACATCCAGGTGCTGAGCCAGGAGCGGCAGCCTTTCTTCCACAC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CCTCTACTCACCCATGGACATCCAGGTGCTGAGCCAGGAGCGGCAGCCTTTCTTCCACAC 960

Qy        961 TCGCTGTGAGGAGGACAATGGCGGCTGCTCCCACCTGTGCCTGCTGTCCCCAAGCGAGCC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TCGCTGTGAGGAGGACAATGGCGGCTGCTCCCACCTGTGCCTGCTGTCCCCAAGCGAGCC 1020

Qy       1021 TTTCTACACATGCGCCTGCCCCACGGGTGTGCAGCTGCAGGACAACGGCAGGACGTGTAA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 TTTCTACACATGCGCCTGCCCCACGGGTGTGCAGCTGCAGGACAACGGCAGGACGTGTAA 1080

Qy       1081 GGCAGGAGCCGAGGAGGTGCTGCTGCTGGCCCGGCGGACGGACCTACGGAGGATCTCGCT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 GGCAGGAGCCGAGGAGGTGCTGCTGCTGGCCCGGCGGACGGACCTACGGAGGATCTCGCT 1140

Qy       1141 GGACACGCCGGACTTCACCGACATCGTGCTGCAGGTGGACGACATCCGGCACGCCATTGC 1200
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Db       1141 GGACACGCCGGACTTCACCGACATCGTGCTGCAGGTGGACGACATCCGGCACGCCATTGC 1200

Qy       1201 CATCGACTACGACCCGCTAGAGGGCTATGTCTACTGGACAGATGACGAGGTGCGGGCCAT 1260
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Db       1201 CATCGACTACGACCCGCTAGAGGGCTATGTCTACTGGACAGATGACGAGGTGCGGGCCAT 1260

Qy       1261 CCGCAGGGCGTACCTGGACGGGTCTGGGGCGCAGACGCTGGTCAACACCGAGATCAACGA 1320
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Qy       1321 CCCCGATGGCATCGCGGTCGACTGGGTGGCCCGAAACCTCTACTGGACCGACACGGGCAC 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       1381 GGACCGCATCGAGGTGACGCGCCTCAACGGCACCTCCCGCAAGATCCTGGTGTCGGAGGA 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 GGACCGCATCGAGGTGACGCGCCTCAACGGCACCTCCCGCAAGATCCTGGTGTCGGAGGA 1440

Qy       1441 CCTGGACGAGCCCCGAGCCATCGCACTGCACCCCGTGATGGGCCTCATGTACTGGACAGA 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 CCTGGACGAGCCCCGAGCCATCGCACTGCACCCCGTGATGGGCCTCATGTACTGGACAGA 1500

Qy       1501 CTGGGGAGAGAACCCTAAAATCGAGTGTGCCAACTTGGATGGGCAGGAGCGGCGTGTGCT 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 CTGGGGAGAGAACCCTAAAATCGAGTGTGCCAACTTGGATGGGCAGGAGCGGCGTGTGCT 1560

Qy       1561 GGTCAATGCCTCCCTCGGGTGGCCCAACGGCCTGGCCCTGGACCTGCAGGAGGGGAAGCT 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 GGTCAATGCCTCCCTCGGGTGGCCCAACGGCCTGGCCCTGGACCTGCAGGAGGGGAAGCT 1620

Qy       1621 CTACTGGGGAGACGCCAAGACAGACAAGATCGAGGTGATCAATGTTGATGGGACGAAGAG 1680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 CTACTGGGGAGACGCCAAGACAGACAAGATCGAGGTGATCAATGTTGATGGGACGAAGAG 1680

Qy       1681 GCGGACCCTCCTGGAGGACAAGCTCCCGCACATTTTCGGGTTCACGCTGCTGGGGGACTT 1740
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Qy       1741 CATCTACTGGACTGACTGGCAGCGCCGCAGCATCGAGCGGGTGCACAAGGTCAAGGCCAG 1800
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Db      1861 CAAGGTCGTCGGAACCAACCCGTGTGCGGACAGGAACGGGGGGTGCAGCCACCTGTGCTT 1920

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Db      1981 GAAGACCTGCATCGTGCCTGAGGCCTTCTTGGTCTTCACCAGCAGAGCCGCCATCCACAG 2040

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Qy      2221 TGACTACCCCGAGGGCATGGCCGTTGACTGGATGGGCAAGAACCTCTACTGGGCCGACAC 2280
Db      2221 TGACTACCCCGAGGGCATGGCCGTTGACTGGATGGGCAAGAACCTCTACTGGGCCGACAC 2280

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Db      2521 CCTCTACTGGACCGACCTGGACACCAACATGATCGAGTCGTCCAACATGCTGGGTCAGGA 2580

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Qy      2941 TCGGATGATCCCGGACGACCAGCACAGCCCGGATCTCATCCTGCCCCTGCATGGACTGAG 3000
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Qy      3781 GTGCTCATGCCCAGTCCACCTCGTGCTCCTGCAGAACCTGCTGACCTGTGGAGAGCCGCC 3840
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Qy      3901 CTGGCGCTGTGACGGCTTTCCCGAGTGCGATGACCAGAGCGACGAGGAGGGCTGCCCCGT 3960
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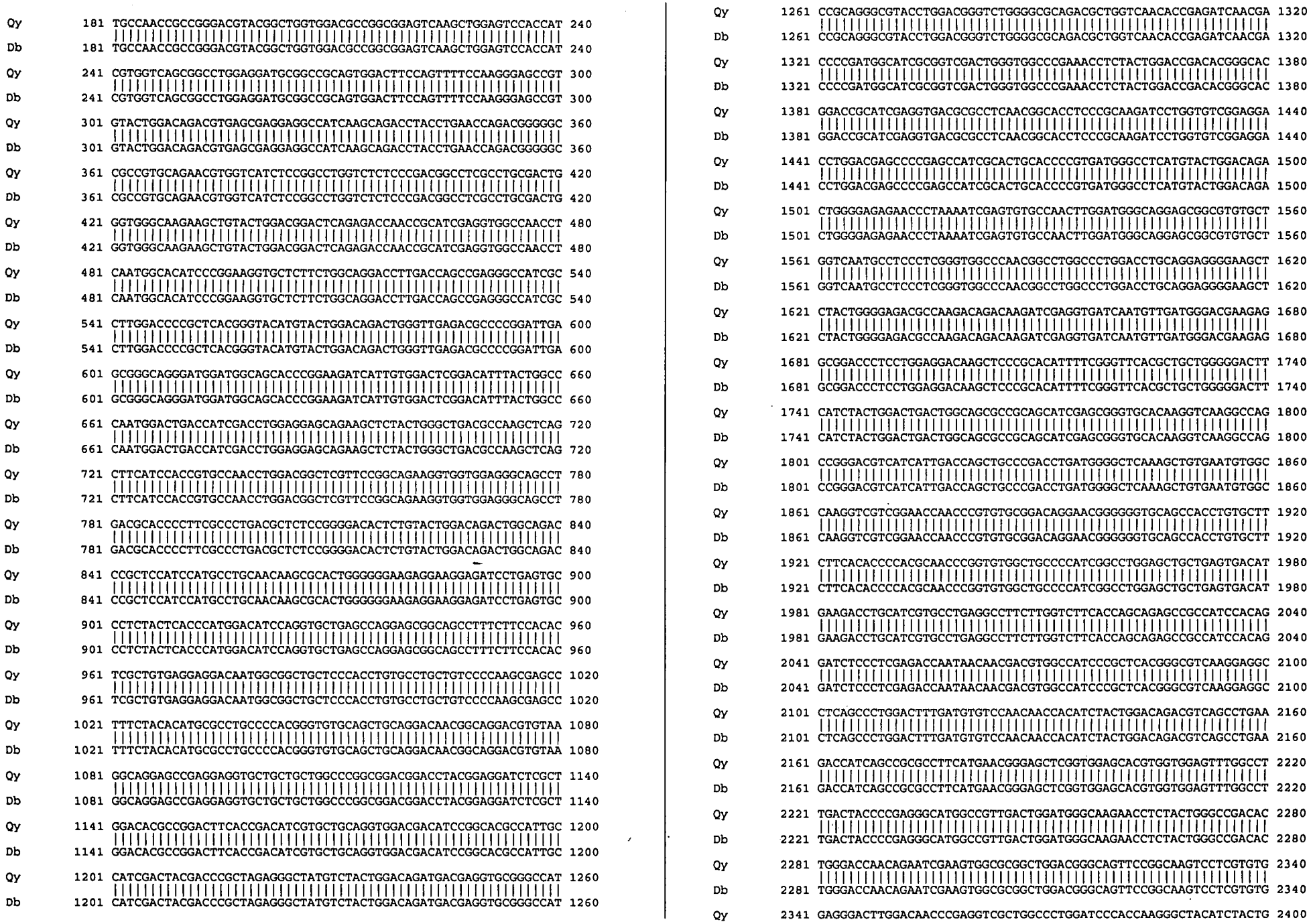
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XX
AC ABA82618;
XX
DT 25-JAN-2002 (first entry)
XX
DE Human HBM gene SEQ ID NO:2.
XX
KW Human; high bone mass; HBM gene; Zmax1 gene; chromosome 11; 11q13.3;
KW sequence tagged site; STS; osteoporosis; osteopathic; gene therapy;
KW antisense therapy; vaccine; bone disorder; Paget's disease; sclerostosis;
KW osteomalacia; fibrous dysplasia; ds.
XX
OS Homo sapiens.
XX
PN WO200177327-A1.
XX
PD 18-OCT-2001.
XX
PF 21-JUN-2000; 2000WO-US016951.
XX
PR 05-APR-2000; 2000US-00543771.
PR 05-APR-2000; 2000US-00544398.
XX
PA (GENO-) GENOME THERAPEUTICS CORP.
XX
PI Carulli JP, Little RD, Recker RR, Johnson ML;
XX
DR WPI; 2001-657171/75.
DR P-PSDB; AAG68170.
XX
PT New high bone mass (HBM) and Zmax1 genes and proteins useful for
PT modulating bone mass for the treatment of e.g. osteoporosis.
XX
PS Claim 1; Page 171-183; 443pp; English.
XX
CC The present invention describes the human Zmax1 gene and the high bone
CC mass (HBM) gene,which are found on chromosome 11q13.3. The Zmax1 and HBM
CC genes have osteopathic activities. The genes can be used in gene therapy,
CC antisense therapy and in the production of vaccines. They can be used in
CC the diagnosis and treatment of bone disorders including osteoporosis,
CC Paget's disease, sclerostosis, osteomalacia and fibrous dysplasia.
CC ABA82038 to ABA82700 and AAG68168 to AAG68193 represent sequences used in
CC the exemplification of the present invention
XX
SQ Sequence 5120 BP; 1037 A; 1657 C; 1547 G; 879 T; 0 U; 0 Other;

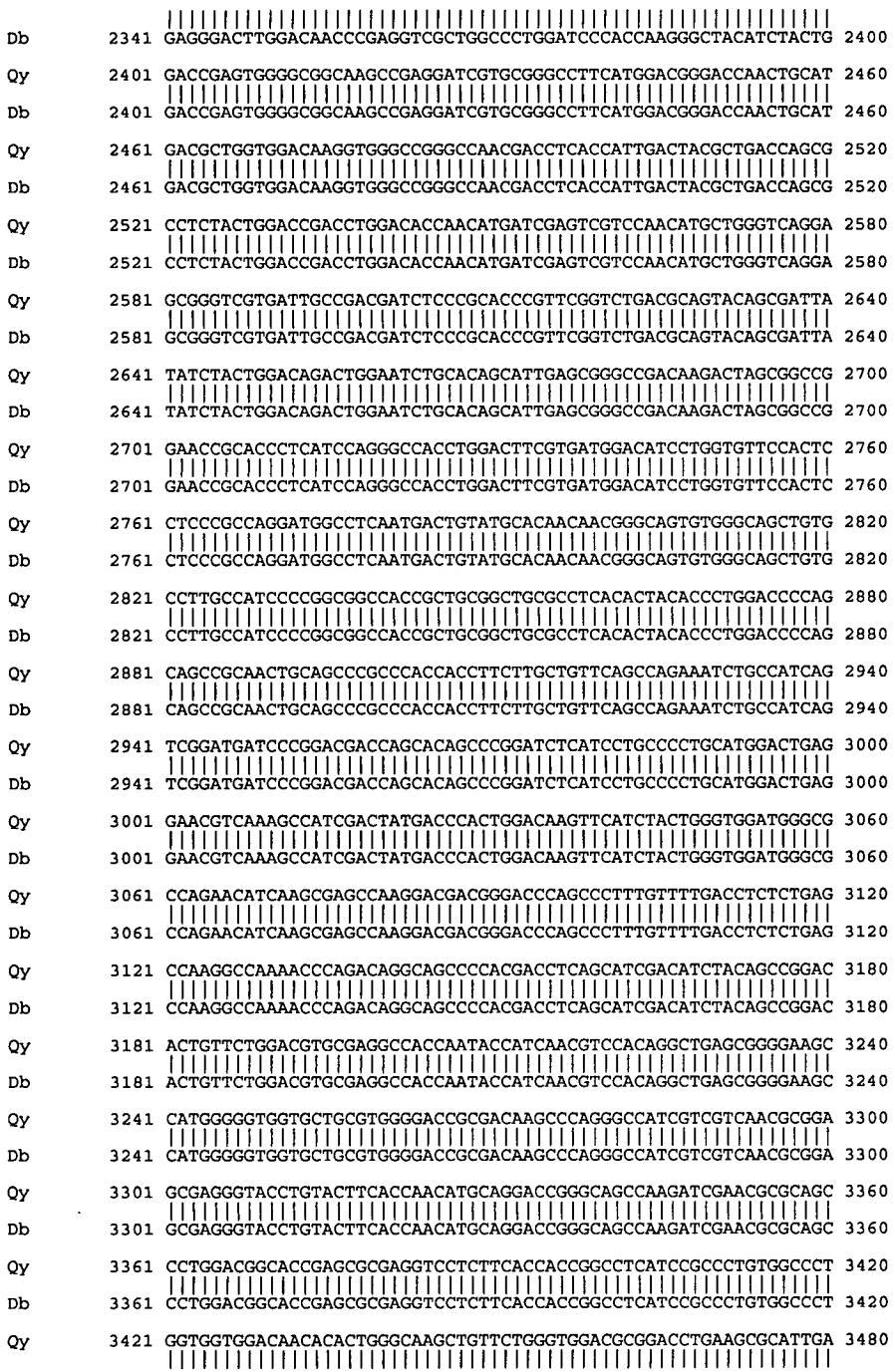
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Qy 1981 GAAGACCTGCATCGTGCCTGAGGCCTTCTTGGTCTTCACCAGCAGAGCCGCCATCCACAG 2040
Db 1981 GAAGACCTGCATCGTGCCTGAGGCCTTCTTGGTCTTCACCAGCAGAGCCGCCATCCACAG 2040
Qy 2041 GATCTCCCTCGAGACCAATAACAACGACGTGGCCATCCCGCTCACGGGCGTCAAGGAGGC 2100
Db 2041 GATCTCCCTCGAGACCAATAACAACGACGTGGCCATCCCGCTCACGGGCGTCAAGGAGGC 2100
Qy 2101 CTCAGCCCTGGACTTTGATGTGTCCAACAACCACATCTACTGGACAGACGTCAGCCTGAA 2160
Db 2101 CTCAGCCCTGGACTTTGATGTGTCCAACAACCACATCTACTGGACAGACGTCAGCCTGAA 2160
Qy 2161 GACCATCAGCCGCGCCTTCATGAACGGGAGCTCGGTGGAGCACGTGGTGGAGTTTGGCCT 2220
Db 2161 GACCATCAGCCGCGCCTTCATGAACGGGAGCTCGGTGGAGCACGTGGTGGAGTTTGGCCT 2220
Qy 2221 TGACTACCCCGAGGGCATGGCCGTTGACTGGATGGGCAAGAACCTCTACTGGGCCGACAC 2280
Db 2221 TGACTACCCCGAGGGCATGGCCGTTGACTGGATGGGCAAGAACCTCTACTGGGCCGACAC 2280
Qy 2281 TGGGACCAACAGAATCGAAGTGGCGCGGCTGGACGGGCAGTTCCGGCAAGTCCTCGTGTG 2340
Db 2281 TGGGACCAACAGAATCGAAGTGGCGCGGCTGGACGGGCAGTTCCGGCAAGTCCTCGTGTG 2340
Qy 2341 GAGGGACTTGGACAACCCGAGGTCGCTGGCCCTGGATCCCACCAAGGGCTACATCTACTG 2400


Db 2341 GAGGGACTTGGACAACCCGAGGTCGCTGGCCCTGGATCCCACCAAGGGCTACATCTACTG 2400
Qy 2401 GACCGAGTGGGGCGGCAAGCCGAGGATCGTGCGGGCCTTCATGGACGGGACCAACTGCAT 2460
Db 2401 GACCGAGTGGGGCGGCAAGCCGAGGATCGTGCGGGCCTTCATGGACGGGACCAACTGCAT 2460
Qy 2461 GACGCTGGTGGACAAGGTGGGCCGGGCCAACGACCTCACCATTGACTACGCTGACCAGCG 2520
Db 2461 GACGCTGGTGGACAAGGTGGGCCGGGCCAACGACCTCACCATTGACTACGCTGACCAGCG 2520
Qy 2521 CCTCTACTGGACCGACCTGGACACCAACATGATCGAGTCGTCCAACATGCTGGGTCAGGA 2580
Db 2521 CCTCTACTGGACCGACCTGGACACCAACATGATCGAGTCGTCCAACATGCTGGGTCAGGA 2580
Qy 2581 GCGGGTCGTGATTGCCGACGATCTCCCGCACCCGTTCGGTCTGACGCAGTACAGCGATTA 2640
Db 2581 GCGGGTCGTGATTGCCGACGATCTCCCGCACCCGTTCGGTCTGACGCAGTACAGCGATTA 2640
Qy 2641 TATCTACTGGACAGACTGGAATCTGCACAGCATTGAGCGGGCCGACAAGACTAGCGGCCG 2700
Db 2641 TATCTACTGGACAGACTGGAATCTGCACAGCATTGAGCGGGCCGACAAGACTAGCGGCCG 2700
Qy 2701 GAACCGCACCCTCATCCAGGGCCACCTGGACTTCGTGATGGACATCCTGGTGTTCCACTC 2760
Db 2701 GAACCGCACCCTCATCCAGGGCCACCTGGACTTCGTGATGGACATCCTGGTGTTCCACTC 2760
Qy 2761 CTCCCGCCAGGATGGCCTCAATGACTGTATGCACAACAACGGGCAGTGTGGGCAGCTGTG 2820
Db 2761 CTCCCGCCAGGATGGCCTCAATGACTGTATGCACAACAACGGGCAGTGTGGGCAGCTGTG 2820
Qy 2821 CCTTGCCATCCCCGGCGGCCACCGCTGCGGCTGCGCCTCACACTACACCCTGGACCCCAG 2880
Db 2821 CCTTGCCATCCCCGGCGGCCACCGCTGCGGCTGCGCCTCACACTACACCCTGGACCCCAG 2880
Qy 2881 CAGCCGCAACTGCAGCCCGCCCACCACCTTCTTGCTGTTCAGCCAGAAATCTGCCATCAG 2940
Db 2881 CAGCCGCAACTGCAGCCCGCCCACCACCTTCTTGCTGTTCAGCCAGAAATCTGCCATCAG 2940
Qy 2941 TCGGATGATCCCGGACGACCAGCACAGCCCGGATCTCATCCTGCCCCTGCATGGACTGAG 3000
Db 2941 TCGGATGATCCCGGACGACCAGCACAGCCCGGATCTCATCCTGCCCCTGCATGGACTGAG 3000
Qy 3001 GAACGTCAAAGCCATCGACTATGACCCACTGGACAAGTTCATCTACTGGGTGGATGGGCG 3060
Db 3001 GAACGTCAAAGCCATCGACTATGACCCACTGGACAAGTTCATCTACTGGGTGGATGGGCG 3060
Qy 3061 CCAGAACATCAAGCGAGCCAAGGACGACGGGACCCAGCCCTTTGTTTTGACCTCTCTGAG 3120
Db 3061 CCAGAACATCAAGCGAGCCAAGGACGACGGGACCCAGCCCTTTGTTTTGACCTCTCTGAG 3120
Qy 3121 CCAAGGCCAAAACCCAGACAGGCAGCCCCACGACCTCAGCATCGACATCTACAGCCGGAC 3180
Db 3121 CCAAGGCCAAAACCCAGACAGGCAGCCCCACGACCTCAGCATCGACATCTACAGCCGGAC 3180
Qy 3181 ACTGTTCTGGACGTGCGAGGCCACCAATACCATCAACGTCCACAGGCTGAGCGGGGAAGC 3240
Db 3181 ACTGTTCTGGACGTGCGAGGCCACCAATACCATCAACGTCCACAGGCTGAGCGGGGAAGC 3240
Qy 3241 CATGGGGGTGGTGCTGCGTGGGGACCGCGACAAGCCCAGGGCCATCGTCGTCAACGCGGA 3300
Db 3241 CATGGGGGTGGTGCTGCGTGGGGACCGCGACAAGCCCAGGGCCATCGTCGTCAACGCGGA 3300
Qy 3301 GCGAGGGTACCTGTACTTCACCAACATGCAGGACCGGGCAGCCAAGATCGAACGCGCAGC 3360
Db 3301 GCGAGGGTACCTGTACTTCACCAACATGCAGGACCGGGCAGCCAAGATCGAACGCGCAGC 3360
Qy 3361 CCTGGACGGCACCGAGCGCGAGGTCCTCTTCACCACCGGCCTCATCCGCCCTGTGGCCCT 3420
Db 3361 CCTGGACGGCACCGAGCGCGAGGTCCTCTTCACCACCGGCCTCATCCGCCCTGTGGCCCT 3420
Qy 3421 GGTGGTGGACAACACACTGGGCAAGCTGTTCTGGGTGGACGCGGACCTGAAGCGCATTGA 3480
Db 3421 GGTGGTGGACAACACACTGGGCAAGCTGTTCTGGGTGGACGCGGACCTGAAGCGCATTGA 3480
Qy 3481 GAGCTGTGACCTGTCAGGGGCCAACCGCCTGACCCTGGAGGACGCCAACATCGTGCAGCC 3540
Db 3481 GAGCTGTGACCTGTCAGGGGCCAACCGCCTGACCCTGGAGGACGCCAACATCGTGCAGCC 3540
Qy 3541 TCTGGGCCTGACCATCCTTGGCAAGCATCTCTACTGGATCGACCGCCAGCAGCAGATGAT 3600
Db 3541 TCTGGGCCTGACCATCCTTGGCAAGCATCTCTACTGGATCGACCGCCAGCAGCAGATGAT 3600
Qy 3601 CGAGCGTGTGGAGAAGACCACCGGGGACAAGCGGACTCGCATCCAGGGCCGTGTCGCCCA 3660
Db 3601 CGAGCGTGTGGAGAAGACCACCGGGGACAAGCGGACTCGCATCCAGGGCCGTGTCGCCCA 3660
Qy 3661 CCTCACTGGCATCCATGCAGTGGAGGAAGTCAGCCTGGAGGAGTTCTCAGCCCACCCATG 3720
Db 3661 CCTCACTGGCATCCATGCAGTGGAGGAAGTCAGCCTGGAGGAGTTCTCAGCCCACCCATG 3720
Qy 3721 TGCCCGTGACAATGGTGGCTGCTCCCACATCTGTATTGCCAAGGGTGATGGGACACCACG 3780
Db 3721 TGCCCGTGACAATGGTGGCTGCTCCCACATCTGTATTGCCAAGGGTGATGGGACACCACG 3780
Qy 3781 GTGCTCATGCCCAGTCCACCTCGTGCTCCTGCAGAACCTGCTGACCTGTGGAGAGCCGCC 3840
Db 3781 GTGCTCATGCCCAGTCCACCTCGTGCTCCTGCAGAACCTGCTGACCTGTGGAGAGCCGCC 3840
Qy 3841 CACCTGCTCCCCGGACCAGTTTGCATGTGCCACAGGGGAGATCGACTGTATCCCCGGGGC 3900
Db 3841 CACCTGCTCCCCGGACCAGTTTGCATGTGCCACAGGGGAGATCGACTGTATCCCCGGGGC 3900
Qy 3901 CTGGCGCTGTGACGGCTTTCCCGAGTGCGATGACCAGAGCGACGAGGAGGGCTGCCCCGT 3960
Db 3901 CTGGCGCTGTGACGGCTTTCCCGAGTGCGATGACCAGAGCGACGAGGAGGGCTGCCCCGT 3960
Qy 3961 GTGCTCCGCCGCCCAGTTCCCCTGCGCGCGGGGTCAGTGTGTGGACCTGCGCCTGCGCTG 4020
Db 3961 GTGCTCCGCCGCCCAGTTCCCCTGCGCGCGGGGTCAGTGTGTGGACCTGCGCCTGCGCTG 4020
Qy 4021 CGACGGCGAGGCAGACTGTCAGGACCGCTCAGACGAGGTGGACTGTGACGCCATCTGCCT 4080
Db 4021 CGACGGCGAGGCAGACTGTCAGGACCGCTCAGACGAGGTGGACTGTGACGCCATCTGCCT 4080
Qy 4081 GCCCAACCAGTTCCGGTGTGCGAGCGGCCAGTGTGTCCTCATCAAACAGCAGTGCGACTC 4140
Db 4081 GCCCAACCAGTTCCGGTGTGCGAGCGGCCAGTGTGTCCTCATCAAACAGCAGTGCGACTC 4140
Qy 4141 CTTCCCCGACTGTATCGACGGCTCCGACGAGCTCATGTGTGAAATCACCAAGCCGCCCTC 4200
Db 4141 CTTCCCCGACTGTATCGACGGCTCCGACGAGCTCATGTGTGAAATCACCAAGCCGCCCTC 4200
Qy 4201 AGACGACAGCCCGGCCCACAGCAGTGCCATCGGGCCCGTCATTGGCATCATCCTCTCTCT 4260
Db 4201 AGACGACAGCCCGGCCCACAGCAGTGCCATCGGGCCCGTCATTGGCATCATCCTCTCTCT 4260
Qy 4261 CTTCGTCATGGGTGGTGTCTATTTTGTGTGCCAGCGCGTGGTGTGCCAGCGCTATGCGGG 4320
Db 4261 CTTCGTCATGGGTGGTGTCTATTTTGTGTGCCAGCGCGTGGTGTGCCAGCGCTATGCGGG 4320
Qy 4321 GGCCAACGGGCCCTTCCCGCACGAGTATGTCAGCGGGACCCCGCACGTGCCCCTCAATTT 4380
Db 4321 GGCCAACGGGCCCTTCCCGCACGAGTATGTCAGCGGGACCCCGCACGTGCCCCTCAATTT 4380
Qy 4381 CATAGCCCCGGGCGGTTCCCAGCATGGCCCCTTCACAGGCATCGCATGCGGAAAGTCCAT 4440
Db 4381 CATAGCCCCGGGCGGTTCCCAGCATGGCCCCTTCACAGGCATCGCATGCGGAAAGTCCAT 4440
Qy 4441 GATGAGCTCCGTGAGCCTGATGGGGGGCCGGGGCGGGGTGCCCCTCTACGACCGGAACCA 4500
Db 4441 GATGAGCTCCGTGAGCCTGATGGGGGGCCGGGGCGGGGTGCCCCTCTACGACCGGAACCA 4500
Qy 4501 CGTCACAGGGGCCTCGTCCAGCAGCTCGTCCAGCACGAAGGCCACGCTGTACCCGCCGAT 4560
Db 4501 CGTCACAGGGGCCTCGTCCAGCAGCTCGTCCAGCACGAAGGCCACGCTGTACCCGCCGAT 4560

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Qy       4561 CCTGAACCCGCCGCCCTCCCCGGCCACGGACCCCTCCCTGTACAACATGGACATGTTCTA 4620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4561 CCTGAACCCGCCGCCCTCCCCGGCCACGGACCCCTCCCTGTACAACATGGACATGTTCTA 4620

Qy       4621 CTCTTCAAACATTCCGGCCACTGCGAGACCGTACAGGCCCTACATCATTCGAGGAATGGC 4680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4621 CTCTTCAAACATTCCGGCCACTGCGAGACCGTACAGGCCCTACATCATTCGAGGAATGGC 4680

Qy       4681 GCCCCCGACGACGCCCTGCAGCACCGACGTGTGTGACAGCGACTACAGCGCCAGCCGCTG 4740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4681 GCCCCCGACGACGCCCTGCAGCACCGACGTGTGTGACAGCGACTACAGCGCCAGCCGCTG 4740

Qy       4741 GAAGGCCAGCAAGTACTACCTGGATTTGAACTCGGACTCAGACCCCTATCCACCCCCACC 4800
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4741 GAAGGCCAGCAAGTACTACCTGGATTTGAACTCGGACTCAGACCCCTATCCACCCCCACC 4800

Qy       4801 CACGCCCCACAGCCAGTACCTGTCGGCGGAGGACAGCTGCCCGCCCTCGCCCGCCACCGA 4860
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4801 CACGCCCCACAGCCAGTACCTGTCGGCGGAGGACAGCTGCCCGCCCTCGCCCGCCACCGA 4860

Qy       4861 GAGGAGCTACTTCCATCTCTTCCCGCCCCCTCCGTCCCCCTGCACGGACTCATCCTGACC 4920
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4861 GAGGAGCTACTTCCATCTCTTCCCGCCCCCTCCGTCCCCCTGCACGGACTCATCCTGACC 4920

Qy       4921 TCGGCCGGGCCACTCTGGCTTCTCTGTGCCCCTGTAAATAGTTTTAAATATGAACAAAGA 4980
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4921 TCGGCCGGGCCACTCTGGCTTCTCTGTGCCCCTGTAAATAGTTTTAAATATGAACAAAGA 4980

Qy       4981 AAAAAATATATTTTATGATTTAAAAAATAAATATAATTGGGATTTTAAAAACATGAGAAA 5040
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4981 AAAAAATATATTTTATGATTTAAAAAATAAATATAATTGGGATTTTAAAAACATGAGAAA 5040

Qy       5041 TGTGAACTGTGATGGGGTGGGCAGGGCTGGGAGAACTTTGTACAGTGGAGAAATATTTAT 5100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5041 TGTGAACTGTGATGGGGTGGGCAGGGCTGGGAGAACTTTGTACAGTGGAGAAATATTTAT 5100

Qy       5101 AAACTTAATTTTGTAAAACA 5120
             ||||||||||||||||||||
Db       5101 AAACTTAATTTTGTAAAACA 5120
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RESULT 8
ACC45358
ID ACC45358 standard; DNA; 5120 BP.
XX
AC ACC45358;
XX
DT 02-JUN-2003 (first entry)
XX
DE Human wild-type LRP5 gene.
XX
KW Human; high bone mass; HBM; LRP5; LRP6; transgenic; bone mass modulation;
KW gene therapy; bone density modulation; bone strength; trabecular number;
KW bone size; bone tissue connectivity; bone disease; osteoporosis;
KW osteomalacia; rickets; Paget's disease; neoplasm of the bone; gene; ds.
XX
OS Homo sapiens.
XX
PN WO200292764-A2.
XX
PD 21-NOV-2002.
XX
PF 13-MAY-2002; 2002WO-US014876.
XX
PR 11-MAY-2001; 2001US-0290071P.
PR 17-MAY-2001; 2001US-0291311P.
PR 01-FEB-2002; 2002US-0353058P.
PR 04-MAR-2002; 2002US-0361293P.
XX
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (AMHP) WYETH.
XX
PI Babij P, Bex FJ, Yaworsky PJ, Bodine PV;
XX
DR WPI; 2003-129278/12.
DR P-PSDB; ABR41093.
XX
PT New transgenic animals (e.g. mice), useful as models for studying bone
PT density modulation, developing drugs for treating or preventing bone
PT diseases (e.g. osteoporosis), or diagnosing diseases characterized by
PT reduced bone density.
XX
PS Disclosure; Fig 6; 603pp; English.
XX
CC The invention relates to novel transgenic animals expressing the high
CC bone mass (HBM) gene, expressing the corresponding wild type HBM gene,
CC comprising an alteration of the gene encoding LRP5 or LRP6, or expressing
CC an LRP5 that is modulated by an altered gene control sequence introduced
CC by homologous or non-homologous recombination. The transgenic animals are
CC for the study of bone density modulation or bone mass modulation. The
CC invention has osteopathic and cytostatic activity. The polynucleotides of
CC the invention may have a use in gene therapy. The transgenic animals and
CC nucleic acids are for the study of bone density modulation, where the
CC bone mass is modulated relative to non-transgenic animals of the same
CC species in more than one parameter selected from bone density, bone
CC strength, trabecular number, bone size, or bone tissue connectivity. The
CC transgenic animals, nucleic acids and methods are useful for identifying
CC molecules involved in bone development, and for developing pharmaceutical
CC compositions, which may be employed for treating or preventing bone
CC diseases, e.g. osteoporosis, osteomalacia, rickets, Paget's disease, or
CC neoplasms of the bone. The transgenic animals and nucleic acids are also
CC useful in methods for diagnosing diseases involved in bone development,
CC or characterised by reduced bone density or mass. The present sequence is
CC used in the exemplification of the invention
XX
SQ Sequence 5120 BP; 1037 A; 1657 C; 1549 G; 877 T; 0 U; 0 Other;

Query Match 100.0%; Score 5118.4; DB 8; Length 5120;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5119; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 ACTAAAGCGCCGCCGCCGCGCCATGGAGCCCGAGTGAGCGCGGCGCGGGCCCGTCCGGCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ACTAAAGCGCCGCCGCCGCGCCATGGAGCCCGAGTGAGCGCGGCGCGGGCCCGTCCGGCC 60

Qy         61 GCCGGACAACATGGAGGCAGCGCCGCCCGGGCCGCCGTGGCCGCTGCTGCTGCTGCTGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCCGGACAACATGGAGGCAGCGCCGCCCGGGCCGCCGTGGCCGCTGCTGCTGCTGCTGCT 120

Qy        121 GCTGCTGCTGGCGCTGTGCGGCTGCCCGGCCCCCGCCGCGGCCTCGCCGCTCCTGCTATT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCTGCTGCTGGCGCTGTGCGGCTGCCCGGCCCCCGCCGCGGCCTCGCCGCTCCTGCTATT 180

Qy        181 TGCCAACCGCCGGGACGTACGGCTGGTGGACGCCGGCGGAGTCAAGCTGGAGTCCACCAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TGCCAACCGCCGGGACGTACGGCTGGTGGACGCCGGCGGAGTCAAGCTGGAGTCCACCAT 240

Qy        241 CGTGGTCAGCGGCCTGGAGGATGCGGCCGCAGTGGACTTCCAGTTTTCCAAGGGAGCCGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CGTGGTCAGCGGCCTGGAGGATGCGGCCGCAGTGGACTTCCAGTTTTCCAAGGGAGCCGT 300

Qy        301 GTACTGGACAGACGTGAGCGAGGAGGCCATCAAGCAGACCTACCTGAACCAGACGGGGGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GTACTGGACAGACGTGAGCGAGGAGGCCATCAAGCAGACCTACCTGAACCAGACGGGGGC 360

Qy        361 CGCCGTGCAGAACGTGGTCATCTCCGGCCTGGTCTCTCCCGACGGCCTCGCCTGCGACTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CGCCGTGCAGAACGTGGTCATCTCCGGCCTGGTCTCTCCCGACGGCCTCGCCTGCGACTG 420

Qy        421 GGTGGGCAAGAAGCTGTACTGGACGGACTCAGAGACCAACCGCATCGAGGTGGCCAACCT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GGTGGGCAAGAAGCTGTACTGGACGGACTCAGAGACCAACCGCATCGAGGTGGCCAACCT 480

Qy        481 CAATGGCACATCCCGGAAGGTGCTCTTCTGGCAGGACCTTGACCAGCCGAGGGCCATCGC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        481 CAATGGCACATCCCGGAAGGTGCTCTTCTGGCAGGACCTTGACCAGCCGAGGGCCATCGC 540
Qy        541 CTTGGACCCCGCTCACGGGTACATGTACTGGACAGACTGGGTTGAGACGCCCCGGATTGA 600
Db        541 CTTGGACCCCGCTCACGGGTACATGTACTGGACAGACTGGGGTGAGACGCCCCGGATTGA 600
Qy        601 GCGGGCAGGGATGGATGGCAGCACCCGGAAGATCATTGTGGACTCGGACATTTACTGGCC 660
Db        601 GCGGGCAGGGATGGATGGCAGCACCCGGAAGATCATTGTGGACTCGGACATTTACTGGCC 660
Qy        661 CAATGGACTGACCATCGACCTGGAGGAGCAGAAGCTCTACTGGGCTGACGCCAAGCTCAG 720
Db        661 CAATGGACTGACCATCGACCTGGAGGAGCAGAAGCTCTACTGGGCTGACGCCAAGCTCAG 720
Qy        721 CTTCATCCACCGTGCCAACCTGGACGGCTCGTTCCGGCAGAAGGTGGTGGAGGGCAGCCT 780
Db        721 CTTCATCCACCGTGCCAACCTGGACGGCTCGTTCCGGCAGAAGGTGGTGGAGGGCAGCCT 780
Qy        781 GACGCACCCCTTCGCCCTGACGCTCTCCGGGGACACTCTGTACTGGACAGACTGGCAGAC 840
Db        781 GACGCACCCCTTCGCCCTGACGCTCTCCGGGGACACTCTGTACTGGACAGACTGGCAGAC 840
Qy        841 CCGCTCCATCCATGCCTGCAACAAGCGCACTGGGGGGAAGAGGAAGGAGATCCTGAGTGC 900
Db        841 CCGCTCCATCCATGCCTGCAACAAGCGCACTGGGGGGAAGAGGAAGGAGATCCTGAGTGC 900
Qy        901 CCTCTACTCACCCATGGACATCCAGGTGCTGAGCCAGGAGCGGCAGCCTTTCTTCCACAC 960
Db        901 CCTCTACTCACCCATGGACATCCAGGTGCTGAGCCAGGAGCGGCAGCCTTTCTTCCACAC 960
Qy        961 TCGCTGTGAGGAGGACAATGGCGGCTGCTCCCACCTGTGCCTGCTGTCCCCAAGCGAGCC 1020
Db        961 TCGCTGTGAGGAGGACAATGGCGGCTGCTCCCACCTGTGCCTGCTGTCCCCAAGCGAGCC 1020
Qy       1021 TTTCTACACATGCGCCTGCCCCACGGGTGTGCAGCTGCAGGACAACGGCAGGACGTGTAA 1080
Db       1021 TTTCTACACATGCGCCTGCCCCACGGGTGTGCAGCTGCAGGACAACGGCAGGACGTGTAA 1080
Qy       1081 GGCAGGAGCCGAGGAGGTGCTGCTGCTGGCCCGGCGGACGGACCTACGGAGGATCTCGCT 1140
Db       1081 GGCAGGAGCCGAGGAGGTGCTGCTGCTGGCCCGGCGGACGGACCTACGGAGGATCTCGCT 1140
Qy       1141 GGACACGCCGGACTTCACCGACATCGTGCTGCAGGTGGACGACATCCGGCACGCCATTGC 1200
Db       1141 GGACACGCCGGACTTCACCGACATCGTGCTGCAGGTGGACGACATCCGGCACGCCATTGC 1200
Qy       1201 CATCGACTACGACCCGCTAGAGGGCTATGTCTACTGGACAGATGACGAGGTGCGGGCCAT 1260
Db       1201 CATCGACTACGACCCGCTAGAGGGCTATGTCTACTGGACAGATGACGAGGTGCGGGCCAT 1260
Qy       1261 CCGCAGGGCGTACCTGGACGGGTCTGGGGCGCAGACGCTGGTCAACACCGAGATCAACGA 1320
Db       1261 CCGCAGGGCGTACCTGGACGGGTCTGGGGCGCAGACGCTGGTCAACACCGAGATCAACGA 1320
Qy       1321 CCCCGATGGCATCGCGGTCGACTGGGTGGCCCGAAACCTCTACTGGACCGACACGGGCAC 1380
Db       1321 CCCCGATGGCATCGCGGTCGACTGGGTGGCCCGAAACCTCTACTGGACCGACACGGGCAC 1380
Qy       1381 GGACCGCATCGAGGTGACGCGCCTCAACGGCACCTCCCGCAAGATCCTGGTGTCGGAGGA 1440
Db       1381 GGACCGCATCGAGGTGACGCGCCTCAACGGCACCTCCCGCAAGATCCTGGTGTCGGAGGA 1440
Qy       1441 CCTGGACGAGCCCCGAGCCATCGCACTGCACCCCGTGATGGGCCTCATGTACTGGACAGA 1500
Db       1441 CCTGGACGAGCCCCGAGCCATCGCACTGCACCCCGTGATGGGCCTCATGTACTGGACAGA 1500
Qy       1501 CTGGGGAGAGAACCCTAAAATCGAGTGTGCCAACTTGGATGGGCAGGAGCGGCGTGTGCT 1560
Db       1501 CTGGGGAGAGAACCCTAAAATCGAGTGTGCCAACTTGGATGGGCAGGAGCGGCGTGTGCT 1560
Qy       1561 GGTCAATGCCTCCCTCGGGTGGCCCAACGGCCTGGCCCTGGACCTGCAGGAGGGGAAGCT 1620
Db       1561 GGTCAATGCCTCCCTCGGGTGGCCCAACGGCCTGGCCCTGGACCTGCAGGAGGGGAAGCT 1620
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Qy       1621 CTACTGGGGAGACGCCAAGACAGACAAGATCGAGGTGATCAATGTTGATGGGACGAAGAG 1680
Db       1621 CTACTGGGGAGACGCCAAGACAGACAAGATCGAGGTGATCAATGTTGATGGGACGAAGAG 1680
Qy       1681 GCGGACCCTCCTGGAGGACAAGCTCCCGCACATTTTCGGGTTCACGCTGCTGGGGGACTT 1740
Db       1681 GCGGACCCTCCTGGAGGACAAGCTCCCGCACATTTTCGGGTTCACGCTGCTGGGGGACTT 1740
Qy       1741 CATCTACTGGACTGACTGGCAGCGCCGCAGCATCGAGCGGGTGCACAAGGTCAAGGCCAG 1800
Db       1741 CATCTACTGGACTGACTGGCAGCGCCGCAGCATCGAGCGGGTGCACAAGGTCAAGGCCAG 1800
Qy       1801 CCGGGACGTCATCATTGACCAGCTGCCCGACCTGATGGGGCTCAAAGCTGTGAATGTGGC 1860
Db       1801 CCGGGACGTCATCATTGACCAGCTGCCCGACCTGATGGGGCTCAAAGCTGTGAATGTGGC 1860
Qy       1861 CAAGGTCGTCGGAACCAACCCGTGTGCGGACAGGAACGGGGGGTGCAGCCACCTGTGCTT 1920
Db       1861 CAAGGTCGTCGGAACCAACCCGTGTGCGGACAGGAACGGGGGGTGCAGCCACCTGTGCTT 1920
Qy       1921 CTTCACACCCCACGCAACCCGGTGTGGCTGCCCCATCGGCCTGGAGCTGCTGAGTGACAT 1980
Db       1921 CTTCACACCCCACGCAACCCGGTGTGGCTGCCCCATCGGCCTGGAGCTGCTGAGTGACAT 1980
Qy       1981 GAAGACCTGCATCGTGCCTGAGGCCTTCTTGGTCTTCACCAGCAGAGCCGCCATCCACAG 2040
Db       1981 GAAGACCTGCATCGTGCCTGAGGCCTTCTTGGTCTTCACCAGCAGAGCCGCCATCCACAG 2040
Qy       2041 GATCTCCCTCGAGACCAATAACAACGACGTGGCCATCCCGCTCACGGGCGTCAAGGAGGC 2100
Db       2041 GATCTCCCTCGAGACCAATAACAACGACGTGGCCATCCCGCTCACGGGCGTCAAGGAGGC 2100
Qy       2101 CTCAGCCCTGGACTTTGATGTGTCCAACAACCACATCTACTGGACAGACGTCAGCCTGAA 2160
Db       2101 CTCAGCCCTGGACTTTGATGTGTCCAACAACCACATCTACTGGACAGACGTCAGCCTGAA 2160
Qy       2161 GACCATCAGCCGCGCCTTCATGAACGGGAGCTCGGTGGAGCACGTGGTGGAGTTTGGCCT 2220
Db       2161 GACCATCAGCCGCGCCTTCATGAACGGGAGCTCGGTGGAGCACGTGGTGGAGTTTGGCCT 2220
Qy       2221 TGACTACCCCGAGGGCATGGCCGTTGACTGGATGGGCAAGAACCTCTACTGGGCCGACAC 2280
Db       2221 TGACTACCCCGAGGGCATGGCCGTTGACTGGATGGGCAAGAACCTCTACTGGGCCGACAC 2280
Qy       2281 TGGGACCAACAGAATCGAAGTGGCGCGGCTGGACGGGCAGTTCCGGCAAGTCCTCGTGTG 2340
Db       2281 TGGGACCAACAGAATCGAAGTGGCGCGGCTGGACGGGCAGTTCCGGCAAGTCCTCGTGTG 2340
Qy       2341 GAGGGACTTGGACAACCCGAGGTCGCTGGCCCTGGATCCCACCAAGGGCTACATCTACTG 2400
Db       2341 GAGGGACTTGGACAACCCGAGGTCGCTGGCCCTGGATCCCACCAAGGGCTACATCTACTG 2400
Qy       2401 GACCGAGTGGGGCGGCAAGCCGAGGATCGTGCGGGCCTTCATGGACGGGACCAACTGCAT 2460
Db       2401 GACCGAGTGGGGCGGCAAGCCGAGGATCGTGCGGGCCTTCATGGACGGGACCAACTGCAT 2460
Qy       2461 GACGCTGGTGGACAAGGTGGGCCGGGCCAACGACCTCACCATTGACTACGCTGACCAGCG 2520
Db       2461 GACGCTGGTGGACAAGGTGGGCCGGGCCAACGACCTCACCATTGACTACGCTGACCAGCG 2520
Qy       2521 CCTCTACTGGACCGACCTGGACACCAACATGATCGAGTCGTCCAACATGCTGGGTCAGGA 2580
Db       2521 CCTCTACTGGACCGACCTGGACACCAACATGATCGAGTCGTCCAACATGCTGGGTCAGGA 2580
Qy       2581 GCGGGTCGTGATTGCCGACGATCTCCCGCACCCGTTCGGTCTGACGCAGTACAGCGATTA 2640
Db       2581 GCGGGTCGTGATTGCCGACGATCTCCCGCACCCGTTCGGTCTGACGCAGTACAGCGATTA 2640
Qy       2641 TATCTACTGGACAGACTGGAATCTGCACAGCATTGAGCGGGCCGACAAGACTAGCGGCCG 2700
Db       2641 TATCTACTGGACAGACTGGAATCTGCACAGCATTGAGCGGGCCGACAAGACTAGCGGCCG 2700
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Qy       2701 GAACCGCACCCTCATCCAGGGCCACCTGGACTTCGTGATGGACATCCTGGTGTTCCACTC 2760
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Qy       2761 CTCCCGCCAGGATGGCCTCAATGACTGTATGCACAACAACGGGCAGTGTGGGCAGCTGTG 2820
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       2821 CCTTGCCATCCCCGGCGGCCACCGCTGCGGCTGCGCCTCACACTACACCCTGGACCCCAG 2880
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Db       2821 CCTTGCCATCCCCGGCGGCCACCGCTGCGGCTGCGCCTCACACTACACCCTGGACCCCAG 2880

Qy       2881 CAGCCGCAACTGCAGCCCGCCCACCACCTTCTTGCTGTTCAGCCAGAAATCTGCCATCAG 2940
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2881 CAGCCGCAACTGCAGCCCGCCCACCACCTTCTTGCTGTTCAGCCAGAAATCTGCCATCAG 2940

Qy       2941 TCGGATGATCCCGGACGACCAGCACAGCCCGGATCTCATCCTGCCCCTGCATGGACTGAG 3000
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2941 TCGGATGATCCCGGACGACCAGCACAGCCCGGATCTCATCCTGCCCCTGCATGGACTGAG 3000

Qy       3001 GAACGTCAAAGCCATCGACTATGACCCACTGGACAAGTTCATCTACTGGGTGGATGGGCG 3060
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3001 GAACGTCAAAGCCATCGACTATGACCCACTGGACAAGTTCATCTACTGGGTGGATGGGCG 3060

Qy       3061 CCAGAACATCAAGCGAGCCAAGGACGACGGGACCCAGCCCTTTGTTTTGACCTCTCTGAG 3120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       3121 CCAAGGCCAAAACCCAGACAGGCAGCCCCACGACCTCAGCATCGACATCTACAGCCGGAC 3180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3121 CCAAGGCCAAAACCCAGACAGGCAGCCCCACGACCTCAGCATCGACATCTACAGCCGGAC 3180

Qy       3181 ACTGTTCTGGACGTGCGAGGCCACCAATACCATCAACGTCCACAGGCTGAGCGGGGAAGC 3240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3181 ACTGTTCTGGACGTGCGAGGCCACCAATACCATCAACGTCCACAGGCTGAGCGGGGAAGC 3240

Qy       3241 CATGGGGGTGGTGCTGCGTGGGGACCGCGACAAGCCCAGGGCCATCGTCGTCAACGCGGA 3300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3241 CATGGGGGTGGTGCTGCGTGGGGACCGCGACAAGCCCAGGGCCATCGTCGTCAACGCGGA 3300

Qy       3301 GCGAGGGTACCTGTACTTCACCAACATGCAGGACCGGGCAGCCAAGATCGAACGCGCAGC 3360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       3361 CCTGGACGGCACCGAGCGCGAGGTCCTCTTCACCACCGGCCTCATCCGCCCTGTGGCCCT 3420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3361 CCTGGACGGCACCGAGCGCGAGGTCCTCTTCACCACCGGCCTCATCCGCCCTGTGGCCCT 3420

Qy       3421 GGTGGTGGACAACACACTGGGCAAGCTGTTCTGGGTGGACGCGGACCTGAAGCGCATTGA 3480
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Qy       3481 GAGCTGTGACCTGTCAGGGGCCAACCGCCTGACCCTGGAGGACGCCAACATCGTGCAGCC 3540
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Db       3481 GAGCTGTGACCTGTCAGGGGCCAACCGCCTGACCCTGGAGGACGCCAACATCGTGCAGCC 3540

Qy       3541 TCTGGGCCTGACCATCCTTGGCAAGCATCTCTACTGGATCGACCGCCAGCAGCAGATGAT 3600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       3601 CGAGCGTGTGGAGAAGACCACCGGGGACAAGCGGACTCGCATCCAGGGCCGTGTCGCCCA 3660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3601 CGAGCGTGTGGAGAAGACCACCGGGGACAAGCGGACTCGCATCCAGGGCCGTGTCGCCCA 3660

Qy       3661 CCTCACTGGCATCCATGCAGTGGAGGAAGTCAGCCTGGAGGAGTTCTCAGCCCACCCATG 3720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3661 CCTCACTGGCATCCATGCAGTGGAGGAAGTCAGCCTGGAGGAGTTCTCAGCCCACCCATG 3720

Qy       3721 TGCCCGTGACAATGGTGGCTGCTCCCACATCTGTATTGCCAAGGGTGATGGGACACCACG 3780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3721 TGCCCGTGACAATGGTGGCTGCTCCCACATCTGTATTGCCAAGGGTGATGGGACACCACG 3780

Qy       3781 GTGCTCATGCCCAGTCCACCTCGTGCTCCTGCAGAACCTGCTGACCTGTGGAGAGCCGCC 3840
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             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3781 GTGCTCATGCCCAGTCCACCTCGTGCTCCTGCAGAACCTGCTGACCTGTGGAGAGCCGCC 3840

Qy       3841 CACCTGCTCCCCGGACCAGTTTGCATGTGCCACAGGGGAGATCGACTGTATCCCCGGGGC 3900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3841 CACCTGCTCCCCGGACCAGTTTGCATGTGCCACAGGGGAGATCGACTGTATCCCCGGGGC 3900

Qy       3901 CTGGCGCTGTGACGGCTTTCCCGAGTGCGATGACCAGAGCGACGAGGAGGGCTGCCCCGT 3960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3901 CTGGCGCTGTGACGGCTTTCCCGAGTGCGATGACCAGAGCGACGAGGAGGGCTGCCCCGT 3960

Qy       3961 GTGCTCCGCCGCCCAGTTCCCCTGCGCGCGGGGTCAGTGTGTGGACCTGCGCCTGCGCTG 4020
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Db       3961 GTGCTCCGCCGCCCAGTTCCCCTGCGCGCGGGGTCAGTGTGTGGACCTGCGCCTGCGCTG 4020

Qy       4021 CGACGGCGAGGCAGACTGTCAGGACCGCTCAGACGAGGTGGACTGTGACGCCATCTGCCT 4080
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Qy       4081 GCCCAACCAGTTCCGGTGTGCGAGCGGCCAGTGTGTCCTCATCAAACAGCAGTGCGACTC 4140
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Qy       4141 CTTCCCCGACTGTATCGACGGCTCCGACGAGCTCATGTGTGAAATCACCAAGCCGCCCTC 4200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4141 CTTCCCCGACTGTATCGACGGCTCCGACGAGCTCATGTGTGAAATCACCAAGCCGCCCTC 4200

Qy       4201 AGACGACAGCCCGGCCCACAGCAGTGCCATCGGGCCCGTCATTGGCATCATCCTCTCTCT 4260
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Db       4201 AGACGACAGCCCGGCCCACAGCAGTGCCATCGGGCCCGTCATTGGCATCATCCTCTCTCT 4260

Qy       4261 CTTCGTCATGGGTGGTGTCTATTTTGTGTGCCAGCGCGTGGTGTGCCAGCGCTATGCGGG 4320
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Qy       4321 GGCCAACGGGCCCTTCCCGCACGAGTATGTCAGCGGGACCCCGCACGTGCCCCTCAATTT 4380
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Qy       4381 CATAGCCCCGGGCGGTTCCCAGCATGGCCCCTTCACAGGCATCGCATGCGGAAAGTCCAT 4440
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Db       4381 CATAGCCCCGGGCGGTTCCCAGCATGGCCCCTTCACAGGCATCGCATGCGGAAAGTCCAT 4440

Qy       4441 GATGAGCTCCGTGAGCCTGATGGGGGGCCGGGGCGGGGTGCCCCTCTACGACCGGAACCA 4500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4441 GATGAGCTCCGTGAGCCTGATGGGGGGCCGGGGCGGGGTGCCCCTCTACGACCGGAACCA 4500

Qy       4501 CGTCACAGGGGCCTCGTCCAGCAGCTCGTCCAGCACGAAGGCCACGCTGTACCCGCCGAT 4560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4501 CGTCACAGGGGCCTCGTCCAGCAGCTCGTCCAGCACGAAGGCCACGCTGTACCCGCCGAT 4560

Qy       4561 CCTGAACCCGCCGCCCTCCCCGGCCACGGACCCCTCCCTGTACAACATGGACATGTTCTA 4620
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Qy       4621 CTCTTCAAACATTCCGGCCACTGCGAGACCGTACAGGCCCTACATCATTCGAGGAATGGC 4680
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Qy       4681 GCCCCCGACGACGCCCTGCAGCACCGACGTGTGTGACAGCGACTACAGCGCCAGCCGCTG 4740
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Db       4681 GCCCCCGACGACGCCCTGCAGCACCGACGTGTGTGACAGCGACTACAGCGCCAGCCGCTG 4740

Qy       4741 GAAGGCCAGCAAGTACTACCTGGATTTGAACTCGGACTCAGACCCCTATCCACCCCCACC 4800
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Db       4741 GAAGGCCAGCAAGTACTACCTGGATTTGAACTCGGACTCAGACCCCTATCCACCCCCACC 4800

Qy       4801 CACGCCCCACAGCCAGTACCTGTCGGCGGAGGACAGCTGCCCGCCCTCGCCCGCCACCGA 4860
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Db       4801 CACGCCCCACAGCCAGTACCTGTCGGCGGAGGACAGCTGCCCGCCCTCGCCCGCCACCGA 4860

Qy       4861 GAGGAGCTACTTCCATCTCTTCCCGCCCCCTCCGTCCCCCTGCACGGACTCATCCTGACC 4920
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Db       4861 GAGGAGCTACTTCCATCTCTTCCCGCCCCCTCCGTCCCCCTGCACGGACTCATCCTGACC 4920

Qy       4921 TCGGCCGGGCCACTCTGGCTTCTCTGTGCCCCTGTAAATAGTTTTAAATATGAACAAAGA 4980
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Db       4921 TCGGCCGGGCCACTCTGGCTTCTCTGTGCCCCTGTAAATAGTTTTAAATATGAACAAAGA 4980

Qy       4981 AAAAAATATATTTTATGATTTAAAAAATAAATATAATTGGGATTTTAAAAACATGAGAAA 5040
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Db       4981 AAAAAATATATTTTATGATTTAAAAAATAAATATAATTGGGATTTTAAAAACATGAGAAA 5040

Qy       5041 TGTGAACTGTGATGGGGTGGGCAGGGCTGGGAGAACTTTGTACAGTGGAGAAATATTTAT 5100
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Qy       5101 AAACTTAATTTTGTAAAACA 5120
             ||||||||||||||||||||
Db       5101 AAACTTAATTTTGTAAAACA 5120


RESULT 9
ADB99038
ID   ADB99038 standard; DNA; 5120 BP.
XX
AC   ADB99038;
XX
DT   04-DEC-2003  (first entry)
XX
DE   Human LRP5 coding sequence.
XX
KW   Osteopathic; Gene therapy; High Bone Mass; HBM; LRP5; Zmax1; LRP6;
KW   bone mass modulation; osteoporosis; human; gene; ds.
XX
OS   Homo sapiens.
XX
PN   WO200292000-A2.
XX
PD   21-NOV-2002.
XX
PF   13-MAY-2002; 2002WO-US014877.
XX
PR   11-MAY-2001; 2001US-0290071P.
PR   17-MAY-2001; 2001US-0291311P.
PR   01-FEB-2002; 2002US-0353058P.
PR   04-MAR-2002; 2002US-0361293P.
XX
PA   (GENO-) GENOME THERAPEUTICS CORP.
PA   (AMHP ) WYETH.
XX
PI   Allen K,  Anisowicz A,  Graham JR,  Morales A,  Yaworsky PJ,  Liu W;
XX
DR   WPI; 2003-129214/12.
DR   P-PSDB; ADB98058.
XX
PT   New nucleic acid comprising a mutation in LRP5 or LRP6, useful for
PT   diagnosing a HBM-like phenotype in a subject and for preparing a
PT   composition for modulating bone mass and/or lipid levels in a subject
PT   suffering from e.g. osteoporosis.
XX
PS   Disclosure; Fig 6; 629pp; English.
XX
CC   The present invention relates to High Bone Mass (HBM), LRP5 (Zmax1) and
CC   LRP6 mutants, which results in a HBM-like phenotype when expressed in a
CC   cell. The HBM-like phenotype results in bone mass modulation and/or lipid
CC   level modulation. The invention is useful for diagnosing a HBM-like
CC   phenotype in a subject and for preparing a composition for modulating
CC   bone mass and/or lipid levels in a subject suffering from e.g.
CC   osteoporosis. The present sequence is the wild-type coding sequence for
CC   human LRP5.
XX
SQ   Sequence 5120 BP; 1037 A; 1657 C; 1549 G; 877 T; 0 U; 0 Other;

  Query Match           100.0%;  Score 5118.4;  DB 10;  Length 5120;
  Best Local Similarity  100.0%;  Pred. No. 0;

  Matches 5119;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ACTAAAGCGCCGCCGCCGCGCCATGGAGCCCGAGTGAGCGCGGCGCGGGCCCGTCCGGCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy         61 GCCGGACAACATGGAGGCAGCGCCGCCCGGGCCGCCGTGGCCGCTGCTGCTGCTGCTGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCCGGACAACATGGAGGCAGCGCCGCCCGGGCCGCCGTGGCCGCTGCTGCTGCTGCTGCT 120

Qy        121 GCTGCTGCTGGCGCTGTGCGGCTGCCCGGCCCCCGCCGCGGCCTCGCCGCTCCTGCTATT 180
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Db        121 GCTGCTGCTGGCGCTGTGCGGCTGCCCGGCCCCCGCCGCGGCCTCGCCGCTCCTGCTATT 180

Qy        181 TGCCAACCGCCGGGACGTACGGCTGGTGGACGCCGGCGGAGTCAAGCTGGAGTCCACCAT 240
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Db        181 TGCCAACCGCCGGGACGTACGGCTGGTGGACGCCGGCGGAGTCAAGCTGGAGTCCACCAT 240

Qy        241 CGTGGTCAGCGGCCTGGAGGATGCGGCCGCAGTGGACTTCCAGTTTTCCAAGGGAGCCGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CGTGGTCAGCGGCCTGGAGGATGCGGCCGCAGTGGACTTCCAGTTTTCCAAGGGAGCCGT 300

Qy        301 GTACTGGACAGACGTGAGCGAGGAGGCCATCAAGCAGACCTACCTGAACCAGACGGGGGC 360
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Db        301 GTACTGGACAGACGTGAGCGAGGAGGCCATCAAGCAGACCTACCTGAACCAGACGGGGGC 360

Qy        361 CGCCGTGCAGAACGTGGTCATCTCCGGCCTGGTCTCTCCCGACGGCCTCGCCTGCGACTG 420
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Db        361 CGCCGTGCAGAACGTGGTCATCTCCGGCCTGGTCTCTCCCGACGGCCTCGCCTGCGACTG 420

Qy        421 GGTGGGCAAGAAGCTGTACTGGACGGACTCAGAGACCAACCGCATCGAGGTGGCCAACCT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        481 CAATGGCACATCCCGGAAGGTGCTCTTCTGGCAGGACCTTGACCAGCCGAGGGCCATCGC 540
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Qy        541 CTTGGACCCCGCTCACGGGTACATGTACTGGACAGACTGGGTTGAGACGCCCCGGATTGA 600
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db        541 CTTGGACCCCGCTCACGGGTACATGTACTGGACAGACTGGGGTGAGACGCCCCGGATTGA 600

Qy        601 GCGGGCAGGGATGGATGGCAGCACCCGGAAGATCATTGTGGACTCGGACATTTACTGGCC 660
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Db        601 GCGGGCAGGGATGGATGGCAGCACCCGGAAGATCATTGTGGACTCGGACATTTACTGGCC 660

Qy        661 CAATGGACTGACCATCGACCTGGAGGAGCAGAAGCTCTACTGGGCTGACGCCAAGCTCAG 720
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Qy        721 CTTCATCCACCGTGCCAACCTGGACGGCTCGTTCCGGCAGAAGGTGGTGGAGGGCAGCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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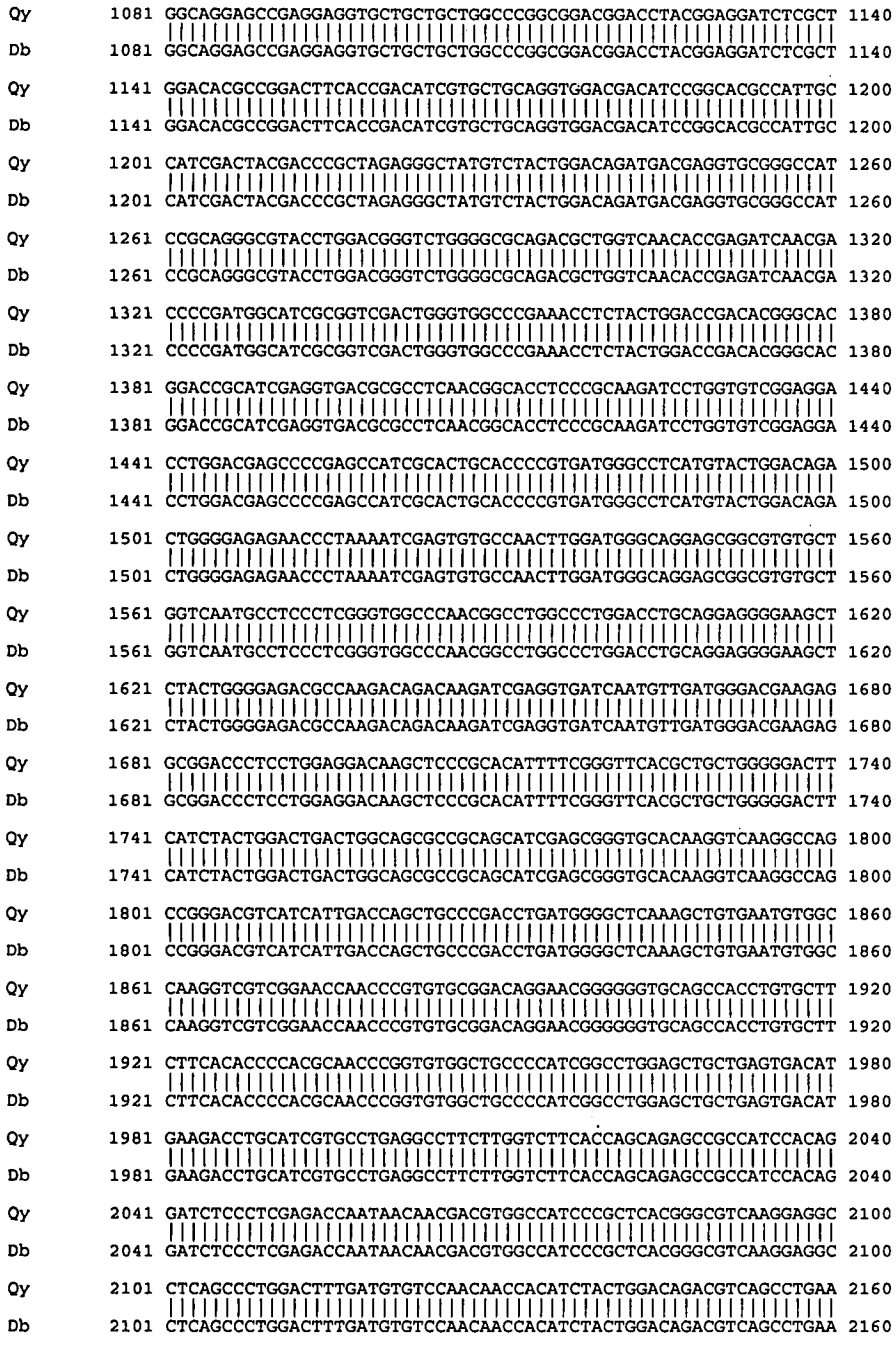
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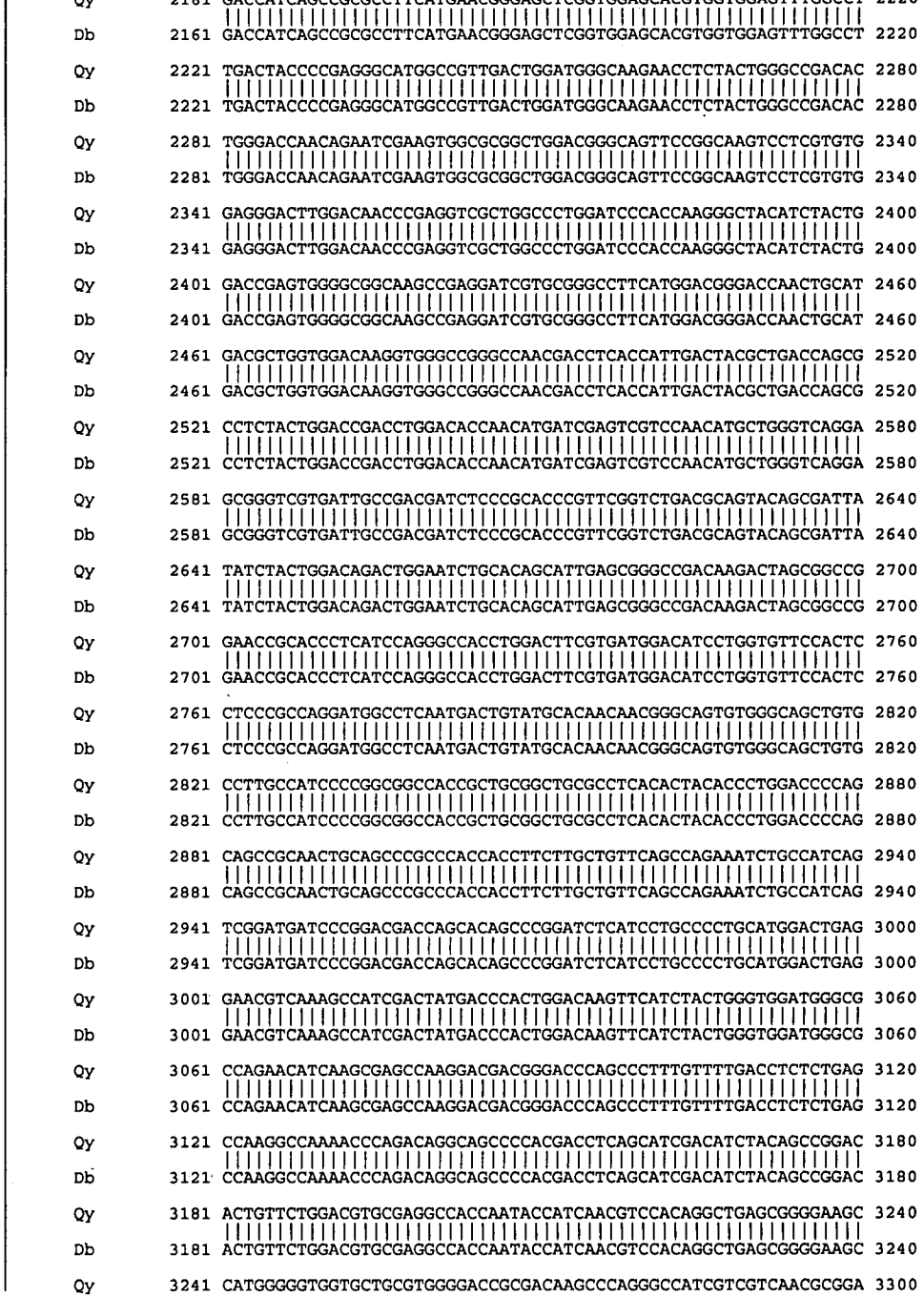
Qy        841 CCGCTCCATCCATGCCTGCAACAAGCGCACTGGGGGGAAGAGGAAGGAGATCCTGAGTGC 900
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Db        841 CCGCTCCATCCATGCCTGCAACAAGCGCACTGGGGGGAAGAGGAAGGAGATCCTGAGTGC 900

Qy        901 CCTCTACTCACCCATGGACATCCAGGTGCTGAGCCAGGAGCGGCAGCCTTTCTTCCACAC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CCTCTACTCACCCATGGACATCCAGGTGCTGAGCCAGGAGCGGCAGCCTTTCTTCCACAC 960

Qy        961 TCGCTGTGAGGAGGACAATGGCGGCTGCTCCCACCTGTGCCTGCTGTCCCCAAGCGAGCC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TCGCTGTGAGGAGGACAATGGCGGCTGCTCCCACCTGTGCCTGCTGTCCCCAAGCGAGCC 1020

Qy       1021 TTTCTACACATGCGCCTGCCCCACGGGTGTGCAGCTGCAGGACAACGGCAGGACGTGTAA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 TTTCTACACATGCGCCTGCCCCACGGGTGTGCAGCTGCAGGACAACGGCAGGACGTGTAA 1080
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Qy 1081 GGCAGGAGCCGAGGAGGTGCTGCTGCTGGCCCGGCGGACGGACCTACGGAGGATCTCGCT 1140
Db 1081 GGCAGGAGCCGAGGAGGTGCTGCTGCTGGCCCGGCGGACGGACCTACGGAGGATCTCGCT 1140
Qy 1141 GGACACGCCGGACTTCACCGACATCGTGCTGCAGGTGGACGACATCCGGCACGCCATTGC 1200
Db 1141 GGACACGCCGGACTTCACCGACATCGTGCTGCAGGTGGACGACATCCGGCACGCCATTGC 1200
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Qy 1381 GGACCGCATCGAGGTGACGCGCCTCAACGGCACCTCCCGCAAGATCCTGGTGTCGGAGGA 1440
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Db 1441 CCTGGACGAGCCCCGAGCCATCGCACTGCACCCCGTGATGGGCCTCATGTACTGGACAGA 1500
Qy 1501 CTGGGGAGAGAACCCTAAAATCGAGTGTGCCAACTTGGATGGGCAGGAGCGGCGTGTGCT 1560
Db 1501 CTGGGGAGAGAACCCTAAAATCGAGTGTGCCAACTTGGATGGGCAGGAGCGGCGTGTGCT 1560
Qy 1561 GGTCAATGCCTCCCTCGGGTGGCCCAACGGCCTGGCCCTGGACCTGCAGGAGGGGAAGCT 1620
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Qy 2161 GACCATCAGCCGCGCCTTCATGAACGGGAGCTCGGTGGAGCACGTGGTGGAGTTTGGCCT 2220
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Db 2221 TGACTACCCCGAGGGCATGGCCGTTGACTGGATGGGCAAGAACCTCTACTGGGCCGACAC 2280
Qy 2281 TGGGACCAACAGAATCGAAGTGGCGCGGCTGGACGGGCAGTTCCGGCAAGTCCTCGTGTG 2340
Db 2281 TGGGACCAACAGAATCGAAGTGGCGCGGCTGGACGGGCAGTTCCGGCAAGTCCTCGTGTG 2340
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Db 2581 GCGGGTCGTGATTGCCGACGATCTCCCGCACCCGTTCGGTCTGACGCAGTACAGCGATTA 2640
Qy 2641 TATCTACTGGACAGACTGGAATCTGCACAGCATTGAGCGGGCCGACAAGACTAGCGGCCG 2700
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Db 2701 GAACCGCACCCTCATCCAGGGCCACCTGGACTTCGTGATGGACATCCTGGTGTTCCACTC 2760
Qy 2761 CTCCCGCCAGGATGGCCTCAATGACTGTATGCACAACAACGGGCAGTGTGGGCAGCTGTG 2820
Db 2761 CTCCCGCCAGGATGGCCTCAATGACTGTATGCACAACAACGGGCAGTGTGGGCAGCTGTG 2820
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Qy 2941 TCGGATGATCCCGGACGACCAGCACAGCCCGGATCTCATCCTGCCCCTGCATGGACTGAG 3000
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Qy 3121 CCAAGGCCAAAACCCAGACAGGCAGCCCCACGACCTCAGCATCGACATCTACAGCCGGAC 3180
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Qy 3181 ACTGTTCTGGACGTGCGAGGCCACCAATACCATCAACGTCCACAGGCTGAGCGGGGAAGC 3240
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Qy 3241 CATGGGGGTGGTGCTGCGTGGGGACCGCGACAAGCCCAGGGCCATCGTCGTCAACGCGGA 3300

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Qy       3361 CCTGGACGGCACCGAGCGCGAGGTCCTCTTCACCACCGGCCTCATCCGCCCTGTGGCCCT 3420
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Qy       3481 GAGCTGTGACCTGTCAGGGGCCAACCGCCTGACCCTGGAGGACGCCAACATCGTGCAGCC 3540
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Qy       3601 CGAGCGTGTGGAGAAGACCACCGGGGACAAGCGGACTCGCATCCAGGGCCGTGTCGCCCA 3660
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Qy       3661 CCTCACTGGCATCCATGCAGTGGAGGAAGTCAGCCTGGAGGAGTTCTCAGCCCACCCATG 3720
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Qy       3721 TGCCCGTGACAATGGTGGCTGCTCCCACATCTGTATTGCCAAGGGTGATGGGACACCACG 3780
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Db       3721 TGCCCGTGACAATGGTGGCTGCTCCCACATCTGTATTGCCAAGGGTGATGGGACACCACG 3780

Qy       3781 GTGCTCATGCCCAGTCCACCTCGTGCTCCTGCAGAACCTGCTGACCTGTGGAGAGCCGCC 3840
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Db       3781 GTGCTCATGCCCAGTCCACCTCGTGCTCCTGCAGAACCTGCTGACCTGTGGAGAGCCGCC 3840

Qy       3841 CACCTGCTCCCCGGACCAGTTTGCATGTGCCACAGGGGAGATCGACTGTATCCCCGGGGC 3900
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Db       3841 CACCTGCTCCCCGGACCAGTTTGCATGTGCCACAGGGGAGATCGACTGTATCCCCGGGGC 3900

Qy       3901 CTGGCGCTGTGACGGCTTTCCCGAGTGCGATGACCAGAGCGACGAGGAGGGCTGCCCCGT 3960
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Qy       3961 GTGCTCCGCCGCCCAGTTCCCCTGCGCGCGGGGTCAGTGTGTGGACCTGCGCCTGCGCTG 4020
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Qy       4081 GCCCAACCAGTTCCGGTGTGCGAGCGGCCAGTGTGTCCTCATCAAACAGCAGTGCGACTC 4140
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Qy       4141 CTTCCCCGACTGTATCGACGGCTCCGACGAGCTCATGTGTGAAATCACCAAGCCGCCCTC 4200
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Db       4141 CTTCCCCGACTGTATCGACGGCTCCGACGAGCTCATGTGTGAAATCACCAAGCCGCCCTC 4200

Qy       4201 AGACGACAGCCCGGCCCACAGCAGTGCCATCGGGCCCGTCATTGGCATCATCCTCTCTCT 4260
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Qy       4261 CTTCGTCATGGGTGGTGTCTATTTTGTGTGCCAGCGCGTGGTGTGCCAGCGCTATGCGGG 4320
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Qy       4381 CATAGCCCCGGGCGGTTCCCAGCATGGCCCCTTCACAGGCATCGCATGCGGAAAGTCCAT 4440
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Qy       4441 GATGAGCTCCGTGAGCCTGATGGGGGGCCGGGGCGGGGTGCCCCTCTACGACCGGAACCA 4500
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Qy       4501 CGTCACAGGGGCCTCGTCCAGCAGCTCGTCCAGCACGAAGGCCACGCTGTACCCGCCGAT 4560
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Qy       4561 CCTGAACCCGCCGCCCTCCCCGGCCACGGACCCCTCCCTGTACAACATGGACATGTTCTA 4620
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Qy       4621 CTCTTCAAACATTCCGGCCACTGCGAGACCGTACAGGCCCTACATCATTCGAGGAATGGC 4680
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Qy       4681 GCCCCCGACGACGCCCTGCAGCACCGACGTGTGTGACAGCGACTACAGCGCCAGCCGCTG 4740
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Qy       4741 GAAGGCCAGCAAGTACTACCTGGATTTGAACTCGGACTCAGACCCCTATCCACCCCCACC 4800
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Qy       4801 CACGCCCCACAGCCAGTACCTGTCGGCGGAGGACAGCTGCCCGCCCTCGCCCGCCACCGA 4860
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Db       4801 CACGCCCCACAGCCAGTACCTGTCGGCGGAGGACAGCTGCCCGCCCTCGCCCGCCACCGA 4860

Qy       4861 GAGGAGCTACTTCCATCTCTTCCCGCCCCCTCCGTCCCCCTGCACGGACTCATCCTGACC 4920
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Db       4861 GAGGAGCTACTTCCATCTCTTCCCGCCCCCTCCGTCCCCCTGCACGGACTCATCCTGACC 4920

Qy       4921 TCGGCCGGGCCACTCTGGCTTCTCTGTGCCCCTGTAAATAGTTTTAAATATGAACAAAGA 4980
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Qy       5041 TGTGAACTGTGATGGGGTGGGCAGGGCTGGGAGAACTTTGTACAGTGGAGAAATATTTAT 5100
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Qy       5101 AAACTTAATTTTGTAAAACA 5120
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Db       5101 AAACTTAATTTTGTAAAACA 5120
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RESULT 10
ADE82639
ID ADE82639 standard; DNA; 5120 BP.
XX
AC ADE82639;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human Zmax1 gene encoding sequence.
XX
KW LRP5; LRP6; HBM; Dkk activity; Osteopathic; Antiinflammatory;
KW Antiarthritic; bone mass disorders; osteoporosis; hypercalcaemia;
KW hyperostosis; osteogenesis; Wnt signaling; ds.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT CDS   71. .4915

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PN   WO200292015-A2.
XX
PD   21-NOV-2002.
XX
PF   17-MAY-2002; 2002WO-US015982.
XX
PR   17-MAY-2001; 2001US-0291311P.
PR   01-FEB-2002; 2002US-0353058P.
PR   04-MAR-2002; 2002US-0361293P.
XX
PA   (GENO-) GENOME THERAPEUTICS CORP.
PA   (AMHP ) WYETH.
XX
PI   Allen K,  Anisowicz A,  Bhat BM,  Damagnez V,  Robinson JA;
PI   Yaworsky PJ;
XX
DR   WPI; 2003-129219/12.
DR   P-PSDB; ADE82427.
XX
PT   Regulating LRP5, LRP6 or HBM activity in a subject, useful for modulating
PT   lipid levels and/or bone mass, and for in treating bone mass disorders,
PT   e.g. osteoporosis, comprises administering a composition which modulates
PT   a Dkk activity.
XX
PS   Disclosure; SEQ ID NO 1; 173pp; English.
XX
CC   The present invention relates to regulating LRP5, LRP6 or HBM activity in
CC   a subject comprising administering a composition which modulates a Dkk
CC   activity. The method is useful for modulating lipid levels and/or bone
CC   mass, and is useful in treating or diagnosing abnormal lipid levels and
CC   bone mass disorders, such as osteoporosis, bond fracture, age-related
CC   loss of bone, a chondrodystrophy, drug-induced bone disorder, high bone
CC   turnover, hypercalcaemia, hyperostosis, osteogenesis, imperfecta,
CC   osteomalacia, osteomyelitis, Paget's disease, osteoarthritis, and
CC   rickets. Modulators of Dkk activity are useful for as reagents in
CC   studying bone mass and lipid level modulation, in modulating Wnt
CC   signaling, or treating Dkk-mediated disorders. The present sequence
CC   represents human Zmax1 gene encoding sequence.
XX
SQ   Sequence 5120 BP; 1037 A; 1657 C; 1549 G; 877 T; 0 U; 0 Other;

  Query Match           100.0%;  Score 5118.4;  DB 10;  Length 5120;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 5119;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ACTAAAGCGCCGCCGCCGCGCCATGGAGCCCGAGTGAGCGCGGCGCGGGCCCGTCCGGCC 60
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Qy        361 CGCCGTGCAGAACGTGGTCATCTCCGGCCTGGTCTCTCCCGACGGCCTCGCCTGCGACTG 420
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Qy        421 GGTGGGCAAGAAGCTGTACTGGACGGACTCAGAGACCAACCGCATCGAGGTGGCCAACCT 480
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Db        421 GGTGGGCAAGAAGCTGTACTGGACGGACTCAGAGACCAACCGCATCGAGGTGGCCAACCT 480

Qy        481 CAATGGCACATCCCGGAAGGTGCTCTTCTGGCAGGACCTTGACCAGCCGAGGGCCATCGC 540
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Qy        541 CTTGGACCCCGCTCACGGGTACATGTACTGGACAGACTGGGTTGAGACGCCCCGGATTGA 600
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Db        541 CTTGGACCCCGCTCACGGGTACATGTACTGGACAGACTGGGGTGAGACGCCCCGGATTGA 600

Qy        601 GCGGGCAGGGATGGATGGCAGCACCCGGAAGATCATTGTGGACTCGGACATTTACTGGCC 660
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Qy        901 CCTCTACTCACCCATGGACATCCAGGTGCTGAGCCAGGAGCGGCAGCCTTTCTTCCACAC 960
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Qy        961 TCGCTGTGAGGAGGACAATGGCGGCTGCTCCCACCTGTGCCTGCTGTCCCCAAGCGAGCC 1020
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Qy       1021 TTTCTACACATGCGCCTGCCCCACGGGTGTGCAGCTGCAGGACAACGGCAGGACGTGTAA 1080
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Qy       1141 GGACACGCCGGACTTCACCGACATCGTGCTGCAGGTGGACGACATCCGGCACGCCATTGC 1200
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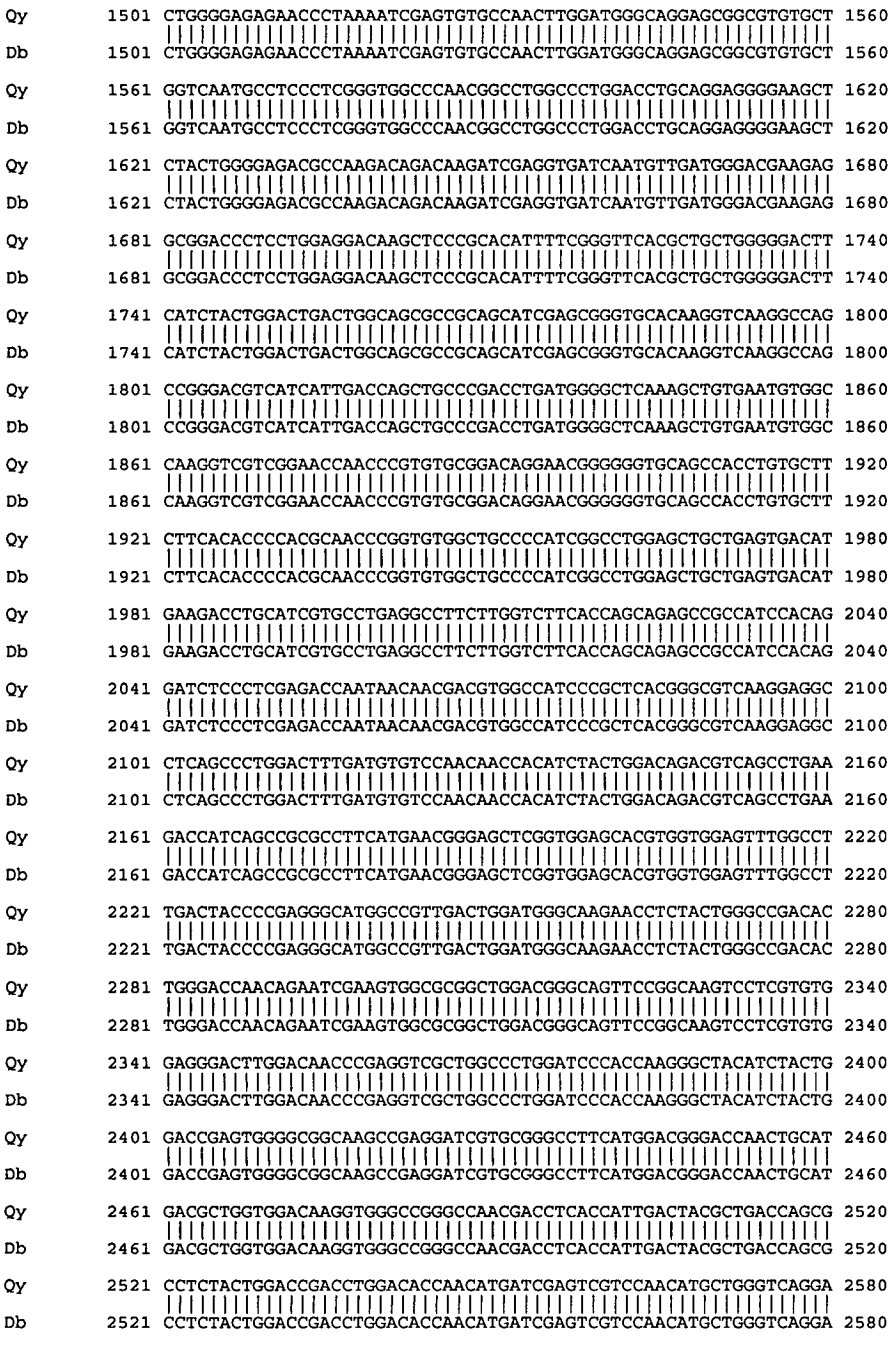
Qy       1201 CATCGACTACGACCCGCTAGAGGGCTATGTCTACTGGACAGATGACGAGGTGCGGGCCAT 1260
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Db       1201 CATCGACTACGACCCGCTAGAGGGCTATGTCTACTGGACAGATGACGAGGTGCGGGCCAT 1260

Qy       1261 CCGCAGGGCGTACCTGGACGGGTCTGGGGCGCAGACGCTGGTCAACACCGAGATCAACGA 1320
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Db       1261 CCGCAGGGCGTACCTGGACGGGTCTGGGGCGCAGACGCTGGTCAACACCGAGATCAACGA 1320

Qy       1321 CCCCGATGGCATCGCGGTCGACTGGGTGGCCCGAAACCTCTACTGGACCGACACGGGCAC 1380
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Qy       1381 GGACCGCATCGAGGTGACGCGCCTCAACGGCACCTCCCGCAAGATCCTGGTGTCGGAGGA 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       1441 CCTGGACGAGCCCCGAGCCATCGCACTGCACCCCGTGATGGGCCTCATGTACTGGACAGA 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 CCTGGACGAGCCCCGAGCCATCGCACTGCACCCCGTGATGGGCCTCATGTACTGGACAGA 1500
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Qy 1501 CTGGGGAGAGAACCCTAAAATCGAGTGTGCCAACTTGGATGGGCAGGAGCGGCGTGTGCT 1560
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Qy 1561 GGTCAATGCCTCCCTCGGGTGGCCCAACGGCCTGGCCCTGGACCTGCAGGAGGGGAAGCT 1620
Db 1561 GGTCAATGCCTCCCTCGGGTGGCCCAACGGCCTGGCCCTGGACCTGCAGGAGGGGAAGCT 1620
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Db 1621 CTACTGGGGAGACGCCAAGACAGACAAGATCGAGGTGATCAATGTTGATGGGACGAAGAG 1680
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Db 1681 GCGGACCCTCCTGGAGGACAAGCTCCCGCACATTTTCGGGTTCACGCTGCTGGGGGACTT 1740
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Db 1801 CCGGGACGTCATCATTGACCAGCTGCCCGACCTGATGGGGCTCAAAGCTGTGAATGTGGC 1860
Qy 1861 CAAGGTCGTCGGAACCAACCCGTGTGCGGACAGGAACGGGGGGGTGCAGCCACCTGTGCTT 1920
Db 1861 CAAGGTCGTCGGAACCAACCCGTGTGCGGACAGGAACGGGGGGTGCAGCCACCTGTGCTT 1920
Qy 1921 CTTCACACCCCACGCAACCCGGTGTGGCTGCCCCATCGGCCTGGAGCTGCTGAGTGACAT 1980
Db 1921 CTTCACACCCCACGCAACCCGGTGTGGCTGCCCCATCGGCCTGGAGCTGCTGAGTGACAT 1980
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Db 2221 TGACTACCCCGAGGGCATGGCCGTTGACTGGATGGGCAAGAACCTCTACTGGGCCGACAC 2280
Qy 2281 TGGGACCAACAGAATCGAAGTGGCGCGGCTGGACGGGCAGTTCCGGCAAGTCCTCGTGTG 2340
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Qy 2401 GACCGAGTGGGGCGGCAAGCCGAGGATCGTGCGGGCCTTCATGGACGGGACCAACTGCAT 2460
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Qy 3241 CATGGGGGTGGTGCTGCGTGGGGACCGCGACAAGCCCAGGGCCATCGTCGTCAACGCGGA 3300
Db 3241 CATGGGGGTGGTGCTGCGTGGGGACCGCGACAAGCCCAGGGCCATCGTCGTCAACGCGGA 3300
Qy 3301 GCGAGGGTACCTGTACTTCACCAACATGCAGGACCGGGCAGCCAAGATCGAACGCGCAGC 3360
Db 3301 GCGAGGGTACCTGTACTTCACCAACATGCAGGACCGGGCAGCCAAGATCGAACGCGCAGC 3360
Qy 3361 CCTGGACGGCACCGAGCGCGAGGTCCTCTTCACCACCGGCCTCATCCGCCCTGTGGCCCT 3420
Db 3361 CCTGGACGGCACCGAGCGCGAGGTCCTCTTCACCACCGGCCTCATCCGCCCTGTGGCCCT 3420
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Qy 3481 GAGCTGTGACCTGTCAGGGGCCAACCGCCTGACCCTGGAGGACGCCAACATCGTGCAGCC 3540
Db 3481 GAGCTGTGACCTGTCAGGGGCCAACCGCCTGACCCTGGAGGACGCCAACATCGTGCAGCC 3540
Qy 3541 TCTGGGCCTGACCATCCTTGGCAAGCATCTCTACTGGATCGACCGCCAGCAGCAGATGAT 3600
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Qy 3661 CCTCACTGGCATCCATGCAGTGGAGGAAGTCAGCCTGGAGGAGTTCTCAGCCCACCCATG 3720

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Db       3661 CCTCACTGGCATCCATGCAGTGGAGGAAGTCAGCCTGGAGGAGTTCTCAGCCCACCCATG 3720

Qy       3721 TGCCCGTGACAATGGTGGCTGCTCCCACATCTGTATTGCCAAGGGTGATGGGACACCACG 3780
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Db       3721 TGCCCGTGACAATGGTGGCTGCTCCCACATCTGTATTGCCAAGGGTGATGGGACACCACG 3780

Qy       3781 GTGCTCATGCCCAGTCCACCTCGTGCTCCTGCAGAACCTGCTGACCTGTGGAGAGCCGCC 3840
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Db       3781 GTGCTCATGCCCAGTCCACCTCGTGCTCCTGCAGAACCTGCTGACCTGTGGAGAGCCGCC 3840

Qy       3841 CACCTGCTCCCCGGACCAGTTTGCATGTGCCACAGGGGAGATCGACTGTATCCCCGGGGC 3900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       3901 CTGGCGCTGTGACGGCTTTCCCGAGTGCGATGACCAGAGCGACGAGGAGGGCTGCCCCGT 3960
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Qy       3961 GTGCTCCGCCGCCCAGTTCCCCTGCGCGCGGGGTCAGTGTGTGGACCTGCGCCTGCGCTG 4020
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Db       3961 GTGCTCCGCCGCCCAGTTCCCCTGCGCGCGGGGTCAGTGTGTGGACCTGCGCCTGCGCTG 4020

Qy       4021 CGACGGCGAGGCAGACTGTCAGGACCGCTCAGACGAGGTGGACTGTGACGCCATCTGCCT 4080
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Db       4021 CGACGGCGAGGCAGACTGTCAGGACCGCTCAGACGAGGTGGACTGTGACGCCATCTGCCT 4080

Qy       4081 GCCCAACCAGTTCCGGTGTGCGAGCGGCCAGTGTGTCCTCATCAAACAGCAGTGCGACTC 4140
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Qy       4141 CTTCCCCGACTGTATCGACGGCTCCGACGAGCTCATGTGTGAAATCACCAAGCCGCCCTC 4200
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Qy       4201 AGACGACAGCCCGGCCCACAGCAGTGCCATCGGGCCCGTCATTGGCATCATCCTCTCTCT 4260
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Qy       4261 CTTCGTCATGGGTGGTGTCTATTTTGTGTGCCAGCGCGTGGTGTGCCAGCGCTATGCGGG 4320
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Qy       4321 GGCCAACGGGCCCTTCCCGCACGAGTATGTCAGCGGGACCCCGCACGTGCCCCTCAATTT 4380
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Qy       4381 CATAGCCCCGGGCGGTTCCCAGCATGGCCCCTTCACAGGCATCGCATGCGGAAAGTCCAT 4440
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Qy       4441 GATGAGCTCCGTGAGCCTGATGGGGGGCCGGGGCGGGGTGCCCCTCTACGACCGGAACCA 4500
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Qy       4561 CCTGAACCCGCCGCCCTCCCCGGCCACGGACCCCTCCCTGTACAACATGGACATGTTCTA 4620
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Qy       4621 CTCTTCAAACATTCCGGCCACTGCGAGACCGTACAGGCCCTACATCATTCGAGGAATGGC 4680
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Qy       4681 GCCCCCGACGACGCCCTGCAGCACCGACGTGTGTGACAGCGACTACAGCGCCAGCCGCTG 4740
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Qy       4741 GAAGGCCAGCAAGTACTACCTGGATTTGAACTCGGACTCAGACCCCTATCCACCCCCACC 4800
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Db       4741 GAAGGCCAGCAAGTACTACCTGGATTTGAACTCGGACTCAGACCCCTATCCACCCCCACC 4800

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Qy       4861 GAGGAGCTACTTCCATCTCTTCCCGCCCCCTCCGTCCCCCTGCACGGACTCATCCTGACC 4920
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Qy       4981 AAAAAATATATTTTATGATTTAAAAAATAAATATAATTGGGATTTTAAAAACATGAGAAA 5040
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Qy       5041 TGTGAACTGTGATGGGGTGGGCAGGGCTGGGAGAACTTTGTACAGTGGAGAAATATTTAT 5100
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Qy       5101 AAACTTAATTTTGTAAAACA 5120
             ||||||||||||||||||||
Db       5101 AAACTTAATTTTGTAAAACA 5120
```

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RESULT 11
ADR16919
ID   ADR16919 standard; DNA; 5120 BP.
XX
AC   ADR16919;
XX
DT   04-NOV-2004  (first entry)
XX
DE   Human high bone mass gene, wild type allele Zmax1 DNA.
XX
KW   Human; high bone mass; Zmax1; ds; gene; HBM; osteoporosis;
KW   chromosome 11q13.3; osteopathic; LDL receptor; bone development;
KW   metabolic bone disease; SNP; single nucleotide polymorphism.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
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FT                   /*tag=  a
FT                   /product= "Zmax1 protein"
FT                   /transl_except= (pos:530. .532,aa:Lys)
FT                   /note= "Applies to SEQ ID 3 only"
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FT                   /note= "Applies to SEQ ID 3 only"
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FT                   /note= "Applies to SEQ ID 3 only"
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FT                   /*tag=  b
FT                   /standard_name= "Single nucleotide polymorphism"
XX
PN   US6780609-B1.
XX
PD   24-AUG-2004.
XX
PF   05-APR-2000; 2000US-00543771.
XX
PR   13-JAN-1998;  98US-0071449P.
PR   23-OCT-1998;  98US-0105511P.
PR   13-JAN-1999;  99US-00229319.
XX
PA   (GENO-) GENOME THERAPEUTICS CORP.
XX
PI   Carulli JP,  Little RD,  Recker RR,  Johnson ML;
XX
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DR WPI; 2004-623529/60.
DR P-PSDB; ADR16921, ADR17560.
XX
PT New high bone mass gene of chromosome 1.1Q13.3, encoding protein useful
PT for treating, diagnosing, preventing, or screening for normal and
PT abnormal conditions of bone, including metabolic bone diseases, e.g.
PT osteoporosis.
XX
PS Disclosure; SEQ ID NO 1; 284pp; English.
XX
CC The invention relates to an isolated amino acid protein sequence selected
CC from an amino acid sequence appearing as ADR16922 or an amino acid
CC sequence comprising or consisting of the extracellular domain of
CC ADR16922(amino acids 23-1385). ADR16922 is encoded by the HBM (high bone
CC mass) allele of the human Zmax1 gene and has sequence similarity to LDL
CC receptors. Also disclosed are nucleic acids, proteins, cloning vectors,
CC expression vectors, transformed hosts, methods of developing
CC pharmaceutical compositions, methods of identifying molecules involved in
CC bone development, and methods of diagnosing and treating diseases
CC involved in bone development. Specifically disclosed is the Zmax1 gene
CC and the high bone mass (HBM) allele on chromosome 11q13.3 encoding
CC ADR16922. The protein is useful for treating, diagnosing, preventing, or
CC screening for normal and abnormal conditions of bone, including metabolic
CC bone diseases, e.g. osteoporosis. The present sequence is the wild type
CC human Zmax1 DNA (probably a cDNA since 23 exons are disclosed yet this
CC sequence is uninterrupted by introns).
XX
SQ Sequence 5120 BP; 1037 A; 1657 C; 1549 G; 877 T; 0 U; 0 Other;

Query Match 100.0%; Score 5118.4; DB 13; Length 5120;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5119; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 ACTAAAGCGCCGCCGCCGCGCCATGGAGCCCGAGTGAGCGCGGCGCGGGCCCGTCCGGCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy         61 GCCGGACAACATGGAGGCAGCGCCGCCCGGGCCGCCGTGGCCGCTGCTGCTGCTGCTGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCCGGACAACATGGAGGCAGCGCCGCCCGGGCCGCCGTGGCCGCTGCTGCTGCTGCTGCT 120

Qy        121 GCTGCTGCTGGCGCTGTGCGGCTGCCCGGCCCCCGCCGCGGCCTCGCCGCTCCTGCTATT 180
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Qy        181 TGCCAACCGCCGGGACGTACGGCTGGTGGACGCCGGCGGAGTCAAGCTGGAGTCCACCAT 240
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Qy        241 CGTGGTCAGCGGCCTGGAGGATGCGGCCGCAGTGGACTTCCAGTTTTCCAAGGGAGCCGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CGTGGTCAGCGGCCTGGAGGATGCGGCCGCAGTGGACTTCCAGTTTTCCAAGGGAGCCGT 300

Qy        301 GTACTGGACAGACGTGAGCGAGGAGGCCATCAAGCAGACCTACCTGAACCAGACGGGGGC 360
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Db        301 GTACTGGACAGACGTGAGCGAGGAGGCCATCAAGCAGACCTACCTGAACCAGACGGGGGC 360

Qy        361 CGCCGTGCAGAACGTGGTCATCTCCGGCCTGGTCTCTCCCGACGGCCTCGCCTGCGACTG 420
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Qy        421 GGTGGGCAAGAAGCTGTACTGGACGGACTCAGAGACCAACCGCATCGAGGTGGCCAACCT 480
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Qy        481 CAATGGCACATCCCGGAAGGTGCTCTTCTGGCAGGACCTTGACCAGCCGAGGGCCATCGC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CAATGGCACATCCCGGAAGGTGCTCTTCTGGCAGGACCTTGACCAGCCGAGGGCCATCGC 540

Qy        541 CTTGGACCCCGCTCACGGGTACATGTACTGGACAGACTGGGTTGAGACGCCCCGGATTGA 600
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db        541 CTTGGACCCCGCTCACGGGTACATGTACTGGACAGACTGGGGTGAGACGCCCCGGATTGA 600

Qy        601 GCGGGCAGGGATGGATGGCAGCACCCGGAAGATCATTGTGGACTCGGACATTTACTGGCC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GCGGGCAGGGATGGATGGCAGCACCCGGAAGATCATTGTGGACTCGGACATTTACTGGCC 660

Qy        661 CAATGGACTGACCATCGACCTGGAGGAGCAGAAGCTCTACTGGGCTGACGCCAAGCTCAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAATGGACTGACCATCGACCTGGAGGAGCAGAAGCTCTACTGGGCTGACGCCAAGCTCAG 720

Qy        721 CTTCATCCACCGTGCCAACCTGGACGGCTCGTTCCGGCAGAAGGTGGTGGAGGGCAGCCT 780
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Qy        781 GACGCACCCCTTCGCCCTGACGCTCTCCGGGGACACTCTGTACTGGACAGACTGGCAGAC 840
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Qy        841 CCGCTCCATCCATGCCTGCAACAAGCGCACTGGGGGGAAGAGGAAGGAGATCCTGAGTGC 900
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Db        841 CCGCTCCATCCATGCCTGCAACAAGCGCACTGGGGGGAAGAGGAAGGAGATCCTGAGTGC 900

Qy        901 CCTCTACTCACCCATGGACATCCAGGTGCTGAGCCAGGAGCGGCAGCCTTTCTTCCACAC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CCTCTACTCACCCATGGACATCCAGGTGCTGAGCCAGGAGCGGCAGCCTTTCTTCCACAC 960

Qy        961 TCGCTGTGAGGAGGACAATGGCGGCTGCTCCCACCTGTGCCTGCTGTCCCCAAGCGAGCC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TCGCTGTGAGGAGGACAATGGCGGCTGCTCCCACCTGTGCCTGCTGTCCCCAAGCGAGCC 1020

Qy       1021 TTTCTACACATGCGCCTGCCCCACGGGTGTGCAGCTGCAGGACAACGGCAGGACGTGTAA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 TTTCTACACATGCGCCTGCCCCACGGGTGTGCAGCTGCAGGACAACGGCAGGACGTGTAA 1080

Qy       1081 GGCAGGAGCCGAGGAGGTGCTGCTGCTGGCCCGGCGGACGGACCTACGGAGGATCTCGCT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 GGCAGGAGCCGAGGAGGTGCTGCTGCTGGCCCGGCGGACGGACCTACGGAGGATCTCGCT 1140

Qy       1141 GGACACGCCGGACTTCACCGACATCGTGCTGCAGGTGGACGACATCCGGCACGCCATTGC 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GGACACGCCGGACTTCACCGACATCGTGCTGCAGGTGGACGACATCCGGCACGCCATTGC 1200

Qy       1201 CATCGACTACGACCCGCTAGAGGGCTATGTCTACTGGACAGATGACGAGGTGCGGGCCAT 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 CATCGACTACGACCCGCTAGAGGGCTATGTCTACTGGACAGATGACGAGGTGCGGGCCAT 1260

Qy       1261 CCGCAGGGCGTACCTGGACGGGTCTGGGGCGCAGACGCTGGTCAACACCGAGATCAACGA 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 CCGCAGGGCGTACCTGGACGGGTCTGGGGCGCAGACGCTGGTCAACACCGAGATCAACGA 1320

Qy       1321 CCCCGATGGCATCGCGGTCGACTGGGTGGCCCGAAACCTCTACTGGACCGACACGGGCAC 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 CCCCGATGGCATCGCGGTCGACTGGGTGGCCCGAAACCTCTACTGGACCGACACGGGCAC 1380

Qy       1381 GGACCGCATCGAGGTGACGCGCCTCAACGGCACCTCCCGCAAGATCCTGGTGTCGGAGGA 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 GGACCGCATCGAGGTGACGCGCCTCAACGGCACCTCCCGCAAGATCCTGGTGTCGGAGGA 1440

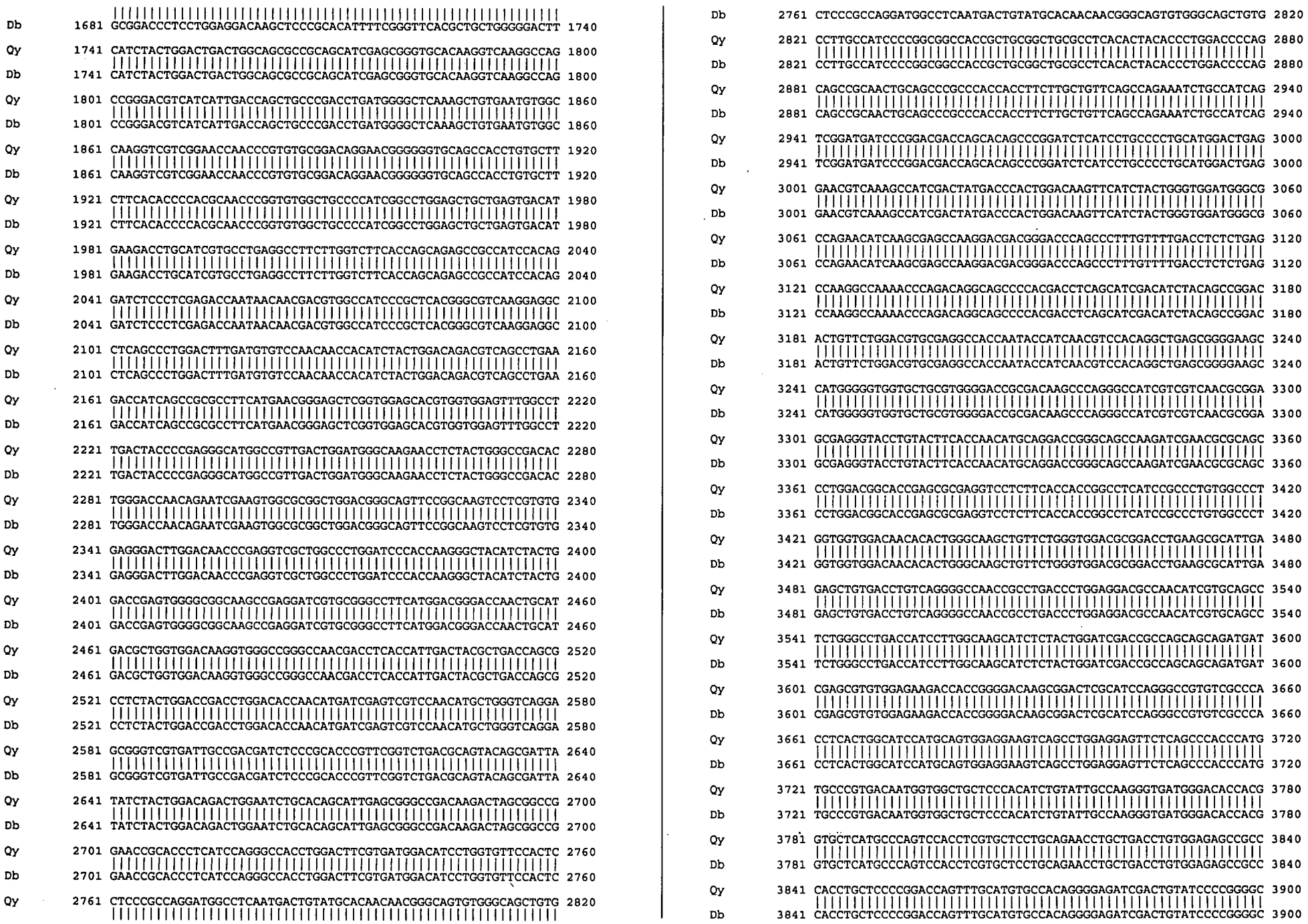
Qy       1441 CCTGGACGAGCCCCGAGCCATCGCACTGCACCCCGTGATGGGCCTCATGTACTGGACAGA 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 CCTGGACGAGCCCCGAGCCATCGCACTGCACCCCGTGATGGGCCTCATGTACTGGACAGA 1500

Qy       1501 CTGGGGAGAGAACCCTAAAATCGAGTGTGCCAACTTGGATGGGCAGGAGCGGCGTGTGCT 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 CTGGGGAGAGAACCCTAAAATCGAGTGTGCCAACTTGGATGGGCAGGAGCGGCGTGTGCT 1560

Qy       1561 GGTCAATGCCTCCCTCGGGTGGCCCAACGGCCTGGCCCTGGACCTGCAGGAGGGGAAGCT 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 GGTCAATGCCTCCCTCGGGTGGCCCAACGGCCTGGCCCTGGACCTGCAGGAGGGGAAGCT 1620

Qy       1621 CTACTGGGGAGACGCCAAGACAGACAAGATCGAGGTGATCAATGTTGATGGGACGAAGAG 1680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 CTACTGGGGAGACGCCAAGACAGACAAGATCGAGGTGATCAATGTTGATGGGACGAAGAG 1680

Qy       1681 GCGGACCCTCCTGGAGGACAAGCTCCCGCACATTTTCGGGTTCACGCTGCTGGGGGACTT 1740
```


Db 1681 GCGGACCCTCCTGGAGGACAAGCTCCCGCACATTTTCGGGTTCACGCTGCTGGGGGACTT 1740
Qy 1741 CATCTACTGGACTGACTGGCAGCGCCGCAGCATCGAGCGGGTGCACAAGGTCAAGGCCAG 1800
Db 1741 CATCTACTGGACTGACTGGCAGCGCCGCAGCATCGAGCGGGTGCACAAGGTCAAGGCCAG 1800
Qy 1801 CCGGGACGTCATCATTGACCAGCTGCCCGACCTGATGGGGCTCAAAGCTGTGAATGTGGC 1860
Db 1801 CCGGGACGTCATCATTGACCAGCTGCCCGACCTGATGGGGCTCAAAGCTGTGAATGTGGC 1860
Qy 1861 CAAGGTCGTCGGAACCAACCCGTGTGCGGACAGGAACGGGGGGTGCAGCCACCTGTGCTT 1920
Db 1861 CAAGGTCGTCGGAACCAACCCGTGTGCGGACAGGAACGGGGGGTGCAGCCACCTGTGCTT 1920
Qy 1921 CTTCACACCCCACGCAACCCGGTGTGGCTGCCCCATCGGCCTGGAGCTGCTGAGTGACAT 1980
Db 1921 CTTCACACCCCACGCAACCCGGTGTGGCTGCCCCATCGGCCTGGAGCTGCTGAGTGACAT 1980
Qy 1981 GAAGACCTGCATCGTGCCTGAGGCCTTCTTGGTCTTCACCAGCAGAGCCGCCATCCACAG 2040
Db 1981 GAAGACCTGCATCGTGCCTGAGGCCTTCTTGGTCTTCACCAGCAGAGCCGCCATCCACAG 2040
Qy 2041 GATCTCCCTCGAGACCAATAACAACGACGTGGCCATCCCGCTCACGGGCGTCAAGGAGGC 2100
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Db 2101 CTCAGCCCTGGACTTTGATGTGTCCAACAACCACATCTACTGGACAGACGTCAGCCTGAA 2160
Qy 2161 GACCATCAGCCGCGCCTTCATGAACGGGAGCTCGGTGGAGCACGTGGTGGAGTTTGGCCT 2220
Db 2161 GACCATCAGCCGCGCCTTCATGAACGGGAGCTCGGTGGAGCACGTGGTGGAGTTTGGCCT 2220
Qy 2221 TGACTACCCCGAGGGCATGGCCGTTGACTGGATGGGCAAGAACCTCTACTGGGCCGACAC 2280
Db 2221 TGACTACCCCGAGGGCATGGCCGTTGACTGGATGGGCAAGAACCTCTACTGGGCCGACAC 2280
Qy 2281 TGGGACCAACAGAATCGAAGTGGCGCGGCTGGACGGGCAGTTCCGGCAAGTCCTCGTGTG 2340
Db 2281 TGGGACCAACAGAATCGAAGTGGCGCGGCTGGACGGGCAGTTCCGGCAAGTCCTCGTGTG 2340
Qy 2341 GAGGGACTTGGACAACCCGAGGTCGCTGGCCCTGGATCCCACCAAGGGCTACATCTACTG 2400
Db 2341 GAGGGACTTGGACAACCCGAGGTCGCTGGCCCTGGATCCCACCAAGGGCTACATCTACTG 2400
Qy 2401 GACCGAGTGGGGCGGCAAGCCGAGGATCGTGCGGGCCTTCATGGACGGGACCAACTGCAT 2460
Db 2401 GACCGAGTGGGGCGGCAAGCCGAGGATCGTGCGGGCCTTCATGGACGGGACCAACTGCAT 2460
Qy 2461 GACGCTGGTGGACAAGGTGGGCCGGGCCAACGACCTCACCATTGACTACGCTGACCAGCG 2520
Db 2461 GACGCTGGTGGACAAGGTGGGCCGGGCCAACGACCTCACCATTGACTACGCTGACCAGCG 2520
Qy 2521 CCTCTACTGGACCGACCTGGACACCAACATGATCGAGTCGTCCAACATGCTGGGTCAGGA 2580
Db 2521 CCTCTACTGGACCGACCTGGACACCAACATGATCGAGTCGTCCAACATGCTGGGTCAGGA 2580
Qy 2581 GCGGGTCGTGATTGCCGACGATCTCCCGCACCCGTTCGGTCTGACGCAGTACAGCGATTA 2640
Db 2581 GCGGGTCGTGATTGCCGACGATCTCCCGCACCCGTTCGGTCTGACGCAGTACAGCGATTA 2640
Qy 2641 TATCTACTGGACAGACTGGAATCTGCACAGCATTGAGCGGGCCGACAAGACTAGCGGCCG 2700
Db 2641 TATCTACTGGACAGACTGGAATCTGCACAGCATTGAGCGGGCCGACAAGACTAGCGGCCG 2700
Qy 2701 GAACCGCACCCTCATCCAGGGCCACCTGGACTTCGTGATGGACATCCTGGTGTTCCACTC 2760
Db 2701 GAACCGCACCCTCATCCAGGGCCACCTGGACTTCGTGATGGACATCCTGGTGTTCCACTC 2760
Qy 2761 CTCCCGCCAGGATGGCCTCAATGACTGTATGCACAACAACGGGCAGTGTGGGCAGCTGTG 2820
Db 2761 CTCCCGCCAGGATGGCCTCAATGACTGTATGCACAACAACGGGCAGTGTGGGCAGCTGTG 2820
Qy 2821 CCTTGCCATCCCCGGCGGCCACCGCTGCGGCTGCGCCTCACACTACACCCTGGACCCCAG 2880
Db 2821 CCTTGCCATCCCCGGCGGCCACCGCTGCGGCTGCGCCTCACACTACACCCTGGACCCCAG 2880
Qy 2881 CAGCCGCAACTGCAGCCCGCCCACCACCTTCTTGCTGTTCAGCCAGAAATCTGCCATCAG 2940
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Qy 2941 TCGGATGATCCCGGACGACCAGCACAGCCCGGATCTCATCCTGCCCCTGCATGGACTGAG 3000
Db 2941 TCGGATGATCCCGGACGACCAGCACAGCCCGGATCTCATCCTGCCCCTGCATGGACTGAG 3000
Qy 3001 GAACGTCAAAGCCATCGACTATGACCCACTGGACAAGTTCATCTACTGGGTGGATGGGCG 3060
Db 3001 GAACGTCAAAGCCATCGACTATGACCCACTGGACAAGTTCATCTACTGGGTGGATGGGCG 3060
Qy 3061 CCAGAACATCAAGCGAGCCAAGGACGACGGGACCCAGCCCTTTGTTTTGACCTCTCTGAG 3120
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Db 3121 CCAAGGCCAAAACCCAGACAGGCAGCCCCACGACCTCAGCATCGACATCTACAGCCGGAC 3180
Qy 3181 ACTGTTCTGGACGTGCGAGGCCACCAATACCATCAACGTCCACAGGCTGAGCGGGGAAGC 3240
Db 3181 ACTGTTCTGGACGTGCGAGGCCACCAATACCATCAACGTCCACAGGCTGAGCGGGGAAGC 3240
Qy 3241 CATGGGGGTGGTGCTGCGTGGGGACCGCGACAAGCCCAGGGCCATCGTCGTCAACGCGGA 3300
Db 3241 CATGGGGGTGGTGCTGCGTGGGGACCGCGACAAGCCCAGGGCCATCGTCGTCAACGCGGA 3300
Qy 3301 GCGAGGGTACCTGTACTTCACCAACATGCAGGACCGGGCAGCCAAGATCGAACGCGCAGC 3360
Db 3301 GCGAGGGTACCTGTACTTCACCAACATGCAGGACCGGGCAGCCAAGATCGAACGCGCAGC 3360
Qy 3361 CCTGGACGGCACCGAGCGCGAGGTCCTCTTCACCACCGGCCTCATCCGCCCTGTGGCCCT 3420
Db 3361 CCTGGACGGCACCGAGCGCGAGGTCCTCTTCACCACCGGCCTCATCCGCCCTGTGGCCCT 3420
Qy 3421 GGTGGTGGACAACACACTGGGCAAGCTGTTCTGGGTGGACGCGGACCTGAAGCGCATTGA 3480
Db 3421 GGTGGTGGACAACACACTGGGCAAGCTGTTCTGGGTGGACGCGGACCTGAAGCGCATTGA 3480
Qy 3481 GAGCTGTGACCTGTCAGGGGCCAACCGCCTGACCCTGGAGGACGCCAACATCGTGCAGCC 3540
Db 3481 GAGCTGTGACCTGTCAGGGGCCAACCGCCTGACCCTGGAGGACGCCAACATCGTGCAGCC 3540
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Db 3541 TCTGGGCCTGACCATCCTTGGCAAGCATCTCTACTGGATCGACCGCCAGCAGCAGATGAT 3600
Qy 3601 CGAGCGTGTGGAGAAGACCACCGGGGACAAGCGGACTCGCATCCAGGGCCGTGTCGCCCA 3660
Db 3601 CGAGCGTGTGGAGAAGACCACCGGGGACAAGCGGACTCGCATCCAGGGCCGTGTCGCCCA 3660
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Db 3661 CCTCACTGGCATCCATGCAGTGGAGGAAGTCAGCCTGGAGGAGTTCTCAGCCCACCCATG 3720
Qy 3721 TGCCCGTGACAATGGTGGCTGCTCCCACATCTGTATTGCCAAGGGTGATGGGACACCACG 3780
Db 3721 TGCCCGTGACAATGGTGGCTGCTCCCACATCTGTATTGCCAAGGGTGATGGGACACCACG 3780
Qy 3781 GTGCTCATGCCCAGTCCACCTCGTGCTCCTGCAGAACCTGCTGACCTGTGGAGAGCCGCC 3840
Db 3781 GTGCTCATGCCCAGTCCACCTCGTGCTCCTGCAGAACCTGCTGACCTGTGGAGAGCCGCC 3840
Qy 3841 CACCTGCTCCCCGGACCAGTTTGCATGTGCCACAGGGGAGATCGACTGTATCCCCGGGGC 3900
Db 3841 CACCTGCTCCCCGGACCAGTTTGCATGTGCCACAGGGGAGATCGACTGTATCCCCGGGGC 3900

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Qy       3901 CTGGCGCTGTGACGGCTTTCCCGAGTGCGATGACCAGAGCGACGAGGAGGGCTGCCCCGT 3960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       3961 GTGCTCCGCCGCCCAGTTCCCCTGCGCGCGGGGTCAGTGTGTGGACCTGCGCCTGCGCTG 4020
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Qy       4021 CGACGGCGAGGCAGACTGTCAGGACCGCTCAGACGAGGTGGACTGTGACGCCATCTGCCT 4080
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Qy       4081 GCCCAACCAGTTCCGGTGTGCGAGCGGCCAGTGTGTCCTCATCAAACAGCAGTGCGACTC 4140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4081 GCCCAACCAGTTCCGGTGTGCGAGCGGCCAGTGTGTCCTCATCAAACAGCAGTGCGACTC 4140

Qy       4141 CTTCCCCGACTGTATCGACGGCTCCGACGAGCTCATGTGTGAAATCACCAAGCCGCCCTC 4200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4141 CTTCCCCGACTGTATCGACGGCTCCGACGAGCTCATGTGTGAAATCACCAAGCCGCCCTC 4200

Qy       4201 AGACGACAGCCCGGCCCACAGCAGTGCCATCGGGCCCGTCATTGGCATCATCCTCTCTCT 4260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4201 AGACGACAGCCCGGCCCACAGCAGTGCCATCGGGCCCGTCATTGGCATCATCCTCTCTCT 4260

Qy       4261 CTTCGTCATGGGTGGTGTCTATTTTGTGTGCCAGCGCGTGGTGTGCCAGCGCTATGCGGG 4320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4261 CTTCGTCATGGGTGGTGTCTATTTTGTGTGCCAGCGCGTGGTGTGCCAGCGCTATGCGGG 4320

Qy       4321 GGCCAACGGGCCCTTCCCGCACGAGTATGTCAGCGGGACCCCGCACGTGCCCCTCAATTT 4380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4321 GGCCAACGGGCCCTTCCCGCACGAGTATGTCAGCGGGACCCCGCACGTGCCCCTCAATTT 4380

Qy       4381 CATAGCCCCGGGCGGTTCCCAGCATGGCCCCTTCACAGGCATCGCATGCGGAAAGTCCAT 4440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4381 CATAGCCCCGGGCGGTTCCCAGCATGGCCCCTTCACAGGCATCGCATGCGGAAAGTCCAT 4440

Qy       4441 GATGAGCTCCGTGAGCCTGATGGGGGGCCGGGGCGGGGTGCCCCTCTACGACCGGAACCA 4500
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Qy       4621 CTCTTCAAACATTCCGGCCACTGCGAGACCGTACAGGCCCTACATCATTCGAGGAATGGC 4680
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Db       4621 CTCTTCAAACATTCCGGCCACTGCGAGACCGTACAGGCCCTACATCATTCGAGGAATGGC 4680

Qy       4681 GCCCCCGACGACGCCCTGCAGCACCGACGTGTGTGACAGCGACTACAGCGCCAGCCGCTG 4740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4681 GCCCCCGACGACGCCCTGCAGCACCGACGTGTGTGACAGCGACTACAGCGCCAGCCGCTG 4740

Qy       4741 GAAGGCCAGCAAGTACTACCTGGATTTGAACTCGGACTCAGACCCCTATCCACCCCCACC 4800
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4741 GAAGGCCAGCAAGTACTACCTGGATTTGAACTCGGACTCAGACCCCTATCCACCCCCACC 4800

Qy       4801 CACGCCCCACAGCCAGTACCTGTCGGCGGAGGACAGCTGCCCGCCCTCGCCCGCCACCGA 4860
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4801 CACGCCCCACAGCCAGTACCTGTCGGCGGAGGACAGCTGCCCGCCCTCGCCCGCCACCGA 4860

Qy       4861 GAGGAGCTACTTCCATCTCTTCCCGCCCCCTCCGTCCCCCTGCACGGACTCATCCTGACC 4920
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4861 GAGGAGCTACTTCCATCTCTTCCCGCCCCCTCCGTCCCCCTGCACGGACTCATCCTGACC 4920

Qy       4921 TCGGCCGGGCCACTCTGGCTTCTCTGTGCCCCTGTAAATAGTTTTAAATATGAACAAAGA 4980
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4921 TCGGCCGGGCCACTCTGGCTTCTCTGTGCCCCTGTAAATAGTTTTAAATATGAACAAAGA 4980

Qy       4981 AAAAAATATATTTTATGATTTAAAAAATAAATATAATTGGGATTTTAAAAACATGAGAAA 5040
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4981 AAAAAATATATTTTATGATTTAAAAAATAAATATAATTGGGATTTTAAAAACATGAGAAA 5040

Qy       5041 TGTGAACTGTGATGGGGTGGGCAGGGCTGGGAGAACTTTGTACAGTGGAGAAATATTTAT 5100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5041 TGTGAACTGTGATGGGGTGGGCAGGGCTGGGAGAACTTTGTACAGTGGAGAAATATTTAT 5100

Qy       5101 AAACTTAATTTTGTAAAACA 5120
             ||||||||||||||||||||
Db       5101 AAACTTAATTTTGTAAAACA 5120
```

RESULT 12
ACC46078
ID ACC46078 standard; DNA; 5278 BP.
XX
AC ACC46078;
XX
DT 02-JUN-2003 (first entry)
XX
DE Mouse HBMGI_2AS vector insert.
XX
KW Mouse; high bone mass; HBM; LRP5; LRP6; transgenic; bone mass modulation;
KW gene therapy; bone density modulation; bone strength; trabecular number;
KW bone size; bone tissue connectivity; bone disease; osteoporosis;
KW osteomalacia; rickets; Paget's disease; neoplasm of the bone; gene; ds.
XX
OS Mus sp.
XX
PN WO200292764-A2.
XX
PD 21-NOV-2002.
XX
PF 13-MAY-2002; 2002WO-US014876.
XX
PR 11-MAY-2001; 2001US-0290071P.
PR 17-MAY-2001; 2001US-0291311P.
PR 01-FEB-2002; 2002US-0353058P.
PR 04-MAR-2002; 2002US-0361293P.
XX
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (AMHP) WYETH.
XX
PI Babij P, Bex FJ, Yaworsky PJ, Bodine PV;
XX
DR WPI; 2003-129278/12.
XX
PT New transgenic animals (e.g. mice), useful as models for studying bone
PT density modulation, developing drugs for treating or preventing bone
PT diseases (e.g. osteoporosis), or diagnosing diseases characterized by
PT reduced bone density.
XX
PS Disclosure; Fig 24; 603pp; English.
XX
CC The invention relates to novel transgenic animals expressing the high
CC bone mass (HBM) gene, expressing the corresponding wild type HBM gene,
CC comprising an alteration of the gene encoding LRP5 or LRP6, or expressing
CC an LRP5 that is modulated by an altered gene control sequence introduced
CC by homologous or non-homologous recombination. The transgenic animals are
CC for the study of bone density modulation or bone mass modulation. The
CC invention has osteopathic and cytostatic activity. The polynucleotides of
CC the invention may have a use in gene therapy. The transgenic animals and
CC nucleic acids are for the study of bone density modulation, where the
CC bone mass is modulated relative to non-transgenic animals of the same
CC species in more than one parameter selected from bone density, bone
CC strength, trabecular number, bone size, or bone tissue connectivity. The
CC transgenic animals, nucleic acids and methods are useful for identifying
CC molecules involved in bone development, and for developing pharmaceutical
CC compositions, which may be employed for treating or preventing bone
CC diseases, e.g. osteoporosis, osteomalacia, rickets, Paget's disease, or
CC neoplasms of the bone. The transgenic animals and nucleic acids are also
CC useful in methods for diagnosing diseases involved in bone development,

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CC   or characterised by reduced bone density or mass. The present sequence is
CC   used in the exemplification of the invention
XX
SQ   Sequence 5278 BP; 1162 A; 1672 C; 1561 G; 883 T; 0 U; 0 Other;

  Query Match             99.9%;  Score 5116.8;  DB 8;  Length 5278;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 5118;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ACTAAAGCGCCGCCGCCGCGCCATGGAGCCCGAGTGAGCGCGGCGCGGGCCCGTCCGGCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         30 ACTAAAGCGCCGCCGCCGCGCCATGGAGCCCGAGTGAGCGCGGCGCGGGCCCGTCCGGCC 89

Qy         61 GCCGGACAACATGGAGGCAGCGCCGCCCGGGCCGCCGTGGCCGCTGCTGCTGCTGCTGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         90 GCCGGACAACATGGAGGCAGCGCCGCCCGGGCCGCCGTGGCCGCTGCTGCTGCTGCTGCT 149

Qy        121 GCTGCTGCTGGCGCTGTGCGGCTGCCCGGCCCCCGCCGCGGCCTCGCCGCTCCTGCTATT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        150 GCTGCTGCTGGCGCTGTGCGGCTGCCCGGCCCCCGCCGCGGCCTCGCCGCTCCTGCTATT 209

Qy        181 TGCCAACCGCCGGGACGTACGGCTGGTGGACGCCGGCGGAGTCAAGCTGGAGTCCACCAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        210 TGCCAACCGCCGGGACGTACGGCTGGTGGACGCCGGCGGAGTCAAGCTGGAGTCCACCAT 269

Qy        241 CGTGGTCAGCGGCCTGGAGGATGCGGCCGCAGTGGACTTCCAGTTTTCCAAGGGAGCCGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        270 CGTGGTCAGCGGCCTGGAGGATGCGGCCGCAGTGGACTTCCAGTTTTCCAAGGGAGCCGT 329

Qy        301 GTACTGGACAGACGTGAGCGAGGAGGCCATCAAGCAGACCTACCTGAACCAGACGGGGGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        330 GTACTGGACAGACGTGAGCGAGGAGGCCATCAAGCAGACCTACCTGAACCAGACGGGGGC 389

Qy        361 CGCCGTGCAGAACGTGGTCATCTCCGGCCTGGTCTCTCCCGACGGCCTCGCCTGCGACTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        390 CGCCGTGCAGAACGTGGTCATCTCCGGCCTGGTCTCTCCCGACGGCCTCGCCTGCGACTG 449

Qy        421 GGTGGGCAAGAAGCTGTACTGGACGGACTCAGAGACCAACCGCATCGAGGTGGCCAACCT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        450 GGTGGGCAAGAAGCTGTACTGGACGGACTCAGAGACCAACCGCATCGAGGTGGCCAACCT 509

Qy        481 CAATGGCACATCCCGGAAGGTGCTCTTCTGGCAGGACCTTGACCAGCCGAGGGCCATCGC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        510 CAATGGCACATCCCGGAAGGTGCTCTTCTGGCAGGACCTTGACCAGCCGAGGGCCATCGC 569

Qy        541 CTTGGACCCCGCTCACGGGTACATGTACTGGACAGACTGGGTTGAGACGCCCCGGATTGA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        570 CTTGGACCCCGCTCACGGGTACATGTACTGGACAGACTGGGTTGAGACGCCCCGGATTGA 629

Qy        601 GCGGGCAGGGATGGATGGCAGCACCCGGAAGATCATTGTGGACTCGGACATTTACTGGCC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        630 GCGGGCAGGGATGGATGGCAGCACCCGGAAGATCATTGTGGACTCGGACATTTACTGGCC 689

Qy        661 CAATGGACTGACCATCGACCTGGAGGAGCAGAAGCTCTACTGGGCTGACGCCAAGCTCAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        690 CAATGGACTGACCATCGACCTGGAGGAGCAGAAGCTCTACTGGGCTGACGCCAAGCTCAG 749

Qy        721 CTTCATCCACCGTGCCAACCTGGACGGCTCGTTCCGGCAGAAGGTGGTGGAGGGCAGCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        750 CTTCATCCACCGTGCCAACCTGGACGGCTCGTTCCGGCAGAAGGTGGTGGAGGGCAGCCT 809

Qy        781 GACGCACCCCTTCGCCCTGACGCTCTCCGGGGACACTCTGTACTGGACAGACTGGCAGAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        810 GACGCACCCCTTCGCCCTGACGCTCTCCGGGGACACTCTGTACTGGACAGACTGGCAGAC 869

Qy        841 CCGCTCCATCCATGCCTGCAACAAGCGCACTGGGGGGAAGAGGAAGGAGATCCTGAGTGC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        870 CCGCTCCATCCATGCCTGCAACAAGCGCACTGGGGGGAAGAGGAAGGAGATCCTGAGTGC 929

Qy        901 CCTCTACTCACCCATGGACATCCAGGTGCTGAGCCAGGAGCGGCAGCCTTTCTTCCACAC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        930 CCTCTACTCACCCATGGACATCCAGGTGCTGAGCCAGGAGCGGCAGCCTTTCTTCCACAC 989

Qy        961 TCGCTGTGAGGAGGACAATGGCGGCTGCTCCCACCTGTGCCTGCTGTCCCCAAGCGAGCC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        990 TCGCTGTGAGGAGGACAATGGCGGCTGCTCCCACCTGTGCCTGCTGTCCCCAAGCGAGCC 1049

Qy       1021 TTTCTACACATGCGCCTGCCCCACGGGTGTGCAGCTGCAGGACAACGGCAGGACGTGTAA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1050 TTTCTACACATGCGCCTGCCCCACGGGTGTGCAGCTGCAGGACAACGGCAGGACGTGTAA 1109

Qy       1081 GGCAGGAGCCGAGGAGGTGCTGCTGCTGGCCCGGCGGACGGACCTACGGAGGATCTCGCT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1110 GGCAGGAGCCGAGGAGGTGCTGCTGCTGGCCCGGCGGACGGACCTACGGAGGATCTCGCT 1169

Qy       1141 GGACACGCCGGACTTCACCGACATCGTGCTGCAGGTGGACGACATCCGGCACGCCATTGC 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1170 GGACACGCCGGACTTCACCGACATCGTGCTGCAGGTGGACGACATCCGGCACGCCATTGC 1229

Qy       1201 CATCGACTACGACCCGCTAGAGGGCTATGTCTACTGGACAGATGACGAGGTGCGGGCCAT 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1230 CATCGACTACGACCCGCTAGAGGGCTATGTCTACTGGACAGATGACGAGGTGCGGGCCAT 1289

Qy       1261 CCGCAGGGCGTACCTGGACGGGTCTGGGGCGCAGACGCTGGTCAACACCGAGATCAACGA 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1290 CCGCAGGGCGTACCTGGACGGGTCTGGGGCGCAGACGCTGGTCAACACCGAGATCAACGA 1349

Qy       1321 CCCCGATGGCATCGCGGTCGACTGGGTGGCCCGAAACCTCTACTGGACCGACACGGGCAC 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1350 CCCCGATGGCATCGCGGTCGACTGGGTGGCCCGAAACCTCTACTGGACCGACACGGGCAC 1409

Qy       1381 GGACCGCATCGAGGTGACGCGCCTCAACGGCACCTCCCGCAAGATCCTGGTGTCGGAGGA 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1410 GGACCGCATCGAGGTGACGCGCCTCAACGGCACCTCCCGCAAGATCCTGGTGTCGGAGGA 1469

Qy       1441 CCTGGACGAGCCCCGAGCCATCGCACTGCACCCCGTGATGGGCCTCATGTACTGGACAGA 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1470 CCTGGACGAGCCCCGAGCCATCGCACTGCACCCCGTGATGGGCCTCATGTACTGGACAGA 1529

Qy       1501 CTGGGGAGAGAACCCTAAAATCGAGTGTGCCAACTTGGATGGGCAGGAGCGGCGTGTGCT 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1530 CTGGGGAGAGAACCCTAAAATCGAGTGTGCCAACTTGGATGGGCAGGAGCGGCGTGTGCT 1589

Qy       1561 GGTCAATGCCTCCCTCGGGTGGCCCAACGGCCTGGCCCTGGACCTGCAGGAGGGGAAGCT 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1590 GGTCAATGCCTCCCTCGGGTGGCCCAACGGCCTGGCCCTGGACCTGCAGGAGGGGAAGCT 1649

Qy       1621 CTACTGGGGAGACGCCAAGACAGACAAGATCGAGGTGATCAATGTTGATGGGACGAAGAG 1680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1650 CTACTGGGGAGACGCCAAGACAGACAAGATCGAGGTGATCAATGTTGATGGGACGAAGAG 1709

Qy       1681 GCGGACCCTCCTGGAGGACAAGCTCCCGCACATTTTCGGGTTCACGCTGCTGGGGGACTT 1740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1710 GCGGACCCTCCTGGAGGACAAGCTCCCGCACATTTTCGGGTTCACGCTGCTGGGGGACTT 1769

Qy       1741 CATCTACTGGACTGACTGGCAGCGCCGCAGCATCGAGCGGGTGCACAAGGTCAAGGCCAG 1800
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1770 CATCTACTGGACTGACTGGCAGCGCCGCAGCATCGAGCGGGTGCACAAGGTCAAGGCCAG 1829

Qy       1801 CCGGGACGTCATCATTGACCAGCTGCCCGACCTGATGGGGCTCAAAGCTGTGAATGTGGC 1860
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1830 CCGGGACGTCATCATTGACCAGCTGCCCGACCTGATGGGGCTCAAAGCTGTGAATGTGGC 1889

Qy       1861 CAAGGTCGTCGGAACCAACCCGTGTGCGGACAGGAACGGGGGGTGCAGCCACCTGTGCTT 1920
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1890 CAAGGTCGTCGGAACCAACCCGTGTGCGGACAGGAACGGGGGGTGCAGCCACCTGTGCTT 1949

Qy       1921 CTTCACACCCCACGCAACCCGGTGTGGCTGCCCCATCGGCCTGGAGCTGCTGAGTGACAT 1980
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1950 CTTCACACCCCACGCAACCCGGTGTGGCTGCCCCATCGGCCTGGAGCTGCTGAGTGACAT 2009

Qy       1981 GAAGACCTGCATCGTGCCTGAGGCCTTCTTGGTCTTCACCAGCAGAGCCGCCATCCACAG 2040
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2010 GAAGACCTGCATCGTGCCTGAGGCCTTCTTGGTCTTCACCAGCAGAGCCGCCATCCACAG 2069

Qy       2041 GATCTCCCTCGAGACCAATAACAACGACGTGGCCATCCCGCTCACGGGCGTCAAGGAGGC 2100
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Db      2070 GATCTCCCTCGAGACCAATAACAACGACGTGGCCATCCCGCTCACGGGCGTCAAGGAGGC 2129
Qy      2101 CTCAGCCCTGGACTTTGATGTGTCCAACAACCACATCTACTGGACAGACGTCAGCCTGAA 2160
Db      2130 CTCAGCCCTGGACTTTGATGTGTCCAACAACCACATCTACTGGACAGACGTCAGCCTGAA 2189
Qy      2161 GACCATCAGCCGCGCCTTCATGAACGGGAGCTCGGTGGAGCACGTGGTGGAGTTTGGCCT 2220
Db      2190 GACCATCAGCCGCGCCTTCATGAACGGGAGCTCGGTGGAGCACGTGGTGGAGTTTGGCCT 2249
Qy      2221 TGACTACCCCGAGGGCATGGCCGTTGACTGGATGGGCAAGAACCTCTACTGGGCCGACAC 2280
Db      2250 TGACTACCCCGAGGGCATGGCCGTTGACTGGATGGGCAAGAACCTCTACTGGGCCGACAC 2309
Qy      2281 TGGGACCAACAGAATCGAAGTGGCGCGGCTGGACGGGCAGTTCCGGCAAGTCCTCGTGTG 2340
Db      2310 TGGGACCAACAGAATCGAAGTGGCGCGGCTGGACGGGCAGTTCCGGCAAGTCCTCGTGTG 2369
Qy      2341 GAGGGACTTGGACAACCCGAGGTCGCTGGCCCTGGATCCCACCAAGGGCTACATCTACTG 2400
Db      2370 GAGGGACTTGGACAACCCGAGGTCGCTGGCCCTGGATCCCACCAAGGGCTACATCTACTG 2429
Qy      2401 GACCGAGTGGGGCGGCAAGCCGAGGATCGTGCGGGCCTTCATGGACGGGACCAACTGCAT 2460
Db      2430 GACCGAGTGGGGCGGCAAGCCGAGGATCGTGCGGGCCTTCATGGACGGGACCAACTGCAT 2489
Qy      2461 GACGCTGGTGGACAAGGTGGGCCGGGCCAACGACCTCACCATTGACTACGCTGACCAGCG 2520
Db      2490 GACGCTGGTGGACAAGGTGGGCCGGGCCAACGACCTCACCATTGACTACGCTGACCAGCG 2549
Qy      2521 CCTCTACTGGACCGACCTGGACACCAACATGATCGAGTCGTCCAACATGCTGGGTCAGGA 2580
Db      2550 CCTCTACTGGACCGACCTGGACACCAACATGATCGAGTCGTCCAACATGCTGGGTCAGGA 2609
Qy      2581 GCGGGTCGTGATTGCCGACGATCTCCCGCACCCGTTCGGTCTGACGCAGTACAGCGATTA 2640
Db      2610 GCGGGTCGTGATTGCCGACGATCTCCCGCACCCGTTCGGTCTGACGCAGTACAGCGATTA 2669
Qy      2641 TATCTACTGGACAGACTGGAATCTGCACAGCATTGAGCGGGCCGACAAGACTAGCGGCCG 2700
Db      2670 TATCTACTGGACAGACTGGAATCTGCACAGCATTGAGCGGGCCGACAAGACTAGCGGCCG 2729
Qy      2701 GAACCGCACCCTCATCCAGGGCCACCTGGACTTCGTGATGGACATCCTGGTGTTCCACTC 2760
Db      2730 GAACCGCACCCTCATCCAGGGCCACCTGGACTTCGTGATGGACATCCTGGTGTTCCACTC 2789
Qy      2761 CTCCCGCCAGGATGGCCTCAATGACTGTATGCACAACAACGGGCAGTGTGGGCAGCTGTG 2820
Db      2790 CTCCCGCCAGGATGGCCTCAATGACTGTATGCACAACAACGGGCAGTGTGGGCAGCTGTG 2849
Qy      2821 CCTTGCCATCCCCGGCGGCCACCGCTGCGGCTGCGCCTCACACTACACCCTGGACCCCAG 2880
Db      2850 CCTTGCCATCCCCGGCGGCCACCGCTGCGGCTGCGCCTCACACTACACCCTGGACCCCAG 2909
Qy      2881 CAGCCGCAACTGCAGCCCGCCCACCACCTTCTTGCTGTTCAGCCAGAAATCTGCCATCAG 2940
Db      2910 CAGCCGCAACTGCAGCCCGCCCACCACCTTCTTGCTGTTCAGCCAGAAATCTGCCATCAG 2969
Qy      2941 TCGGATGATCCCGGACGACCAGCACAGCCCGGATCTCATCCTGCCCCTGCATGGACTGAG 3000
Db      2970 TCGGATGATCCCGGACGACCAGCACAGCCCGGATCTCATCCTGCCCCTGCATGGACTGAG 3029
Qy      3001 GAACGTCAAAGCCATCGACTATGACCCACTGGACAAGTTCATCTACTGGGTGGATGGGCG 3060
Db      3030 GAACGTCAAAGCCATCGACTATGACCCACTGGACAAGTTCATCTACTGGGTGGATGGGCG 3089
Qy      3061 CCAGAACATCAAGCGAGCCAAGGACGACGGGACCCAGCCCTTTGTTTTGACCTCTCTGAG 3120
Db      3090 CCAGAACATCAAGCGAGCCAAGGACGACGGGACCCAGCCCTTTGTTTTGACCTCTCTGAG 3149
Qy      3121 CCAAGGCCAAAACCCAGACAGGCAGCCCCACGACCTCAGCATCGACATCTACAGCCGGAC 3180
Db      3150 CCAAGGCCAAAACCCAGACAGGCAGCCCCACGACCTCAGCATCGACATCTACAGCCGGAC 3209
Qy      3181 ACTGTTCTGGACGTGCGAGGCCACCAATACCATCAACGTCCACAGGCTGAGCGGGGAAGC 3240
Db      3210 ACTGTTCTGGACGTGCGAGGCCACCAATACCATCAACGTCCACAGGCTGAGCGGGGAAGC 3269
Qy      3241 CATGGGGGTGGTGCTGCGTGGGGACCGCGACAAGCCCAGGGCCATCGTCGTCAACGCGGA 3300
Db      3270 CATGGGGGTGGTGCTGCGTGGGGACCGCGACAAGCCCAGGGCCATCGTCGTCAACGCGGA 3329
Qy      3301 GCGAGGGTACCTGTACTTCACCAACATGCAGGACCGGGCAGCCAAGATCGAACGCGCAGC 3360
Db      3330 GCGAGGGTACCTGTACTTCACCAACATGCAGGACCGGGCAGCCAAGATCGAACGCGCAGC 3389
Qy      3361 CCTGGACGGCACCGAGCGCGAGGTCCTCTTCACCACCGGCCTCATCCGCCCTGTGGCCCT 3420
Db      3390 CCTGGACGGCACCGAGCGCGAGGTCCTCTTCACCACCGGCCTCATCCGCCCTGTGGCCCT 3449
Qy      3421 GGTGGTGGACAACACACTGGGCAAGCTGTTCTGGGTGGACGCGGACCTGAAGCGCATTGA 3480
Db      3450 GGTGGTAGACAACACACTGGGCAAGCTGTTCTGGGTGGACGCGGACCTGAAGCGCATTGA 3509
Qy      3481 GAGCTGTGACCTGTCAGGGGCCAACCGCCTGACCCTGGAGGACGCCAACATCGTGCAGCC 3540
Db      3510 GAGCTGTGACCTGTCAGGGGCCAACCGCCTGACCCTGGAGGACGCCAACATCGTGCAGCC 3569
Qy      3541 TCTGGGCCTGACCATCCTTGGCAAGCATCTCTACTGGATCGACCGCCAGCAGCAGATGAT 3600
Db      3570 TCTGGGCCTGACCATCCTTGGCAAGCATCTCTACTGGATCGACCGCCAGCAGCAGATGAT 3629
Qy      3601 CGAGCGTGTGGAGAAGACCACCGGGGACAAGCGGACTCGCATCCAGGGCCGTGTCGCCCA 3660
Db      3630 CGAGCGTGTGGAGAAGACCACCGGGGACAAGCGGACTCGCATCCAGGGCCGTGTCGCCCA 3689
Qy      3661 CCTCACTGGCATCCATGCAGTGGAGGAAGTCAGCCTGGAGGAGTTCTCAGCCCACCCATG 3720
Db      3690 CCTCACTGGCATCCATGCAGTGGAGGAAGTCAGCCTGGAGGAGTTCTCAGCCCACCCATG 3749
Qy      3721 TGCCCGTGACAATGGTGGCTGCTCCCACATCTGTATTGCCAAGGGTGATGGGACACCACG 3780
Db      3750 TGCCCGTGACAATGGTGGCTGCTCCCACATCTGTATTGCCAAGGGTGATGGGACACCACG 3809
Qy      3781 GTGCTCATGCCCAGTCCACCTCGTGCTCCTGCAGAACCTGCTGACCTGTGGAGAGCCGCC 3840
Db      3810 GTGCTCATGCCCAGTCCACCTCGTGCTCCTGCAGAACCTGCTGACCTGTGGAGAGCCGCC 3869
Qy      3841 CACCTGCTCCCCGGACCAGTTTGCATGTGCCACAGGGGAGATCGACTGTATCCCCGGGGC 3900
Db      3870 CACCTGCTCCCCGGACCAGTTTGCATGTGCCACAGGGGAGATCGACTGTATCCCCGGGGC 3929
Qy      3901 CTGGCGCTGTGACGGCTTTCCCGAGTGCGATGACCAGAGCGACGAGGAGGGCTGCCCCGT 3960
Db      3930 CTGGCGCTGTGACGGCTTTCCCGAGTGCGATGACCAGAGCGACGAGGAGGGCTGCCCCGT 3989
Qy      3961 GTGCTCCGCCGCCCAGTTCCCCTGCGCGCGGGGTCAGTGTGTGGACCTGCGCCTGCGCTG 4020
Db      3990 GTGCTCCGCCGCCCAGTTCCCCTGCGCGCGGGGTCAGTGTGTGGACCTGCGCCTGCGCTG 4049
Qy      4021 CGACGGCGAGGCAGACTGTCAGGACCGCTCAGACGAGGTGGACTGTGACGCCATCTGCCT 4080
Db      4050 CGACGGCGAGGCAGACTGTCAGGACCGCTCAGACGAGGCGGACTGTGACGCCATCTGCCT 4109
Qy      4081 GCCCAACCAGTTCCGGTGTGCGAGCGGCCAGTGTGTCCTCATCAAACAGCAGTGCGACTC 4140
Db      4110 GCCCAACCAGTTCCGGTGTGCGAGCGGCCAGTGTGTCCTCATCAAACAGCAGTGCGACTC 4169
Qy      4141 CTTCCCCGACTGTATCGACGGCTCCGACGAGCTCATGTGTGAAATCACCAAGCCGCCCTC 4200
Db      4170 CTTCCCCGACTGTATCGACGGCTCCGACGAGCTCATGTGTGAAATCACCAAGCCGCCCTC 4229
Qy      4201 AGACGACAGCCCGGCCCACAGCAGTGCCATCGGGCCCGTCATTGGCATCATCCTCTCTCT 4260
Db      4230 AGACGACAGCCCGGCCCACAGCAGTGCCATCGGGCCCGTCATTGGCATCATCCTCTCTCT 4289
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Qy       4261 CTTCGTCATGGGTGGTGTCTATTTTGTGTGCCAGCGCGTGGTGTGCCAGCGCTATGCGGG 4320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4290 CTTCGTCATGGGTGGTGTCTATTTTGTGTGCCAGCGCGTGGTGTGCCAGCGCTATGCGGG 4349

Qy       4321 GGCCAACGGGCCCTTCCCGCACGAGTATGTCAGCGGGACCCCGCACGTGCCCCTCAATTT 4380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4350 GGCCAACGGGCCCTTCCCGCACGAGTATGTCAGCGGGACCCCGCACGTGCCCCTCAATTT 4409

Qy       4381 CATAGCCCCGGGCGGTTCCCAGCATGGCCCCTTCACAGGCATCGCATGCGGAAAGTCCAT 4440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4410 CATAGCCCCGGGCGGTTCCCAGCATGGCCCCTTCACAGGCATCGCATGCGGAAAGTCCAT 4469

Qy       4441 GATGAGCTCCGTGAGCCTGATGGGGGGCCGGGGCGGGGTGCCCCTCTACGACCGGAACCA 4500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4470 GATGAGCTCCGTGAGCCTGATGGGGGGCCGGGGCGGGGTGCCCCTCTACGACCGGAACCA 4529

Qy       4501 CGTCACAGGGGCCTCGTCCAGCAGCTCGTCCAGCACGAAGGCCACGCTGTACCCGCCGAT 4560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4530 CGTCACAGGGGCCTCGTCCAGCAGCTCGTCCAGCACGAAGGCCACGCTGTACCCGCCGAT 4589

Qy       4561 CCTGAACCCGCCGCCCTCCCCGGCCACGGACCCCTCCCTGTACAACATGGACATGTTCTA 4620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4590 CCTGAACCCGCCGCCCTCCCCGGCCACGGACCCCTCCCTGTACAACATGGACATGTTCTA 4649

Qy       4621 CTCTTCAAACATTCCGGCCACTGCGAGACCGTACAGGCCCTACATCATTCGAGGAATGGC 4680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4650 CTCTTCAAACATTCCGGCCACTGCGAGACCGTACAGGCCCTACATCATTCGAGGAATGGC 4709

Qy       4681 GCCCCCGACGACGCCCTGCAGCACCGACGTGTGTGACAGCGACTACAGCGCCAGCCGCTG 4740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4710 GCCCCCGACGACGCCCTGCAGCACCGACGTGTGTGACAGCGACTACAGCGCCAGCCGCTG 4769

Qy       4741 GAAGGCCAGCAAGTACTACCTGGATTTGAACTCGGACTCAGACCCCTATCCACCCCCACC 4800
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4770 GAAGGCCAGCAAGTACTACCTGGATTTGAACTCGGACTCAGACCCCTATCCACCCCCACC 4829

Qy       4801 CACGCCCCCACAGCCAGTACCTGTCGGCGGAGGACAGCTGCCCGCCCTCGCCCGCCACCGA 4860
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4830 CACGCCCCCACAGCCAGTACCTGTCGGCGGAGGACAGCTGCCCGCCCTCGCCCGCCACCGA 4889

Qy       4861 GAGGAGCTACTTCCATCTCTTCCCGCCCCCTCCGTCCCCCTGCACGGACTCATCCTGACC 4920
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4890 GAGGAGCTACTTCCATCTCTTCCCGCCCCCTCCGTCCCCCTGCACGGACTCATCCTGACC 4949

Qy       4921 TCGGCCGGGCCACTCTGGCTTCTCTGTGCCCCTGTAAATAGTTTTAAATATGAACAAAGA 4980
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4950 TCGGCCGGGCCACTCTGGCTTCTCTGTGCCCCTGTAAATAGTTTTAAATATGAACAAAGA 5009

Qy       4981 AAAAAATATATTTTATGATTTAAAAAATAAATATAATTGGGATTTTAAAAACATGAGAAA 5040
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5010 AAAAAATATATTTTATGATTTAAAAAATAAATATAATTGGGATTTTAAAAACATGAGAAA 5069

Qy       5041 TGTGAACTGTGATGGGGTGGGCAGGGCTGGGAGAACTTTGTACAGTGGAGAAATATTTAT 5100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5070 TGTGAACTGTGATGGGGTGGGCAGGGCTGGGAGAACTTTGTACAGTGGAGAAATATTTAT 5129

Qy       5101 AAACTTAATTTTGTAAAACA 5120
             ||||||||||||||||||||
Db       5130 AAACTTAATTTTGTAAAACA 5149
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RESULT 13
ADB98796
ID ADB98796 standard; DNA; 5278 BP.
XX
AC ADB98796;
XX
DT 04-DEC-2003 (first entry)
XX
DE Mouse HBMGI-2AS DNA sequence.
XX
KW Osteopathic; Gene therapy; High Bone Mass; HBM; LRP5; Zmax1; LRP6;
KW bone mass modulation; osteoporosis; mouse; ds.
XX
OS Mus sp.
XX
PN WO200292000-A2.
XX
PD 21-NOV-2002.
XX
PF 13-MAY-2002; 2002WO-US014877.
XX
PR 11-MAY-2001; 2001US-0290071P.
PR 17-MAY-2001; 2001US-0291311P.
PR 01-FEB-2002; 2002US-0353058P.
PR 04-MAR-2002; 2002US-0361293P.
XX
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (AMHP) WYETH.
XX
PI Allen K, Anisowicz A, Graham JR, Morales A, Yaworsky PJ, Liu W;
XX
DR WPI; 2003-129214/12.
XX
PT New nucleic acid comprising a mutation in LRP5 or LRP6, useful for
PT diagnosing a HBM-like phenotype in a subject and for preparing a
PT composition for modulating bone mass and/or lipid levels in a subject
PT suffering from e.g. osteoporosis.
XX
PS Disclosure; Fig 24; 629pp; English.
XX
CC The present invention relates to High Bone Mass (HBM), LRP5 (Zmax1) and
CC LRP6 mutants, which results in a HBM-like phenotype when expressed in a
CC cell. The HBM-like phenotype results in bone mass modulation and/or lipid
CC level modulation. The invention is useful for diagnosing a HBM-like
CC phenotype in a subject and for preparing a composition for modulating
CC bone mass and/or lipid levels in a subject suffering from e.g.
CC osteoporosis. The present sequence was used to illustrate the invention.
XX
SQ Sequence 5278 BP; 1162 A; 1672 C; 1561 G; 883 T; 0 U; 0 Other;

Query Match 99.9%; Score 5116.8; DB 10; Length 5278;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5118; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy          1 ACTAAAGCGCCGCCGCCGCGCCATGGAGCCCGAGTGAGCGCGGCGCGGGCCCGTCCGGCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         30 ACTAAAGCGCCGCCGCCGCGCCATGGAGCCCGAGTGAGCGCGGCGCGGGCCCGTCCGGCC 89

Qy         61 GCCGGACAACATGGAGGCAGCGCCGCCCGGGCCGCCGTGGCCGCTGCTGCTGCTGCTGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         90 GCCGGACAACATGGAGGCAGCGCCGCCCGGGCCGCCGTGGCCGCTGCTGCTGCTGCTGCT 149

Qy        121 GCTGCTGCTGGCGCTGTGCGGCTGCCCGGCCCCCGCCGCGGCCTCGCCGCTCCTGCTATT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        150 GCTGCTGCTGGCGCTGTGCGGCTGCCCGGCCCCCGCCGCGGCCTCGCCGCTCCTGCTATT 209

Qy        181 TGCCAACCGCCGGGACGTACGGCTGGTGGACGCCGGCGGAGTCAAGCTGGAGTCCACCAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        210 TGCCAACCGCCGGGACGTACGGCTGGTGGACGCCGGCGGAGTCAAGCTGGAGTCCACCAT 269

Qy        241 CGTGGTCAGCGGCCTGGAGGATGCGGCCGCAGTGGACTTCCAGTTTTCCAAGGGAGCCGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        270 CGTGGTCAGCGGCCTGGAGGATGCGGCCGCAGTGGACTTCCAGTTTTCCAAGGGAGCCGT 329

Qy        301 GTACTGGACAGACGTGAGCGAGGAGGCCATCAAGCAGACCTACCTGAACCAGACGGGGGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        330 GTACTGGACAGACGTGAGCGAGGAGGCCATCAAGCAGACCTACCTGAACCAGACGGGGGC 389

Qy        361 CGCCGTGCAGAACGTGGTCATCTCCGGCCTGGTCTCTCCCGACGGCCTCGCCTGCGACTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        390 CGCCGTGCAGAACGTGGTCATCTCCGGCCTGGTCTCTCCCGACGGCCTCGCCTGCGACTG 449

Qy        421 GGTGGGCAAGAAGCTGTACTGGACGGACTCAGAGACCAACCGCATCGAGGTGGCCAACCT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        450 GGTGGGCAAGAAGCTGTACTGGACGGACTCAGAGACCAACCGCATCGAGGTGGCCAACCT 509

Qy        481 CAATGGCACATCCCGGAAGGTGCTCTTCTGGCAGGACCTTGACCAGCCGAGGGCCATCGC 540

Db        510 CAATGGCACATCCCGGAAGGTGCTCTTCTGGCAGGACCTTGACCAGCCGAGGGCCATCGC 569

Qy        541 CTTGGACCCCGCTCACGGGTACATGTACTGGACAGACTGGGTTGAGACGCCCCGGATTGA 600

Db        570 CTTGGACCCCGCTCACGGGTACATGTACTGGACAGACTGGGTTGAGACGCCCCGGATTGA 629

Qy        601 GCGGGCAGGGATGGATGGCAGCACCCGGAAGATCATTGTGGACTCGGACATTTACTGGCC 660

Db        630 GCGGGCAGGGATGGATGGCAGCACCCGGAAGATCATTGTGGACTCGGACATTTACTGGCC 689

Qy        661 CAATGGACTGACCATCGACCTGGAGGAGCAGAAGCTCTACTGGGCTGACGCCAAGCTCAG 720

Db        690 CAATGGACTGACCATCGACCTGGAGGAGCAGAAGCTCTACTGGGCTGACGCCAAGCTCAG 749

Qy        721 CTTCATCCACCGTGCCAACCTGGACGGCTCGTTCCGGCAGAAGGTGGTGGAGGGCAGCCT 780

Db        750 CTTCATCCACCGTGCCAACCTGGACGGCTCGTTCCGGCAGAAGGTGGTGGAGGGCAGCCT 809

Qy        781 GACGCACCCCTTCGCCCTGACGCTCTCCGGGGACACTCTGTACTGGACAGACTGGCAGAC 840

Db        810 GACGCACCCCTTCGCCCTGACGCTCTCCGGGGACACTCTGTACTGGACAGACTGGCAGAC 869

Qy        841 CCGCTCCATCCATGCCTGCAACAAGCGCACTGGGGGGAAGAGGAAGGAGATCCTGAGTGC 900

Db        870 CCGCTCCATCCATGCCTGCAACAAGCGCACTGGGGGGAAGAGGAAGGAGATCCTGAGTGC 929

Qy        901 CCTCTACTCACCCATGGACATCCAGGTGCTGAGCCAGGAGCGGCAGCCTTTCTTCCACAC 960

Db        930 CCTCTACTCACCCATGGACATCCAGGTGCTGAGCCAGGAGCGGCAGCCTTTCTTCCACAC 989

Qy        961 TCGCTGTGAGGAGGACAATGGCGGCTGCTCCCACCTGTGCCTGCTGTCCCCAAGCGAGCC 1020

Db        990 TCGCTGTGAGGAGGACAATGGCGGCTGCTCCCACCTGTGCCTGCTGTCCCCAAGCGAGCC 1049

Qy       1021 TTTCTACACATGCGCCTGCCCCACGGGTGTGCAGCTGCAGGACAACGGCAGGACGTGTAA 1080

Db       1050 TTTCTACACATGCGCCTGCCCCACGGGTGTGCAGCTGCAGGACAACGGCAGGACGTGTAA 1109

Qy       1081 GGCAGGAGCCGAGGAGGTGCTGCTGCTGGCCCGGCGGACGGACCTACGGAGGATCTCGCT 1140

Db       1110 GGCAGGAGCCGAGGAGGTGCTGCTGCTGGCCCGGCGGACGGACCTACGGAGGATCTCGCT 1169

Qy       1141 GGACACGCCGGACTTCACCGACATCGTGCTGCAGGTGGACGACATCCGGCACGCCATTGC 1200

Db       1170 GGACACGCCGGACTTCACCGACATCGTGCTGCAGGTGGACGACATCCGGCACGCCATTGC 1229

Qy       1201 CATCGACTACGACCCGCTAGAGGGCTATGTCTACTGGACAGATGACGAGGTGCGGGCCAT 1260

Db       1230 CATCGACTACGACCCGCTAGAGGGCTATGTCTACTGGACAGATGACGAGGTGCGGGCCAT 1289

Qy       1261 CCGCAGGGCGTACCTGGACGGGTCTGGGGCGCAGACGCTGGTCAACACCGAGATCAACGA 1320

Db       1290 CCGCAGGGCGTACCTGGACGGGTCTGGGGCGCAGACGCTGGTCAACACCGAGATCAACGA 1349

Qy       1321 CCCCGATGGCATCGCGGTCGACTGGGTGGCCCGAAACCTCTACTGGACCGACACGGGCAC 1380

Db       1350 CCCCGATGGCATCGCGGTCGACTGGGTGGCCCGAAACCTCTACTGGACCGACACGGGCAC 1409

Qy       1381 GGACCGCATCGAGGTGACGCGCCTCAACGGCACCTCCCGCAAGATCCTGGTGTCGGAGGA 1440

Db       1410 GGACCGCATCGAGGTGACGCGCCTCAACGGCACCTCCCGCAAGATCCTGGTGTCGGAGGA 1469

Qy       1441 CCTGGACGAGCCCCGAGCCATCGCACTGCACCCCGTGATGGGCCTCATGTACTGGACAGA 1500

Db       1470 CCTGGACGAGCCCCGAGCCATCGCACTGCACCCCGTGATGGGCCTCATGTACTGGACAGA 1529

Qy       1501 CTGGGGAGAGAACCCTAAAATCGAGTGTGCCAACTTGGATGGGCAGGAGCGGCGTGTGCT 1560

Db       1530 CTGGGGAGAGAACCCTAAAATCGAGTGTGCCAACTTGGATGGGCAGGAGCGGCGTGTGCT 1589

Qy       1561 GGTCAATGCCTCCCTCGGGTGGCCCAACGGCCTGGCCCTGGACCTGCAGGAGGGGAAGCT 1620

Db       1590 GGTCAATGCCTCCCTCGGGTGGCCCAACGGCCTGGCCCTGGACCTGCAGGAGGGGAAGCT 1649

Qy       1621 CTACTGGGGAGACGCCAAGACAGACAAGATCGAGGTGATCAATGTTGATGGGACGAAGAG 1680

Db       1650 CTACTGGGGAGACGCCAAGACAGACAAGATCGAGGTGATCAATGTTGATGGGACGAAGAG 1709

Qy       1681 GCGGACCCTCCTGGAGGACAAGCTCCCGCACATTTTCGGGTTCACGCTGCTGGGGGACTT 1740

Db       1710 GCGGACCCTCCTGGAGGACAAGCTCCCGCACATTTTCGGGTTCACGCTGCTGGGGGACTT 1769

Qy       1741 CATCTACTGGACTGACTGGCAGCGCCGCAGCATCGAGCGGGTGCACAAGGTCAAGGCCAG 1800

Db       1770 CATCTACTGGACTGACTGGCAGCGCCGCAGCATCGAGCGGGTGCACAAGGTCAAGGCCAG 1829

Qy       1801 CCGGGACGTCATCATTGACCAGCTGCCCGACCTGATGGGGCTCAAAGCTGTGAATGTGGC 1860

Db       1830 CCGGGACGTCATCATTGACCAGCTGCCCGACCTGATGGGGCTCAAAGCTGTGAATGTGGC 1889

Qy       1861 CAAGGTCGTCGGAACCAACCCGTGTGCGGACAGGAACGGGGGGTGCAGCCACCTGTGCTT 1920

Db       1890 CAAGGTCGTCGGAACCAACCCGTGTGCGGACAGGAACGGGGGGTGCAGCCACCTGTGCTT 1949

Qy       1921 CTTCACACCCCACGCAACCCGGTGTGGCTGCCCCATCGGCCTGGAGCTGCTGAGTGACAT 1980

Db       1950 CTTCACACCCCACGCAACCCGGTGTGGCTGCCCCATCGGCCTGGAGCTGCTGAGTGACAT 2009

Qy       1981 GAAGACCTGCATCGTGCCTGAGGCCTTCTTGGTCTTCACCAGCAGAGCCGCCATCCACAG 2040

Db       2010 GAAGACCTGCATCGTGCCTGAGGCCTTCTTGGTCTTCACCAGCAGAGCCGCCATCCACAG 2069

Qy       2041 GATCTCCCTCGAGACCAATAACAACGACGTGGCCATCCCGCTCACGGGCGTCAAGGAGGC 2100

Db       2070 GATCTCCCTCGAGACCAATAACAACGACGTGGCCATCCCGCTCACGGGCGTCAAGGAGGC 2129

Qy       2101 CTCAGCCCTGGACTTTGATGTGTCCAACAACCACATCTACTGGACAGACGTCAGCCTGAA 2160

Db       2130 CTCAGCCCTGGACTTTGATGTGTCCAACAACCACATCTACTGGACAGACGTCAGCCTGAA 2189

Qy       2161 GACCATCAGCCGCGCCTTCATGAACGGGAGCTCGGTGGAGCACGTGGTGGAGTTTGGCCT 2220

Db       2190 GACCATCAGCCGCGCCTTCATGAACGGGAGCTCGGTGGAGCACGTGGTGGAGTTTGGCCT 2249

Qy       2221 TGACTACCCCGAGGGCATGGCCGTTGACTGGATGGGCAAGAACCTCTACTGGGCCGACAC 2280

Db       2250 TGACTACCCCGAGGGCATGGCCGTTGACTGGATGGGCAAGAACCTCTACTGGGCCGACAC 2309

Qy       2281 TGGGACCAACAGAATCGAAGTGGCGCGGCTGGACGGGCAGTTCCGGCAAGTCCTCGTGTG 2340

Db       2310 TGGGACCAACAGAATCGAAGTGGCGCGGCTGGACGGGCAGTTCCGGCAAGTCCTCGTGTG 2369

Qy       2341 GAGGGACTTGGACAACCCGAGGTCGCTGGCCCTGGATCCCACCAAGGGCTACATCTACTG 2400

Db       2370 GAGGGACTTGGACAACCCGAGGTCGCTGGCCCTGGATCCCACCAAGGGCTACATCTACTG 2429

Qy       2401 GACCGAGTGGGGCGGCAAGCCGAGGATCGTGCGGGCCTTCATGGACGGGACCAACTGCAT 2460

Db       2430 GACCGAGTGGGGCGGCAAGCCGAGGATCGTGCGGGCCTTCATGGACGGGACCAACTGCAT 2489

Qy       2461 GACGCTGGTGGACAAGGTGGGCCGGGCCAACGACCTCACCATTGACTACGCTGACCAGCG 2520

Db       2490 GACGCTGGTGGACAAGGTGGGCCGGGCCAACGACCTCACCATTGACTACGCTGACCAGCG 2549

Qy       2521 CCTCTACTGGACCGACCTGGACACCAACATGATCGAGTCGTCCAACATGCTGGGTCAGGA 2580

Db       2550 CCTCTACTGGACCGACCTGGACACCAACATGATCGAGTCGTCCAACATGCTGGGTCAGGA 2609

Qy       2581 GCGGGTCGTGATTGCCGACGATCTCCCGCACCCGTTCGGTCTGACGCAGTACAGCGATTA 2640

Db       2610 GCGGGTCGTGATTGCCGACGATCTCCCGCACCCGTTCGGTCTGACGCAGTACAGCGATTA 2669
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Qy       2641 TATCTACTGGACAGACTGGAATCTGCACAGCATTGAGCGGGCCGACAAGACTAGCGGCCG 2700
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Db       2670 TATCTACTGGACAGACTGGAATCTGCACAGCATTGAGCGGGCCGACAAGACTAGCGGCCG 2729

Qy       2701 GAACCGCACCCTCATCCAGGGCCACCTGGACTTCGTGATGGACATCCTGGTGTTCCACTC 2760
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2730 GAACCGCACCCTCATCCAGGGCCACCTGGACTTCGTGATGGACATCCTGGTGTTCCACTC 2789

Qy       2761 CTCCCGCCAGGATGGCCTCAATGACTGTATGCACAACAACGGGCAGTGTGGGCAGCTGTG 2820
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2790 CTCCCGCCAGGATGGCCTCAATGACTGTATGCACAACAACGGGCAGTGTGGGCAGCTGTG 2849

Qy       2821 CCTTGCCATCCCCGGCGGCCACCGCTGCGGCTGCGCCTCACACTACACCCTGGACCCCAG 2880
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2850 CCTTGCCATCCCCGGCGGCCACCGCTGCGGCTGCGCCTCACACTACACCCTGGACCCCAG 2909

Qy       2881 CAGCCGCAACTGCAGCCCGCCCACCACCTTCTTGCTGTTCAGCCAGAAATCTGCCATCAG 2940
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2910 CAGCCGCAACTGCAGCCCGCCCACCACCTTCTTGCTGTTCAGCCAGAAATCTGCCATCAG 2969

Qy       2941 TCGGATGATCCCGGACGACCAGCACAGCCCGGATCTCATCCTGCCCCTGCATGGACTGAG 3000
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2970 TCGGATGATCCCGGACGACCAGCACAGCCCGGATCTCATCCTGCCCCTGCATGGACTGAG 3029

Qy       3001 GAACGTCAAAGCCATCGACTATGACCCACTGGACAAGTTCATCTACTGGGTGGATGGGCG 3060
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3030 GAACGTCAAAGCCATCGACTATGACCCACTGGACAAGTTCATCTACTGGGTGGATGGGCG 3089

Qy       3061 CCAGAACATCAAGCGAGCCAAGGACGACGGGACCCAGCCCTTTGTTTTGACCTCTCTGAG 3120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3090 CCAGAACATCAAGCGAGCCAAGGACGACGGGACCCAGCCCTTTGTTTTGACCTCTCTGAG 3149

Qy       3121 CCAAGGCCAAAACCCAGACAGGCAGCCCCACGACCTCAGCATCGACATCTACAGCCGGAC 3180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3150 CCAAGGCCAAAACCCAGACAGGCAGCCCCACGACCTCAGCATCGACATCTACAGCCGGAC 3209

Qy       3181 ACTGTTCTGGACGTGCGAGGCCACCAATACCATCAACGTCCACAGGCTGAGCGGGGAAGC 3240
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Db       3210 ACTGTTCTGGACGTGCGAGGCCACCAATACCATCAACGTCCACAGGCTGAGCGGGGAAGC 3269

Qy       3241 CATGGGGGTGGTGCTGCGTGGGGACCGCGACAAGCCCAGGGCCATCGTCGTCAACGCGGA 3300
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Db       3270 CATGGGGGTGGTGCTGCGTGGGGACCGCGACAAGCCCAGGGCCATCGTCGTCAACGCGGA 3329

Qy       3301 GCGAGGGTACCTGTACTTCACCAACATGCAGGACCGGGCAGCCAAGATCGAACGCGCAGC 3360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3330 GCGAGGGTACCTGTACTTCACCAACATGCAGGACCGGGCAGCCAAGATCGAACGCGCAGC 3389

Qy       3361 CCTGGACGGCACCGAGCGCGAGGTCCTCTTCACCACCGGCCTCATCCGCCCTGTGGCCCT 3420
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Db       3390 CCTGGACGGCACCGAGCGCGAGGTCCTCTTCACCACCGGCCTCATCCGCCCTGTGGCCCT 3449

Qy       3421 GGTGGTGGACAACACACTGGGCAAGCTGTTCTGGGTGGACGCGGACCTGAAGCGCATTGA 3480
             |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3450 GGTGGTAGACAACACACTGGGCAAGCTGTTCTGGGTGGACGCGGACCTGAAGCGCATTGA 3509

Qy       3481 GAGCTGTGACCTGTCAGGGGCCAACCGCCTGACCCTGGAGGACGCCAACATCGTGCAGCC 3540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3510 GAGCTGTGACCTGTCAGGGGCCAACCGCCTGACCCTGGAGGACGCCAACATCGTGCAGCC 3569

Qy       3541 TCTGGGCCTGACCATCCTTGGCAAGCATCTCTACTGGATCGACCGCCAGCAGCAGATGAT 3600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3570 TCTGGGCCTGACCATCCTTGGCAAGCATCTCTACTGGATCGACCGCCAGCAGCAGATGAT 3629

Qy       3601 CGAGCGTGTGGAGAAGACCACCGGGGACAAGCGGACTCGCATCCAGGGCCGTGTCGCCCA 3660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3630 CGAGCGTGTGGAGAAGACCACCGGGGACAAGCGGACTCGCATCCAGGGCCGTGTCGCCCA 3689

Qy       3661 CCTCACTGGCATCCATGCAGTGGAGGAAGTCAGCCTGGAGGAGTTCTCAGCCCACCCATG 3720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3690 CCTCACTGGCATCCATGCAGTGGAGGAAGTCAGCCTGGAGGAGTTCTCAGCCCACCCATG 3749

Qy       3721 TGCCCGTGACAATGGTGGCTGCTCCCACATCTGTATTGCCAAGGGTGATGGGACACCACG 3780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3750 TGCCCGTGACAATGGTGGCTGCTCCCACATCTGTATTGCCAAGGGTGATGGGACACCACG 3809

Qy       3781 GTGCTCATGCCCAGTCCACCTCGTGCTCCTGCAGAACCTGCTGACCTGTGGAGAGCCGCC 3840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3810 GTGCTCATGCCCAGTCCACCTCGTGCTCCTGCAGAACCTGCTGACCTGTGGAGAGCCGCC 3869

Qy       3841 CACCTGCTCCCCGGACCAGTTTGCATGTGCCACAGGGGAGATCGACTGTATCCCCGGGGC 3900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3870 CACCTGCTCCCCGGACCAGTTTGCATGTGCCACAGGGGAGATCGACTGTATCCCCGGGGC 3929

Qy       3901 CTGGCGCTGTGACGGCTTTCCCGAGTGCGATGACCAGAGCGACGAGGAGGGCTGCCCCGT 3960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3930 CTGGCGCTGTGACGGCTTTCCCGAGTGCGATGACCAGAGCGACGAGGAGGGCTGCCCCGT 3989

Qy       3961 GTGCTCCGCCGCCCCAGTTCCCCTGCGCGCGGGGTCAGTGTGTGGACCTGCGCCTGCGCTG 4020
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Db       3990 GTGCTCCGCCGCCCAGTTCCCCTGCGCGCGGGGTCAGTGTGTGGACCTGCGCCTGCGCTG 4049

Qy       4021 CGACGGCGAGGCAGACTGTCAGGACCGCTCAGACGAGGTGGACTGTGACGCCATCTGCCT 4080
             |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db       4050 CGACGGCGAGGCAGACTGTCAGGACCGCTCAGACGAGGCGGACTGTGACGCCATCTGCCT 4109

Qy       4081 GCCCAACCAGTTCCGGTGTGCGAGCGGCCAGTGTGTCCTCATCAAACAGCAGTGCGACTC 4140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4110 GCCCAACCAGTTCCGGTGTGCGAGCGGCCAGTGTGTCCTCATCAAACAGCAGTGCGACTC 4169

Qy       4141 CTTCCCCGACTGTATCGACGGCTCCGACGAGCTCATGTGTGAAATCACCAAGCCGCCCTC 4200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4170 CTTCCCCGACTGTATCGACGGCTCCGACGAGCTCATGTGTGAAATCACCAAGCCGCCCTC 4229

Qy       4201 AGACGACAGCCCGGCCCACAGCAGTGCCATCGGGCCCGTCATTGGCATCATCCTCTCTCT 4260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4230 AGACGACAGCCCGGCCCACAGCAGTGCCATCGGGCCCGTCATTGGCATCATCCTCTCTCT 4289

Qy       4261 CTTCGTCATGGGTGGTGTCTATTTTGTGTGCCAGCGCGTGGTGTGCCAGCGCTATGCGGG 4320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4290 CTTCGTCATGGGTGGTGTCTATTTTGTGTGCCAGCGCGTGGTGTGCCAGCGCTATGCGGG 4349

Qy       4321 GGCCAACGGGCCCTTCCCGCACGAGTATGTCAGCGGGACCCCGCACGTGCCCCTCAATTT 4380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4350 GGCCAACGGGCCCTTCCCGCACGAGTATGTCAGCGGGACCCCGCACGTGCCCCTCAATTT 4409

Qy       4381 CATAGCCCCGGGCGGTTCCCAGCATGGCCCCTTCACAGGCATCGCATGCGGAAAGTCCAT 4440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4410 CATAGCCCCGGGCGGTTCCCAGCATGGCCCCTTCACAGGCATCGCATGCGGAAAGTCCAT 4469

Qy       4441 GATGAGCTCCGTGAGCCTGATGGGGGGCCGGGGCGGGGTGCCCCTCTACGACCGGAACCA 4500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4470 GATGAGCTCCGTGAGCCTGATGGGGGGCCGGGGCGGGGTGCCCCTCTACGACCGGAACCA 4529

Qy       4501 CGTCACAGGGGCCTCGTCCAGCAGCTCGTCCAGCACGAAGGCCACGCTGTACCCGCCGAT 4560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4530 CGTCACAGGGGCCTCGTCCAGCAGCTCGTCCAGCACGAAGGCCACGCTGTACCCGCCGAT 4589

Qy       4561 CCTGAACCCGCCGCCCTCCCCGGCCACGGACCCCTCCCTGTACAACATGGACATGTTCTA 4620
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Db       4590 CCTGAACCCGCCGCCCTCCCCGGCCACGGACCCCTCCCTGTACAACATGGACATGTTCTA 4649

Qy       4621 CTCTTCAAACATTCCGGCCACTGCGAGACCGTACAGGCCCTACATCATTCGAGGAATGGC 4680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4650 CTCTTCAAACATTCCGGCCACTGCGAGACCGTACAGGCCCTACATCATTCGAGGAATGGC 4709

Qy       4681 GCCCCCGACGACGCCCTGCAGCACCGACGTGTGTGACAGCGACTACAGCGCCAGCCGCTG 4740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4710 GCCCCCGACGACGCCCTGCAGCACCGACGTGTGTGACAGCGACTACAGCGCCAGCCGCTG 4769

Qy       4741 GAAGGCCAGCAAGTACTACCTGGATTTGAACTCGGACTCAGACCCCTATCCACCCCCACC 4800
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4770 GAAGGCCAGCAAGTACTACCTGGATTTGAACTCGGACTCAGACCCCTATCCACCCCCACC 4829

Qy       4801 CACGCCCCACAGCCAGTACCTGTCGGCGGAGGACAGCTGCCCGCCCTCGCCCGCCACCGA 4860
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       4830 CACGCCCCACAGCCAGTACCTGTCGGCGGAGGACAGCTGCCCGCCCTCGCCCGCCACCGA 4889

Qy       4861 GAGGAGCTACTTCCATCTCTTCCCGCCCCCTCCGTCCCCCTGCACGGACTCATCCTGACC 4920
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4890 GAGGAGCTACTTCCATCTCTTCCCGCCCCCTCCGTCCCCCTGCACGGACTCATCCTGACC 4949

Qy       4921 TCGGCCGGGCCACTCTGGCTTCTCTGTGCCCCTGTAAATAGTTTTAAATATGAACAAAGA 4980
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4950 TCGGCCGGGCCACTCTGGCTTCTCTGTGCCCCTGTAAATAGTTTTAAATATGAACAAAGA 5009

Qy       4981 AAAAAATATATTTTATGATTTAAAAAATAAATATAATTGGGATTTTAAAAACATGAGAAA 5040
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5010 AAAAAATATATTTTATGATTTAAAAAATAAATATAATTGGGATTTTAAAAACATGAGAAA 5069

Qy       5041 TGTGAACTGTGATGGGGTGGGCAGGGCTGGGAGAACTTTGTACAGTGGAGAAATATTTAT 5100
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Db       5070 TGTGAACTGTGATGGGGTGGGCAGGGCTGGGAGAACTTTGTACAGTGGAGAAATATTTAT 5129

Qy       5101 AAACTTAATTTTGTAAAACA 5120
             ||||||||||||||||||||
Db       5130 AAACTTAATTTTGTAAAACA 5149
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RESULT 14
ACC46079
ID ACC46079 standard; DNA; 5278 BP.
XX
AC ACC46079;
XX
DT 02-JUN-2003 (first entry)
XX
DE Human ZMAXGI_3AS vector insert.
XX
KW Human; high bone mass; HBM; LRP5; LRP6; transgenic; bone mass modulation;
KW gene therapy; bone density modulation; bone strength; trabecular number;
KW bone size; bone tissue connectivity; bone disease; osteoporosis;
KW osteomalacia; rickets; Paget's disease; neoplasm of the bone; gene; ds.
XX
OS Homo sapiens.
XX
PN WO200292764-A2.
XX
PD 21-NOV-2002.
XX
PF 13-MAY-2002; 2002WO-US014876.
XX
PR 11-MAY-2001; 2001US-0290071P.
PR 17-MAY-2001; 2001US-0291311P.
PR 01-FEB-2002; 2002US-0353058P.
PR 04-MAR-2002; 2002US-0361293P.
XX
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (AMHP) WYETH.
XX
PI Babij P, Bex FJ, Yaworsky PJ, Bodine PV;
XX
DR WPI; 2003-129278/12.
XX
PT New transgenic animals (e.g. mice), useful as models for studying bone
PT density modulation, developing drugs for treating or preventing bone
PT diseases (e.g. osteoporosis), or diagnosing diseases characterized by
PT reduced bone density.
XX
PS Disclosure; Fig 25; 603pp; English.
XX
CC The invention relates to novel transgenic animals expressing the high
CC bone mass (HBM) gene, expressing the corresponding wild type HBM gene,
CC comprising an alteration of the gene encoding LRP5 or LRP6, or expressing
CC an LRP5 that is modulated by an altered gene control sequence introduced
CC by homologous or non-homologous recombination. The transgenic animals are
CC for the study of bone density modulation or bone mass modulation. The
CC invention has osteopathic and cytostatic activity. The polynucleotides of
CC the invention may have a use in gene therapy. The transgenic animals and
CC nucleic acids are for the study of bone density modulation, where the
CC bone mass is modulated relative to non-transgenic animals of the same
CC species in more than one parameter selected from bone density, bone
CC strength, trabecular number, bone size, or bone tissue connectivity. The
CC transgenic animals, nucleic acids and methods are useful for identifying
CC molecules involved in bone development, and for developing pharmaceutical
CC compositions, which may be employed for treating or preventing bone
CC diseases, e.g. osteoporosis, osteomalacia, rickets, Paget's disease, or
CC neoplasms of the bone. The transgenic animals and nucleic acids are also
CC useful in methods for diagnosing diseases involved in bone development,
CC or characterised by reduced bone density or mass. The present sequence is
CC used in the exemplification of the invention
XX
SQ Sequence 5278 BP; 1162 A; 1672 C; 1562 G; 882 T; 0 U; 0 Other;

```
  Query Match           99.9%;  Score 5115.2;  DB 8;  Length 5278;
  Best Local Similarity  99.9%;  Pred. No. 0;
  Matches 5117;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 ACTAAAGCGCCGCCGCCGCGCCATGGAGCCCGAGTGAGCGCGGCGCGGGCCCGTCCGGCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         30 ACTAAAGCGCCGCCGCCGCGCCATGGAGCCCGAGTGAGCGCGGCGCGGGCCCGTCCGGCC 89

Qy         61 GCCGGACAACATGGAGGCAGCGCCGCCCGGGCCGCCGTGGCCGCTGCTGCTGCTGCTGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         90 GCCGGACAACATGGAGGCAGCGCCGCCCGGGCCGCCGTGGCCGCTGCTGCTGCTGCTGCT 149

Qy        121 GCTGCTGCTGGCGCTGTGCGGCTGCCCGGCCCCCGCCGCGGCCTCGCCGCTCCTGCTATT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        150 GCTGCTGCTGGCGCTGTGCGGCTGCCCGGCCCCCGCCGCGGCCTCGCCGCTCCTGCTATT 209

Qy        181 TGCCAACCGCCGGGACGTACGGCTGGTGGACGCCGGCGGAGTCAAGCTGGAGTCCACCAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        210 TGCCAACCGCCGGGACGTACGGCTGGTGGACGCCGGCGGAGTCAAGCTGGAGTCCACCAT 269

Qy        241 CGTGGTCAGCGGCCTGGAGGATGCGGCCGCAGTGGACTTCCAGTTTTCCAAGGGAGCCGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        270 CGTGGTCAGCGGCCTGGAGGATGCGGCCGCAGTGGACTTCCAGTTTTCCAAGGGAGCCGT 329

Qy        301 GTACTGGACAGACGTGAGCGAGGAGGCCATCAAGCAGACCTACCTGAACCAGACGGGGGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        330 GTACTGGACAGACGTGAGCGAGGAGGCCATCAAGCAGACCTACCTGAACCAGACGGGGGC 389

Qy        361 CGCCGTGCAGAACGTGGTCATCTCCGGCCTGGTCTCTCCCGACGGCCTCGCCTGCGACTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        390 CGCCGTGCAGAACGTGGTCATCTCCGGCCTGGTCTCTCCCGACGGCCTCGCCTGCGACTG 449

Qy        421 GGTGGGCAAGAAGCTGTACTGGACGGACTCAGAGACCAACCGCATCGAGGTGGCCAACCT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        450 GGTGGGCAAGAAGCTGTACTGGACGGACTCAGAGACCAACCGCATCGAGGTGGCCAACCT 509

Qy        481 CAATGGCACATCCCGGAAGGTGCTCTTCTGGCAGGACCTTGACCAGCCGAGGGCCATCGC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        510 CAATGGCACATCCCGGAAGGTGCTCTTCTGGCAGGACCTTGACCAGCCGAGGGCCATCGC 569

Qy        541 CTTGGACCCCGCTCACGGGTACATGTACTGGACAGACTGGGTTGAGACGCCCCGGATTGA 600
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db        570 CTTGGACCCCGCTCACGGGTACATGTACTGGACAGACTGGGGTGAGACGCCCCGGATTGA 629

Qy        601 GCGGGCAGGGATGGATGGCAGCACCCGGAAGATCATTGTGGACTCGGACATTTACTGGCC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        630 GCGGGCAGGGATGGATGGCAGCACCCGGAAGATCATTGTGGACTCGGACATTTACTGGCC 689

Qy        661 CAATGGACTGACCATCGACCTGGAGGAGCAGAAGCTCTACTGGGCTGACGCCAAGCTCAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        690 CAATGGACTGACCATCGACCTGGAGGAGCAGAAGCTCTACTGGGCTGACGCCAAGCTCAG 749

Qy        721 CTTCATCCACCGTGCCAACCTGGACGGCTCGTTCCGGCAGAAGGTGGTGGAGGGCAGCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        750 CTTCATCCACCGTGCCAACCTGGACGGCTCGTTCCGGCAGAAGGTGGTGGAGGGCAGCCT 809

Qy        781 GACGCACCCCTTCGCCCTGACGCTCTCCGGGGACACTCTGTACTGGACAGACTGGCAGAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        810 GACGCACCCCTTCGCCCTGACGCTCTCCGGGGACACTCTGTACTGGACAGACTGGCAGAC 869

Qy        841 CCGCTCCATCCATGCCTGCAACAAGCGCACTGGGGGGAAGAGGAAGGAGATCCTGAGTGC 900

Db        870 CCGCTCCATCCATGCCTGCAACAAGCGCACTGGGGGGAAGAGGAAGGAGATCCTGAGTGC 929

Qy        901 CCTCTACTCACCCATGGACATCCAGGTGCTGAGCCAGGAGCGGCAGCCTTTCTTCCACAC 960

Db        930 CCTCTACTCACCCATGGACATCCAGGTGCTGAGCCAGGAGCGGCAGCCTTTCTTCCACAC 989

Qy        961 TCGCTGTGAGGAGGACAATGGCGGCTGCTCCCACCTGTGCCTGCTGTCCCCAAGCGAGCC 1020

Db        990 TCGCTGTGAGGAGGACAATGGCGGCTGCTCCCACCTGTGCCTGCTGTCCCCAAGCGAGCC 1049

Qy       1021 TTTCTACACATGCGCCTGCCCCACGGGTGTGCAGCTGCAGGACAACGGCAGGACGTGTAA 1080

Db       1050 TTTCTACACATGCGCCTGCCCCACGGGTGTGCAGCTGCAGGACAACGGCAGGACGTGTAA 1109

Qy       1081 GGCAGGAGCCGAGGAGGTGCTGCTGCTGGCCCGGCGGACGGACCTACGGAGGATCTCGCT 1140

Db       1110 GGCAGGAGCCGAGGAGGTGCTGCTGCTGGCCCGGCGGACGGACCTACGGAGGATCTCGCT 1169

Qy       1141 GGACACGCCGGACTTCACCGACATCGTGCTGCAGGTGGACGACATCCGGCACGCCATTGC 1200

Db       1170 GGACACGCCGGACTTCACCGACATCGTGCTGCAGGTGGACGACATCCGGCACGCCATTGC 1229

Qy       1201 CATCGACTACGACCCGCTAGAGGGCTATGTCTACTGGACAGATGACGAGGTGCGGGCCAT 1260

Db       1230 CATCGACTACGACCCGCTAGAGGGCTATGTCTACTGGACAGATGACGAGGTGCGGGCCAT 1289

Qy       1261 CCGCAGGGCGTACCTGGACGGGTCTGGGGCGCAGACGCTGGTCAACACCGAGATCAACGA 1320

Db       1290 CCGCAGGGCGTACCTGGACGGGTCTGGGGCGCAGACGCTGGTCAACACCGAGATCAACGA 1349

Qy       1321 CCCCGATGGCATCGCGGTCGACTGGGTGGCCCGAAACCTCTACTGGACCGACACGGGCAC 1380

Db       1350 CCCCGATGGCATCGCGGTCGACTGGGTGGCCCGAAACCTCTACTGGACCGACACGGGCAC 1409

Qy       1381 GGACCGCATCGAGGTGACGCGCCTCAACGGCACCTCCCGCAAGATCCTGGTGTCGGAGGA 1440

Db       1410 GGACCGCATCGAGGTGACGCGCCTCAACGGCACCTCCCGCAAGATCCTGGTGTCGGAGGA 1469

Qy       1441 CCTGGACGAGCCCCGAGCCATCGCACTGCACCCCGTGATGGGCCTCATGTACTGGACAGA 1500

Db       1470 CCTGGACGAGCCCCGAGCCATCGCACTGCACCCCGTGATGGGCCTCATGTACTGGACAGA 1529

Qy       1501 CTGGGGAGAGAACCCTAAAATCGAGTGTGCCAACTTGGATGGGCAGGAGCGGCGTGTGCT 1560

Db       1530 CTGGGGAGAGAACCCTAAAATCGAGTGTGCCAACTTGGATGGGCAGGAGCGGCGTGTGCT 1589

Qy       1561 GGTCAATGCCTCCCTCGGGTGGCCCAACGGCCTGGCCCTGGACCTGCAGGAGGGGAAGCT 1620

Db       1590 GGTCAATGCCTCCCTCGGGTGGCCCAACGGCCTGGCCCTGGACCTGCAGGAGGGGAAGCT 1649

Qy       1621 CTACTGGGGAGACGCCAAGACAGACAAGATCGAGGTGATCAATGTTGATGGGACGAAGAG 1680

Db       1650 CTACTGGGGAGACGCCAAGACAGACAAGATCGAGGTGATCAATGTTGATGGGACGAAGAG 1709

Qy       1681 GCGGACCCTCCTGGAGGACAAGCTCCCGCACATTTTCGGGTTCACGCTGCTGGGGGACTT 1740

Db       1710 GCGGACCCTCCTGGAGGACAAGCTCCCGCACATTTTCGGGTTCACGCTGCTGGGGGACTT 1769

Qy       1741 CATCTACTGGACTGACTGGCAGCGCCGCAGCATCGAGCGGGTGCACAAGGTCAAGGCCAG 1800

Db       1770 CATCTACTGGACTGACTGGCAGCGCCGCAGCATCGAGCGGGTGCACAAGGTCAAGGCCAG 1829

Qy       1801 CCGGGACGTCATCATTGACCAGCTGCCCGACCTGATGGGGCTCAAAGCTGTGAATGTGGC 1860

Db       1830 CCGGGACGTCATCATTGACCAGCTGCCCGACCTGATGGGGCTCAAAGCTGTGAATGTGGC 1889

Qy       1861 CAAGGTCGTCGGAACCAACCCGTGTGCGGACAGGAACGGGGGGTGCAGCCACCTGTGCTT 1920

Db       1890 CAAGGTCGTCGGAACCAACCCGTGTGCGGACAGGAACGGGGGGTGCAGCCACCTGTGCTT 1949
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Qy       1921 CTTCACACCCCACGCAACCCGGTGTGGCTGCCCCATCGGCCTGGAGCTGCTGAGTGACAT 1980

Db       1950 CTTCACACCCCACGCAACCCGGTGTGGCTGCCCCATCGGCCTGGAGCTGCTGAGTGACAT 2009

Qy       1981 GAAGACCTGCATCGTGCCTGAGGCCTTCTTGGTCTTCACCAGCAGAGCCGCCATCCACAG 2040

Db       2010 GAAGACCTGCATCGTGCCTGAGGCCTTCTTGGTCTTCACCAGCAGAGCCGCCATCCACAG 2069

Qy       2041 GATCTCCCTCGAGACCAATAACAACGACGTGGCCATCCCGCTCACGGGCGTCAAGGAGGC 2100

Db       2070 GATCTCCCTCGAGACCAATAACAACGACGTGGCCATCCCGCTCACGGGCGTCAAGGAGGC 2129

Qy       2101 CTCAGCCCTGGACTTTGATGTGTCCAACAACCACATCTACTGGACAGACGTCAGCCTGAA 2160

Db       2130 CTCAGCCCTGGACTTTGATGTGTCCAACAACCACATCTACTGGACAGACGTCAGCCTGAA 2189

Qy       2161 GACCATCAGCCGCGCCTTCATGAACGGGAGCTCGGTGGAGCACGTGGTGGAGTTTGGCCT 2220

Db       2190 GACCATCAGCCGCGCCTTCATGAACGGGAGCTCGGTGGAGCACGTGGTGGAGTTTGGCCT 2249

Qy       2221 TGACTACCCCGAGGGCATGGCCGTTGACTGGATGGGCAAGAACCTCTACTGGGCCGACAC 2280

Db       2250 TGACTACCCCGAGGGCATGGCCGTTGACTGGATGGGCAAGAACCTCTACTGGGCCGACAC 2309

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Qy       2341 GAGGGACTTGGACAACCCGAGGTCGCTGGCCCTGGATCCCACCAAGGGCTACATCTACTG 2400

Db       2370 GAGGGACTTGGACAACCCGAGGTCGCTGGCCCTGGATCCCACCAAGGGCTACATCTACTG 2429

Qy       2401 GACCGAGTGGGGCGGCAAGCCGAGGATCGTGCGGGCCTTCATGGACGGGACCAACTGCAT 2460

Db       2430 GACCGAGTGGGGCGGCAAGCCGAGGATCGTGCGGGCCTTCATGGACGGGACCAACTGCAT 2489

Qy       2461 GACGCTGGTGGACAAGGTGGGCCGGGCCAACGACCTCACCATTGACTACGCTGACCAGCG 2520

Db       2490 GACGCTGGTGGACAAGGTGGGCCGGGCCAACGACCTCACCATTGACTACGCTGACCAGCG 2549

Qy       2521 CCTCTACTGGACCGACCTGGACACCAACATGATCGAGTCGTCCAACATGCTGGGTCAGGA 2580

Db       2550 CCTCTACTGGACCGACCTGGACACCAACATGATCGAGTCGTCCAACATGCTGGGTCAGGA 2609

Qy       2581 GCGGGTCGTGATTGCCGACGATCTCCCGCACCCGTTCGGTCTGACGCAGTACAGCGATTA 2640

Db       2610 GCGGGTCGTGATTGCCGACGATCTCCCGCACCCGTTCGGTCTGACGCAGTACAGCGATTA 2669

Qy       2641 TATCTACTGGACAGACTGGAATCTGCACAGCATTGAGCGGGCCGACAAGACTAGCGGCCG 2700

Db       2670 TATCTACTGGACAGACTGGAATCTGCACAGCATTGAGCGGGCCGACAAGACTAGCGGCCG 2729

Qy       2701 GAACCGCACCCTCATCCAGGGCCACCTGGACTTCGTGATGGACATCCTGGTGTTCCACTC 2760

Db       2730 GAACCGCACCCTCATCCAGGGCCACCTGGACTTCGTGATGGACATCCTGGTGTTCCACTC 2789

Qy       2761 CTCCCGCCAGGATGGCCTCAATGACTGTATGCACAACAACGGGCAGTGTGGGCAGCTGTG 2820

Db       2790 CTCCCGCCAGGATGGCCTCAATGACTGTATGCACAACAACGGGCAGTGTGGGCAGCTGTG 2849

Qy       2821 CCTTGCCATCCCCGGCGGCCACCGCTGCGGCTGCGCCTCACACTACACCCTGGACCCCAG 2880

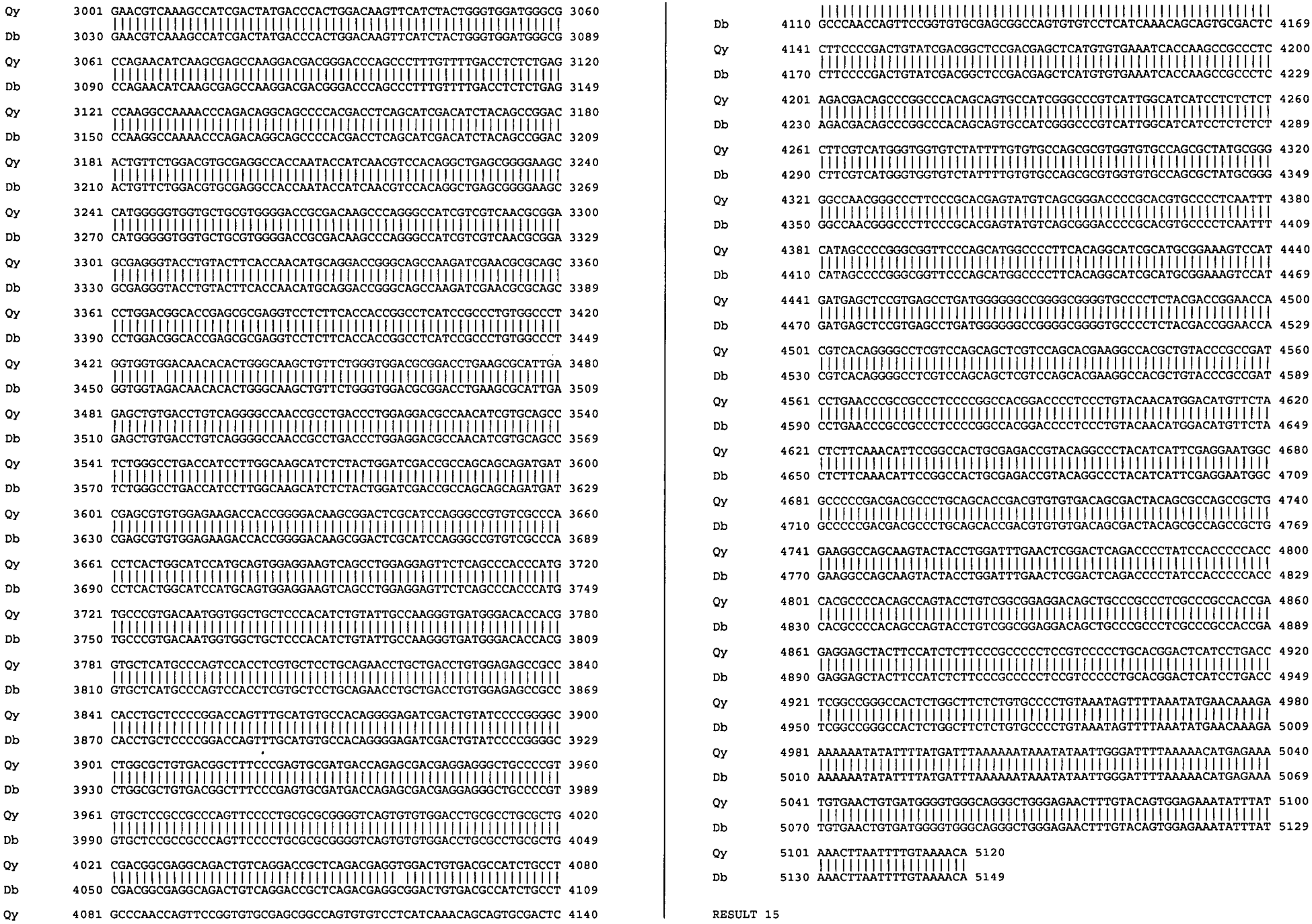
Db       2850 CCTTGCCATCCCCGGCGGCCACCGCTGCGGCTGCGCCTCACACTACACCCTGGACCCCAG 2909

Qy       2881 CAGCCGCAACTGCAGCCCGCCCACCACCTTCTTGCTGTTCAGCCAGAAATCTGCCATCAG 2940

Db       2910 CAGCCGCAACTGCAGCCCGCCCACCACCTTCTTGCTGTTCAGCCAGAAATCTGCCATCAG 2969

Qy       2941 TCGGATGATCCCGGACGACCAGCACAGCCCGGATCTCATCCTGCCCCTGCATGGACTGAG 3000

Db       2970 TCGGATGATCCCGGACGACCAGCACAGCCCGGATCTCATCCTGCCCCTGCATGGACTGAG 3029
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ADB98797
ID   ADB98797 standard; DNA; 5278 BP.
XX
AC   ADB98797;
XX
DT   04-DEC-2003  (first entry)
XX
DE   Human ZMAXGI-3AS DNA sequence.
XX
KW   Osteopathic; Gene therapy; High Bone Mass; HBM; LRP5; Zmax1; LRP6;
KW   bone mass modulation; osteoporosis; human; ds.
XX
OS   Homo sapiens.
XX
PN   WO200292000-A2.
XX
PD   21-NOV-2002.
XX
PF   13-MAY-2002; 2002WO-US014877.
XX
PR   11-MAY-2001; 2001US-0290071P.
PR   17-MAY-2001; 2001US-0291311P.
PR   01-FEB-2002; 2002US-0353058P.
PR   04-MAR-2002; 2002US-0361293P.
XX
PA   (GENO-) GENOME THERAPEUTICS CORP.
PA   (AMHP ) WYETH.
XX
PI   Allen K, Anisowicz A, Graham JR, Morales A, Yaworsky PJ, Liu W;
XX
DR   WPI; 2003-129214/12.
XX
PT   New nucleic acid comprising a mutation in LRP5 or LRP6, useful for
PT   diagnosing a HBM-like phenotype in a subject and for preparing a
PT   composition for modulating bone mass and/or lipid levels in a subject
PT   suffering from e.g. osteoporosis.
XX
PS   Disclosure; Fig 25; 629pp; English.
XX
CC   The present invention relates to High Bone Mass (HBM), LRP5 (Zmax1) and
CC   LRP6 mutants, which results in a HBM-like phenotype when expressed in a
CC   cell. The HBM-like phenotype results in bone mass modulation and/or lipid
CC   level modulation. The invention is useful for diagnosing a HBM-like
CC   phenotype in a subject and for preparing a composition for modulating
CC   bone mass and/or lipid levels in a subject suffering from e.g.
CC   osteoporosis. The present sequence was used to illustrate the invention.
XX
SQ   Sequence 5278 BP; 1162 A; 1672 C; 1562 G; 882 T; 0 U; 0 Other;

  Query Match             99.9%;  Score 5115.2;  DB 10;  Length 5278;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 5117;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 ACTAAAGCGCCGCCGCCGCGCCATGGAGCCCGAGTGAGCGCGGCGCGGGCCCGTCCGGCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         30 ACTAAAGCGCCGCCGCCGCGCCATGGAGCCCGAGTGAGCGCGGCGCGGGCCCGTCCGGCC 89

Qy         61 GCCGGACAACATGGAGGCAGCGCCGCCCGGGCCGCCGTGGCCGCTGCTGCTGCTGCTGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         90 GCCGGACAACATGGAGGCAGCGCCGCCCGGGCCGCCGTGGCCGCTGCTGCTGCTGCTGCT 149

Qy        121 GCTGCTGCTGGCGCTGTGCGGCTGCCCGGCCCCCGCCGCGGCCTCGCCGCTCCTGCTATT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        150 GCTGCTGCTGGCGCTGTGCGGCTGCCCGGCCCCCGCCGCGGCCTCGCCGCTCCTGCTATT 209

Qy        181 TGCCAACCGCCGGGACGTACGGCTGGTGGACGCCGGCGGAGTCAAGCTGGAGTCCACCAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        210 TGCCAACCGCCGGGACGTACGGCTGGTGGACGCCGGCGGAGTCAAGCTGGAGTCCACCAT 269

Qy        241 CGTGGTCAGCGGCCTGGAGGATGCGGCCGCAGTGGACTTCCAGTTTTCCAAGGGAGCCGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        270 CGTGGTCAGCGGCCTGGAGGATGCGGCCGCAGTGGACTTCCAGTTTTCCAAGGGAGCCGT 329

Qy        301 GTACTGGACAGACGTGAGCGAGGAGGCCATCAAGCAGACCTACCTGAACCAGACGGGGGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        330 GTACTGGACAGACGTGAGCGAGGAGGCCATCAAGCAGACCTACCTGAACCAGACGGGGGC 389

Qy        361 CGCCGTGCAGAACGTGGTCATCTCCGGCCTGGTCTCTCCCGACGGCCTCGCCTGCGACTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        390 CGCCGTGCAGAACGTGGTCATCTCCGGCCTGGTCTCTCCCGACGGCCTCGCCTGCGACTG 449

Qy        421 GGTGGGCAAGAAGCTGTACTGGACGGACTCAGAGACCAACCGCATCGAGGTGGCCAACCT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        450 GGTGGGCAAGAAGCTGTACTGGACGGACTCAGAGACCAACCGCATCGAGGTGGCCAACCT 509

Qy        481 CAATGGCACATCCCGGAAGGTGCTCTTCTGGCAGGACCTTGACCAGCCGAGGGCCATCGC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        510 CAATGGCACATCCCGGAAGGTGCTCTTCTGGCAGGACCTTGACCAGCCGAGGGCCATCGC 569

Qy        541 CTTGGACCCCGCTCACGGGTACATGTACTGGACAGACTGGGTTGAGACGCCCCGGATTGA 600
              |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db        570 CTTGGACCCCGCTCACGGGTACATGTACTGGACAGACTGGGGTGAGACGCCCCGGATTGA 629

Qy        601 GCGGGCAGGGATGGATGGCAGCACCCGGAAGATCATTGTGGACTCGGACATTTACTGGCC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        630 GCGGGCAGGGATGGATGGCAGCACCCGGAAGATCATTGTGGACTCGGACATTTACTGGCC 689

Qy        661 CAATGGACTGACCATCGACCTGGAGGAGCAGAAGCTCTACTGGGCTGACGCCAAGCTCAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        690 CAATGGACTGACCATCGACCTGGAGGAGCAGAAGCTCTACTGGGCTGACGCCAAGCTCAG 749

Qy        721 CTTCATCCACCGTGCCAACCTGGACGGCTCGTTCCGGCAGAAGGTGGTGGAGGGCAGCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        750 CTTCATCCACCGTGCCAACCTGGACGGCTCGTTCCGGCAGAAGGTGGTGGAGGGCAGCCT 809

Qy        781 GACGCACCCCTTCGCCCTGACGCTCTCCGGGGACACTCTGTACTGGACAGACTGGCAGAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        810 GACGCACCCCTTCGCCCTGACGCTCTCCGGGGACACTCTGTACTGGACAGACTGGCAGAC 869

Qy        841 CCGCTCCATCCATGCCTGCAACAAGCGCACTGGGGGGAAGAGGAAGGAGATCCTGAGTGC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        870 CCGCTCCATCCATGCCTGCAACAAGCGCACTGGGGGGAAGAGGAAGGAGATCCTGAGTGC 929

Qy        901 CCTCTACTCACCCATGGACATCCAGGTGCTGAGCCAGGAGCGGCAGCCTTTCTTCCACAC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        930 CCTCTACTCACCCATGGACATCCAGGTGCTGAGCCAGGAGCGGCAGCCTTTCTTCCACAC 989

Qy        961 TCGCTGTGAGGAGGACAATGGCGGCTGCTCCCACCTGTGCCTGCTGTCCCCAAGCGAGCC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        990 TCGCTGTGAGGAGGACAATGGCGGCTGCTCCCACCTGTGCCTGCTGTCCCCAAGCGAGCC 1049

Qy       1021 TTTCTACACATGCGCCTGCCCCACGGGTGTGCAGCTGCAGGACAACGGCAGGACGTGTAA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1050 TTTCTACACATGCGCCTGCCCCACGGGTGTGCAGCTGCAGGACAACGGCAGGACGTGTAA 1109

Qy       1081 GGCAGGAGCCGAGGAGGTGCTGCTGCTGGCCCGGCGGACGGACCTACGGAGGATCTCGCT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1110 GGCAGGAGCCGAGGAGGTGCTGCTGCTGGCCCGGCGGACGGACCTACGGAGGATCTCGCT 1169

Qy       1141 GGACACGCCGGACTTCACCGACATCGTGCTGCAGGTGGACGACATCCGGCACGCCATTGC 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1170 GGACACGCCGGACTTCACCGACATCGTGCTGCAGGTGGACGACATCCGGCACGCCATTGC 1229

Qy       1201 CATCGACTACGACCCGCTAGAGGGCTATGTCTACTGGACAGATGACGAGGTGCGGGCCAT 1260
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Db       1230 CATCGACTACGACCCGCTAGAGGGCTATGTCTACTGGACAGATGACGAGGTGCGGGCCAT 1289

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Qy       1381 GGACCGCATCGAGGTGACGCGCCTCAACGGCACCTCCCGCAAGATCCTGGTGTCGGAGGA 1440
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Db      1410 GGACCGCATCGAGGTGACGCGCCTCAACGGCACCTCCCGCAAGATCCTGGTGTCGGAGGA 1469
Qy      1441 CCTGGACGAGCCCCGAGCCATCGCACTGCACCCCGTGATGGGCCTCATGTACTGGACAGA 1500
Db      1470 CCTGGACGAGCCCCGAGCCATCGCACTGCACCCCGTGATGGGCCTCATGTACTGGACAGA 1529
Qy      1501 CTGGGGAGAGAACCCTAAAATCGAGTGTGCCAACTTGGATGGGCAGGAGCGGCGTGTGCT 1560
Db      1530 CTGGGGAGAGAACCCTAAAATCGAGTGTGCCAACTTGGATGGGCAGGAGCGGCGTGTGCT 1589
Qy      1561 GGTCAATGCCTCCCTCGGGTGGCCCAACGGCCTGGCCCTGGACCTGCAGGAGGGGAAGCT 1620
Db      1590 GGTCAATGCCTCCCTCGGGTGGCCCAACGGCCTGGCCCTGGACCTGCAGGAGGGGAAGCT 1649
Qy      1621 CTACTGGGGAGACGCCAAGACAGACAAGATCGAGGTGATCAATGTTGATGGGACGAAGAG 1680
Db      1650 CTACTGGGGAGACGCCAAGACAGACAAGATCGAGGTGATCAATGTTGATGGGACGAAGAG 1709
Qy      1681 GCGGACCCTCCTGGAGGACAAGCTCCCGCACATTTTCGGGTTCACGCTGCTGGGGGACTT 1740
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Qy      1741 CATCTACTGGACTGACTGGCAGCGCCGCAGCATCGAGCGGGTGCACAAGGTCAAGGCCAG 1800
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Qy      1801 CCGGGACGTCATCATTGACCAGCTGCCCGACCTGATGGGGCTCAAAGCTGTGAATGTGGC 1860
Db      1830 CCGGGACGTCATCATTGACCAGCTGCCCGACCTGATGGGGCTCAAAGCTGTGAATGTGGC 1889
Qy      1861 CAAGGTCGTCGGAACCAACCCGTGTGCGGACAGGAACGGGGGGTGCAGCCACCTGTGCTT 1920
Db      1890 CAAGGTCGTCGGAACCAACCCGTGTGCGGACAGGAACGGGGGGTGCAGCCACCTGTGCTT 1949
Qy      1921 CTTCACACCCCACGCAACCCGGTGTGGCTGCCCCATCGGCCTGGAGCTGCTGAGTGACAT 1980
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Qy      1981 GAAGACCTGCATCGTGCCTGAGGCCTTCTTGGTCTTCACCAGCAGAGCCGCCATCCACAG 2040
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Qy      2041 GATCTCCCTCGAGACCAATAACAACGACGTGGCCATCCCGCTCACGGGCGTCAAGGAGGC 2100
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SUMMARIES

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ALIGNMENTS

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; Patent No. 6770461
; GENERAL INFORMATION:
; APPLICANT: Carulli, John P.
; APPLICANT: Little, Randall D.
; APPLICANT: Recker, Robert R.
; APPLICANT: Johnson, Mark L.
; TITLE OF INVENTION: High bone mass gene of 11q13.3
; FILE REFERENCE: 032796-013
; CURRENT APPLICATION NUMBER: US/09/544,398B
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: US 09/229,319
; PRIOR FILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: US 60/071,449
; PRIOR FILING DATE: 1998-01-13
; PRIOR APPLICATION NUMBER: US 60/105,511
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 641
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 5120
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-544-398B-2

Query Match 100.0%; Score 5120; DB 4; Length 5120;
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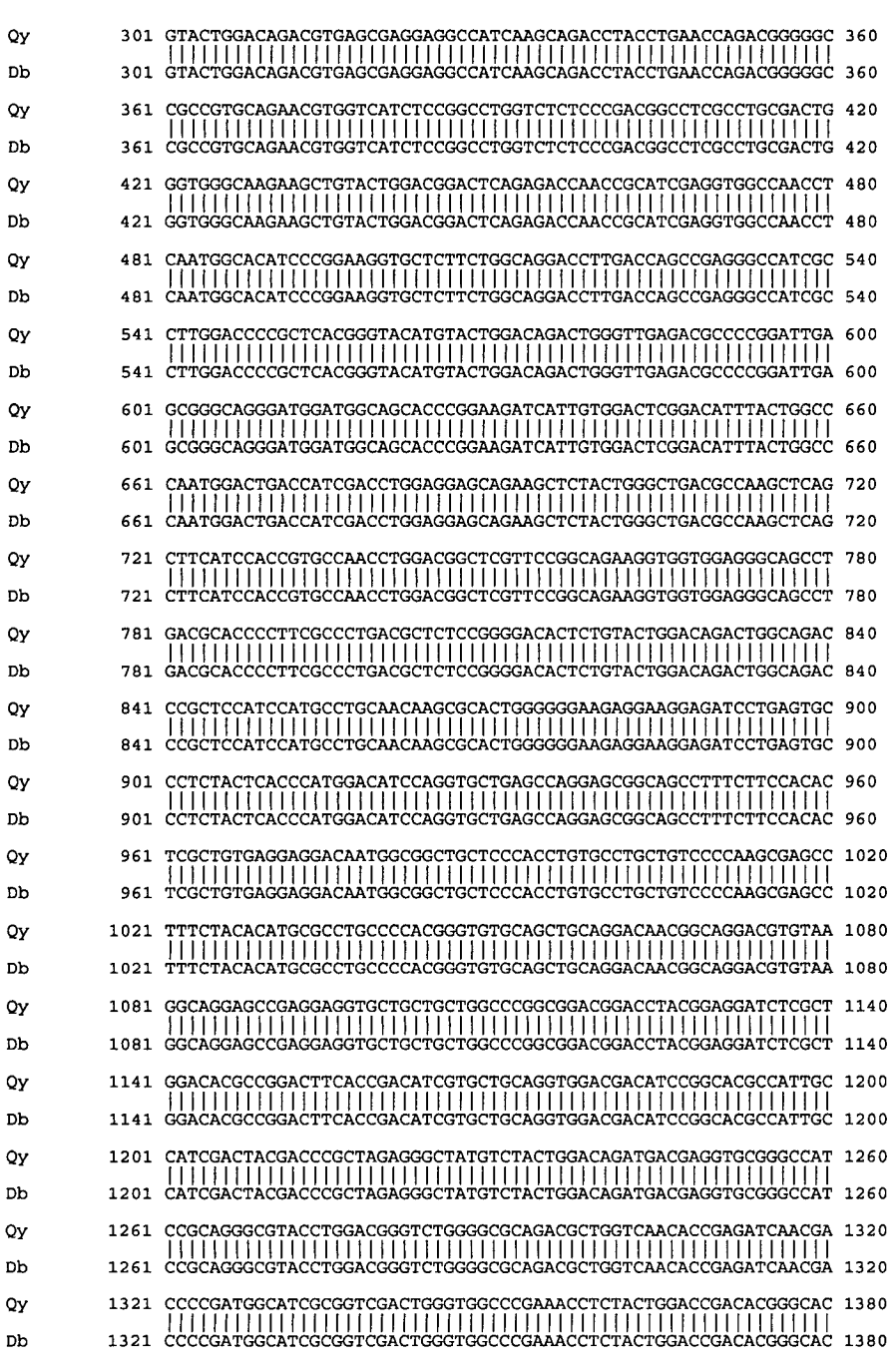
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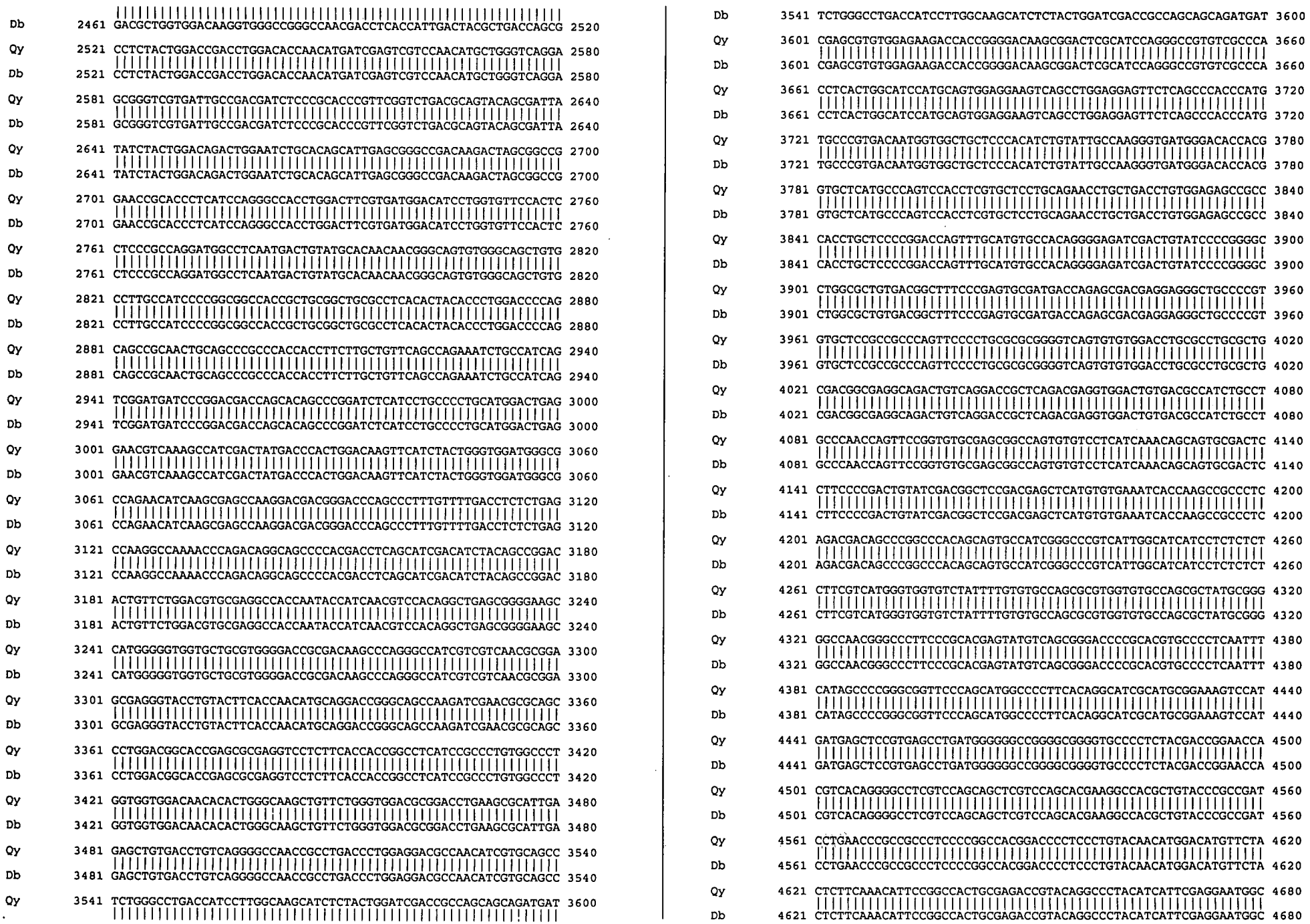
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Db 1141 GGACACGCCGGACTTCACCGACATCGTGCTGCAGGTGGACGACATCCGGCACGCCATTGC 1200
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RESULT 2
US-09-543-771B-2
; Sequence 2, Application US/09543771B
; Patent No. 6780609
; GENERAL INFORMATION:
; APPLICANT: Carulli, John P.
; APPLICANT: Little, Randall D.
; APPLICANT: Recker, Robert R.
; APPLICANT: Johnson, Mark L.
; TITLE OF INVENTION: High bone mass gene of 11q13.3
; FILE REFERENCE: 032796-014
; CURRENT APPLICATION NUMBER: US/09/543,771B
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 09/229,319
; PRIOR FILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: US 60/071,449
; PRIOR FILING DATE: 1998-01-13
; PRIOR APPLICATION NUMBER: US 60/105,511
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 641
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 5120
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-543-771B-2

Query Match 100.0%; Score 5120; DB 4; Length 5120;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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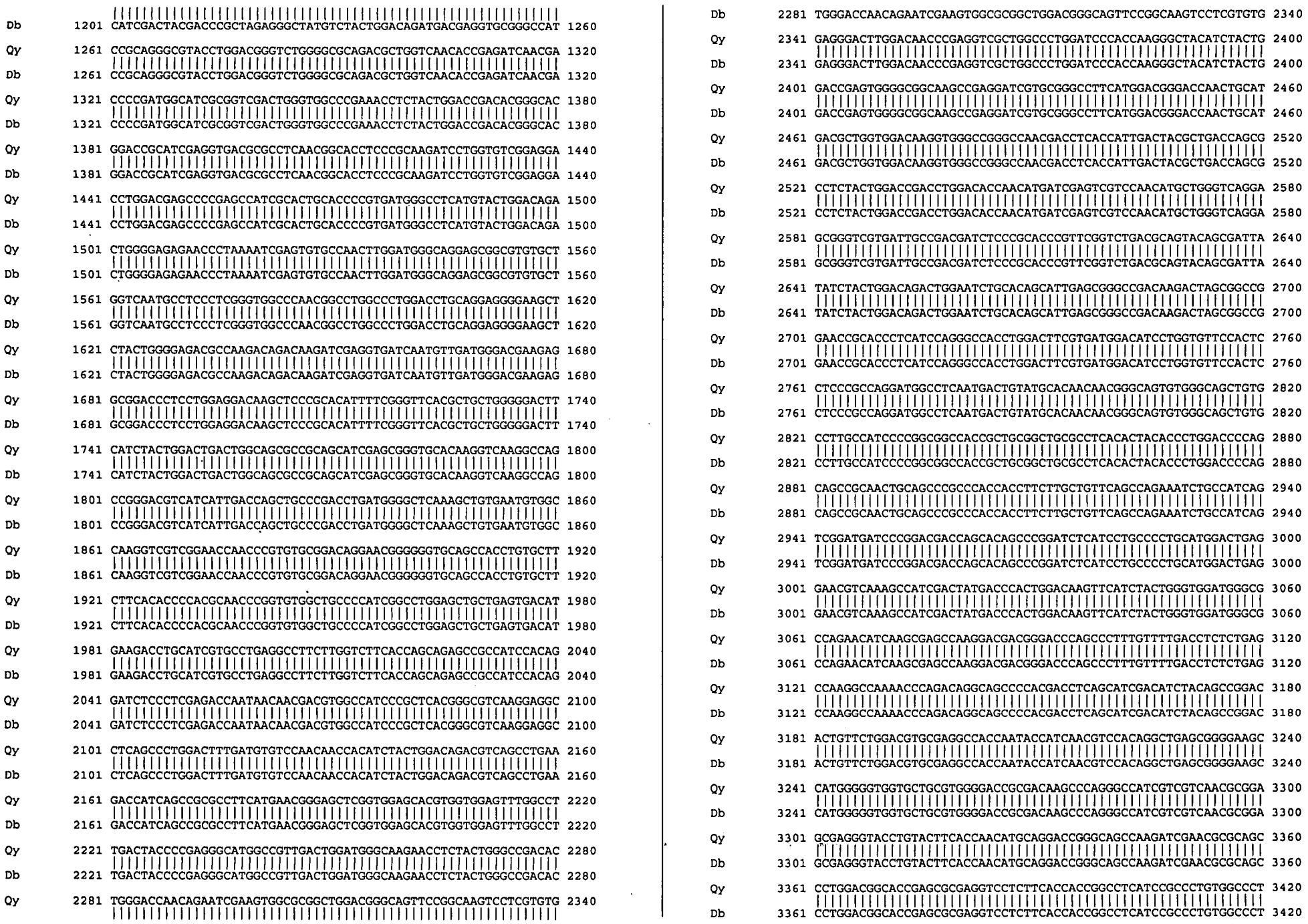
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Qy 1681 GCGGACCCTCCTGGAGGACAAGCTCCCGCACATTTTCGGGTTCACGCTGCTGGGGGACTT 1740
Db 1681 GCGGACCCTCCTGGAGGACAAGCTCCCGCACATTTTCGGGTTCACGCTGCTGGGGGACTT 1740
Qy 1741 CATCTACTGGACTGACTGGCAGCGCCGCAGCATCGAGCGGGTGCACAAGGTCAAGGCCAG 1800
Db 1741 CATCTACTGGACTGACTGGCAGCGCCGCAGCATCGAGCGGGTGCACAAGGTCAAGGCCAG 1800
Qy 1801 CCGGGACGTCATCATTGACCAGCTGCCCGACCTGATGGGGCTCAAAGCTGTGAATGTGGC 1860
Db 1801 CCGGGACGTCATCATTGACCAGCTGCCCGACCTGATGGGGCTCAAAGCTGTGAATGTGGC 1860
Qy 1861 CAAGGTCGTCGGAACCAACCCGTGTGCGGACAGGAACGGGGGGTGCAGCCACCTGTGCTT 1920
Db 1861 CAAGGTCGTCGGAACCAACCCGTGTGCGGACAGGAACGGGGGGTGCAGCCACCTGTGCTT 1920
Qy 1921 CTTCACACCCCACGCAACCCGGTGTGGCTGCCCCATCGGCCTGGAGCTGCTGAGTGACAT 1980
Db 1921 CTTCACACCCCACGCAACCCGGTGTGGCTGCCCCATCGGCCTGGAGCTGCTGAGTGACAT 1980
Qy 1981 GAAGACCTGCATCGTGCCTGAGGCCTTCTTGGTCTTCACCAGCAGAGCCGCCATCCACAG 2040
Db 1981 GAAGACCTGCATCGTGCCTGAGGCCTTCTTGGTCTTCACCAGCAGAGCCGCCATCCACAG 2040
Qy 2041 GATCTCCCTCGAGACCAATAACAACGACGTGGCCATCCCGCTCACGGGCGTCAAGGAGGC 2100
Db 2041 GATCTCCCTCGAGACCAATAACAACGACGTGGCCATCCCGCTCACGGGCGTCAAGGAGGC 2100
Qy 2101 CTCAGCCCTGGACTTTGATGTGTCCAACAACCACATCTACTGGACAGACGTCAGCCTGAA 2160
Db 2101 CTCAGCCCTGGACTTTGATGTGTCCAACAACCACATCTACTGGACAGACGTCAGCCTGAA 2160
Qy 2161 GACCATCAGCCGCGCCTTCATGAACGGGAGCTCGGTGGAGCACGTGGTGGAGTTTGGCCT 2220
Db 2161 GACCATCAGCCGCGCCTTCATGAACGGGAGCTCGGTGGAGCACGTGGTGGAGTTTGGCCT 2220
Qy 2221 TGACTACCCCGAGGGCATGGCCGTTGACTGGATGGGCAAGAACCTCTACTGGGCCGACAC 2280
Db 2221 TGACTACCCCGAGGGCATGGCCGTTGACTGGATGGGCAAGAACCTCTACTGGGCCGACAC 2280
Qy 2281 TGGGACCAACAGAATCGAAGTGGCGCGGCTGGACGGGCAGTTCCGGCAAGTCCTCGTGTG 2340
Db 2281 TGGGACCAACAGAATCGAAGTGGCGCGGCTGGACGGGCAGTTCCGGCAAGTCCTCGTGTG 2340
Qy 2341 GAGGGACTTGGACAACCCGAGGTCGCTGGCCCTGGATCCCACCAAGGGCTACATCTACTG 2400
Db 2341 GAGGGACTTGGACAACCCGAGGTCGCTGGCCCTGGATCCCACCAAGGGCTACATCTACTG 2400
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Db 2401 GACCGAGTGGGGCGGCAAGCCGAGGATCGTGCGGGCCTTCATGGACGGGACCAACTGCAT 2460
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Db 2461 GACGCTGGTGGACAAGGTGGGCCGGGCCAACGACCTCACCATTGACTACGCTGACCAGCG 2520
Qy 2521 CCTCTACTGGACCGACCTGGACACCAACATGATCGAGTCGTCCAACATGCTGGGTCAGGA 2580
Db 2521 CCTCTACTGGACCGACCTGGACACCAACATGATCGAGTCGTCCAACATGCTGGGTCAGGA 2580
Qy 2581 GCGGGTCGTGATTGCCGACGATCTCCCGCACCCGTTCGGTCTGACGCAGTACAGCGATTA 2640
Db 2581 GCGGGTCGTGATTGCCGACGATCTCCCGCACCCGTTCGGTCTGACGCAGTACAGCGATTA 2640
Qy 2641 TATCTACTGGACAGACTGGAATCTGCACAGCATTGAGCGGGCCGACAAGACTAGCGGCCG 2700
Db 2641 TATCTACTGGACAGACTGGAATCTGCACAGCATTGAGCGGGCCGACAAGACTAGCGGCCG 2700
Qy 2701 GAACCGCACCCTCATCCAGGGCCACCTGGACTTCGTGATGGACATCCTGGTGTTCCACTC 2760
Db 2701 GAACCGCACCCTCATCCAGGGCCACCTGGACTTCGTGATGGACATCCTGGTGTTCCACTC 2760
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Db 2881 CAGCCGCAACTGCAGCCCGCCCACCACCTTCTTGCTGTTCAGCCAGAAATCTGCCATCAG 2940
Qy 2941 TCGGATGATCCCGGACGACCAGCACAGCCCGGATCTCATCCTGCCCCTGCATGGACTGAG 3000
Db 2941 TCGGATGATCCCGGACGACCAGCACAGCCCGGATCTCATCCTGCCCCTGCATGGACTGAG 3000
Qy 3001 GAACGTCAAAGCCATCGACTATGACCCACTGGACAAGTTCATCTACTGGGTGGATGGGCG 3060
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Db 3121 CCAAGGCCAAAACCCAGACAGGCAGCCCCACGACCTCAGCATCGACATCTACAGCCGGAC 3180
Qy 3181 ACTGTTCTGGACGTGCGAGGCCACCAATACCATCAACGTCCACAGGCTGAGCGGGGAAGC 3240
Db 3181 ACTGTTCTGGACGTGCGAGGCCACCAATACCATCAACGTCCACAGGCTGAGCGGGGAAGC 3240
Qy 3241 CATGGGGGTGGTGCTGCGTGGGGACCGCGACAAGCCCAGGGCCATCGTCGTCAACGCGGA 3300
Db 3241 CATGGGGGTGGTGCTGCGTGGGGACCGCGACAAGCCCAGGGCCATCGTCGTCAACGCGGA 3300
Qy 3301 GCGAGGGTACCTGTACTTCACCAACATGCAGGACCGGGCAGCCAAGATCGAACGCGCAGC 3360
Db 3301 GCGAGGGTACCTGTACTTCACCAACATGCAGGACCGGGCAGCCAAGATCGAACGCGCAGC 3360
Qy 3361 CCTGGACGGCACCGAGCGCGAGGTCCTCTTCACCACCGGCCTCATCCGCCCTGTGGCCCT 3420
Db 3361 CCTGGACGGCACCGAGCGCGAGGTCCTCTTCACCACCGGCCTCATCCGCCCTGTGGCCCT 3420

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Qy       3421 GGTGGTGGACAACACACTGGGCAAGCTGTTCTGGGTGGACGCGGACCTGAAGCGCATTGA 3480
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Db       3421 GGTGGTGGACAACACACTGGGCAAGCTGTTCTGGGTGGACGCGGACCTGAAGCGCATTGA 3480

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Db       3481 GAGCTGTGACCTGTCAGGGGCCAACCGCCTGACCCTGGAGGACGCCAACATCGTGCAGCC 3540

Qy       3541 TCTGGGCCTGACCATCCTTGGCAAGCATCTCTACTGGATCGACCGCCAGCAGCAGATGAT 3600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3541 TCTGGGCCTGACCATCCTTGGCAAGCATCTCTACTGGATCGACCGCCAGCAGCAGATGAT 3600

Qy       3601 CGAGCGTGTGGAGAAGACCACCGGGGACAAGCGGACTCGCATCCAGGGCCGTGTCGCCCA 3660
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Db       3601 CGAGCGTGTGGAGAAGACCACCGGGGACAAGCGGACTCGCATCCAGGGCCGTGTCGCCCA 3660

Qy       3661 CCTCACTGGCATCCATGCAGTGGAGGAAGTCAGCCTGGAGGAGTTCTCAGCCCACCCATG 3720
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Db       3661 CCTCACTGGCATCCATGCAGTGGAGGAAGTCAGCCTGGAGGAGTTCTCAGCCCACCCATG 3720

Qy       3721 TGCCCGTGACAATGGTGGCTGCTCCCACATCTGTATTGCCAAGGGTGATGGGACACCACG 3780
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Db       3721 TGCCCGTGACAATGGTGGCTGCTCCCACATCTGTATTGCCAAGGGTGATGGGACACCACG 3780

Qy       3781 GTGCTCATGCCCAGTCCACCTCGTGCTCCTGCAGAACCTGCTGACCTGTGGAGAGCCGCC 3840
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Db       3781 GTGCTCATGCCCAGTCCACCTCGTGCTCCTGCAGAACCTGCTGACCTGTGGAGAGCCGCC 3840

Qy       3841 CACCTGCTCCCCGGACCAGTTTGCATGTGCCACAGGGGAGATCGACTGTATCCCCGGGGC 3900
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Db       3841 CACCTGCTCCCCGGACCAGTTTGCATGTGCCACAGGGGAGATCGACTGTATCCCCGGGGC 3900

Qy       3901 CTGGCGCTGTGACGGCTTTCCCGAGTGCGATGACCAGAGCGACGAGGAGGGCTGCCCCGT 3960
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Qy       3961 GTGCTCCGCCGCCCAGTTCCCCTGCGCGCGGGGTCAGTGTGTGGACCTGCGCCTGCGCTG 4020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3961 GTGCTCCGCCGCCCAGTTCCCCTGCGCGCGGGGTCAGTGTGTGGACCTGCGCCTGCGCTG 4020

Qy       4021 CGACGGCGAGGCAGACTGTCAGGACCGCTCAGACGAGGTGGACTGTGACGCCATCTGCCT 4080
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Qy       4081 GCCCAACCAGTTCCGGTGTGCGAGCGGCCAGTGTGTCCTCATCAAACAGCAGTGCGACTC 4140
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Db       4081 GCCCAACCAGTTCCGGTGTGCGAGCGGCCAGTGTGTCCTCATCAAACAGCAGTGCGACTC 4140

Qy       4141 CTTCCCCGACTGTATCGACGGCTCCGACGAGCTCATGTGTGAAATCACCAAGCCGCCCTC 4200
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Db       4141 CTTCCCCGACTGTATCGACGGCTCCGACGAGCTCATGTGTGAAATCACCAAGCCGCCCTC 4200

Qy       4201 AGACGACAGCCCGGCCCACAGCAGTGCCATCGGGCCCGTCATTGGCATCATCCTCTCTCT 4260
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Db       4201 AGACGACAGCCCGGCCCACAGCAGTGCCATCGGGCCCGTCATTGGCATCATCCTCTCTCT 4260

Qy       4261 CTTCGTCATGGGTGGTGTCTATTTTGTGTGCCAGCGCGTGGTGTGCCAGCGCTATGCGGG 4320
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Db       4261 CTTCGTCATGGGTGGTGTCTATTTTGTGTGCCAGCGCGTGGTGTGCCAGCGCTATGCGGG 4320

Qy       4321 GGCCAACGGGCCCTTCCCGCACGAGTATGTCAGCGGGACCCCGCACGTGCCCCTCAATTT 4380
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Db       4321 GGCCAACGGGCCCTTCCCGCACGAGTATGTCAGCGGGACCCCGCACGTGCCCCTCAATTT 4380

Qy       4381 CATAGCCCCGGGCGGTTCCCAGCATGGCCCCTTCACAGGCATCGCATGCGGAAAGTCCAT 4440
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Db       4381 CATAGCCCCGGGCGGTTCCCAGCATGGCCCCTTCACAGGCATCGCATGCGGAAAGTCCAT 4440

Qy       4441 GATGAGCTCCGTGAGCCTGATGGGGGGCCGGGGCGGGGTGCCCCTCTACGACCGGAACCA 4500
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Db       4441 GATGAGCTCCGTGAGCCTGATGGGGGGCCGGGGCGGGGTGCCCCTCTACGACCGGAACCA 4500

Qy       4501 CGTCACAGGGGCCTCGTCCAGCAGCTCGTCCAGCACGAAGGCCACGCTGTACCCGCCGAT 4560
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Db       4501 CGTCACAGGGGCCTCGTCCAGCAGCTCGTCCAGCACGAAGGCCACGCTGTACCCGCCGAT 4560

Qy       4561 CCTGAACCCGCCGCCCTCCCCGGCCACGGACCCCTCCCTGTACAACATGGACATGTTCTA 4620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4561 CCTGAACCCGCCGCCCTCCCCGGCCACGGACCCCTCCCTGTACAACATGGACATGTTCTA 4620

Qy       4621 CTCTTCAAACATTCCGGCCACTGCGAGACCGTACAGGCCCTACATCATTCGAGGAATGGC 4680
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Db       4621 CTCTTCAAACATTCCGGCCACTGCGAGACCGTACAGGCCCTACATCATTCGAGGAATGGC 4680

Qy       4681 GCCCCCGACGACGCCCTGCAGCACCGACGTGTGTGACAGCGACTACAGCGCCAGCCGCTG 4740
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Db       4681 GCCCCCGACGACGCCCTGCAGCACCGACGTGTGTGACAGCGACTACAGCGCCAGCCGCTG 4740

Qy       4741 GAAGGCCAGCAAGTACTACCTGGATTTGAACTCGGACTCAGACCCCTATCCACCCCCACC 4800
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4741 GAAGGCCAGCAAGTACTACCTGGATTTGAACTCGGACTCAGACCCCTATCCACCCCCACC 4800

Qy       4801 CACGCCCCACAGCCAGTACCTGTCGGCGGAGGACAGCTGCCCGCCCTCGCCCGCCACCGA 4860
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4801 CACGCCCCACAGCCAGTACCTGTCGGCGGAGGACAGCTGCCCGCCCTCGCCCGCCACCGA 4860

Qy       4861 GAGGAGCTACTTCCATCTCTTCCCGCCCCCTCCGTCCCCCTGCACGGACTCATCCTGACC 4920
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4861 GAGGAGCTACTTCCATCTCTTCCCGCCCCCTCCGTCCCCCTGCACGGACTCATCCTGACC 4920

Qy       4921 TCGGCCGGGCCACTCTGGCTTCTCTGTGCCCCTGTAAATAGTTTTAAATATGAACAAAGA 4980
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Db       4921 TCGGCCGGGCCACTCTGGCTTCTCTGTGCCCCTGTAAATAGTTTTAAATATGAACAAAGA 4980

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Db       4981 AAAAAATATATTTTATGATTTAAAAAATAAATATAATTGGGATTTTAAAAACATGAGAAA 5040

Qy       5041 TGTGAACTGTGATGGGGTGGGCAGGGCTGGGAGAACTTTGTACAGTGGAGAAATATTTAT 5100
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Db       5101 AAACTTAATTTTGTAAAACA 5120
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RESULT 3
US-09-544-398B-1
; Sequence 1, Application US/09544398B
; Patent No. 6770461
; GENERAL INFORMATION:
; APPLICANT: Carulli, John P.
; APPLICANT: Little, Randall D.
; APPLICANT: Recker, Robert R.
; APPLICANT: Johnson, Mark L.
; TITLE OF INVENTION: High bone mass gene of 11q13.3
; FILE REFERENCE: 032796-013
; CURRENT APPLICATION NUMBER: US/09/544,398B
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: US 09/229,319
; PRIOR FILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: US 60/071,449
; PRIOR FILING DATE: 1998-01-13
; PRIOR APPLICATION NUMBER: US 60/105,511
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 641
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 5120
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-544-398B-1

Query Match 100.0%; Score 5118.4; DB 4; Length 5120;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 5119; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 ACTAAAGCGCCGCCGCCGCGCCATGGAGCCCGAGTGAGCGCGGCGCGGGCCCGTCCGGCC 60
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Qy        121 GCTGCTGCTGGCGCTGTGCGGCTGCCCGGCCCCCGCCGCGGCCTCGCCGCTCCTGCTATT 180
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Db        121 GCTGCTGCTGGCGCTGTGCGGCTGCCCGGCCCCCGCCGCGGCCTCGCCGCTCCTGCTATT 180

Qy        181 TGCCAACCGCCGGGACGTACGGCTGGTGGACGCCGGCGGAGTCAAGCTGGAGTCCACCAT 240
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Qy        241 CGTGGTCAGCGGCCTGGAGGATGCGGCCGCAGTGGACTTCCAGTTTTCCAAGGGAGCCGT 300
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Db        301 GTACTGGACAGACGTGAGCGAGGAGGCCATCAAGCAGACCTACCTGAACCAGACGGGGGC 360

Qy        361 CGCCGTGCAGAACGTGGTCATCTCCGGCCTGGTCTCTCCCGACGGCCTCGCCTGCGACTG 420
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Db        721 CTTCATCCACCGTGCCAACCTGGACGGCTCGTTCCGGCAGAAGGTGGTGGAGGGCAGCCT 780

Qy        781 GACGCACCCCTTCGCCCTGACGCTCTCCGGGGACACTCTGTACTGGACAGACTGGCAGAC 840
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Db        781 GACGCACCCCTTCGCCCTGACGCTCTCCGGGGACACTCTGTACTGGACAGACTGGCAGAC 840

Qy        841 CCGCTCCATCCATGCCTGCAACAAGCGCACTGGGGGGAAGAGGAAGGAGATCCTGAGTGC 900
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Db        841 CCGCTCCATCCATGCCTGCAACAAGCGCACTGGGGGGAAGAGGAAGGAGATCCTGAGTGC 900

Qy        901 CCTCTACTCACCCATGGACATCCAGGTGCTGAGCCAGGAGCGGCAGCCTTTCTTCCACAC 960
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Db        901 CCTCTACTCACCCATGGACATCCAGGTGCTGAGCCAGGAGCGGCAGCCTTTCTTCCACAC 960

Qy        961 TCGCTGTGAGGAGGACAATGGCGGCTGCTCCCACCTGTGCCTGCTGTCCCCAAGCGAGCC 1020
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Qy       1081 GGCAGGAGCCGAGGAGGTGCTGCTGCTGGCCCGGCGGACGGACCTACGGAGGATCTCGCT 1140
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Db       1081 GGCAGGAGCCGAGGAGGTGCTGCTGCTGGCCCGGCGGACGGACCTACGGAGGATCTCGCT 1140

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Db       1201 CATCGACTACGACCCGCTAGAGGGCTATGTCTACTGGACAGATGACGAGGTGCGGGCCAT 1260

Qy       1261 CCGCAGGGCGTACCTGGACGGGTCTGGGGCGCAGACGCTGGTCAACACCGAGATCAACGA 1320
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Db       1261 CCGCAGGGCGTACCTGGACGGGTCTGGGGCGCAGACGCTGGTCAACACCGAGATCAACGA 1320

Qy       1321 CCCCGATGGCATCGCGGTCGACTGGGTGGCCCGAAACCTCTACTGGACCGACACGGGCAC 1380
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Db       1321 CCCCGATGGCATCGCGGTCGACTGGGTGGCCCGAAACCTCTACTGGACCGACACGGGCAC 1380

Qy       1381 GGACCGCATCGAGGTGACGCGCCTCAACGGCACCTCCCGCAAGATCCTGGTGTCGGAGGA 1440
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Db       1381 GGACCGCATCGAGGTGACGCGCCTCAACGGCACCTCCCGCAAGATCCTGGTGTCGGAGGA 1440

Qy       1441 CCTGGACGAGCCCCGAGCCATCGCACTGCACCCCGTGATGGGCCTCATGTACTGGACAGA 1500
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Qy       1501 CTGGGGAGAGAACCCTAAAATCGAGTGTGCCAACTTGGATGGGCAGGAGCGGCGTGTGCT 1560
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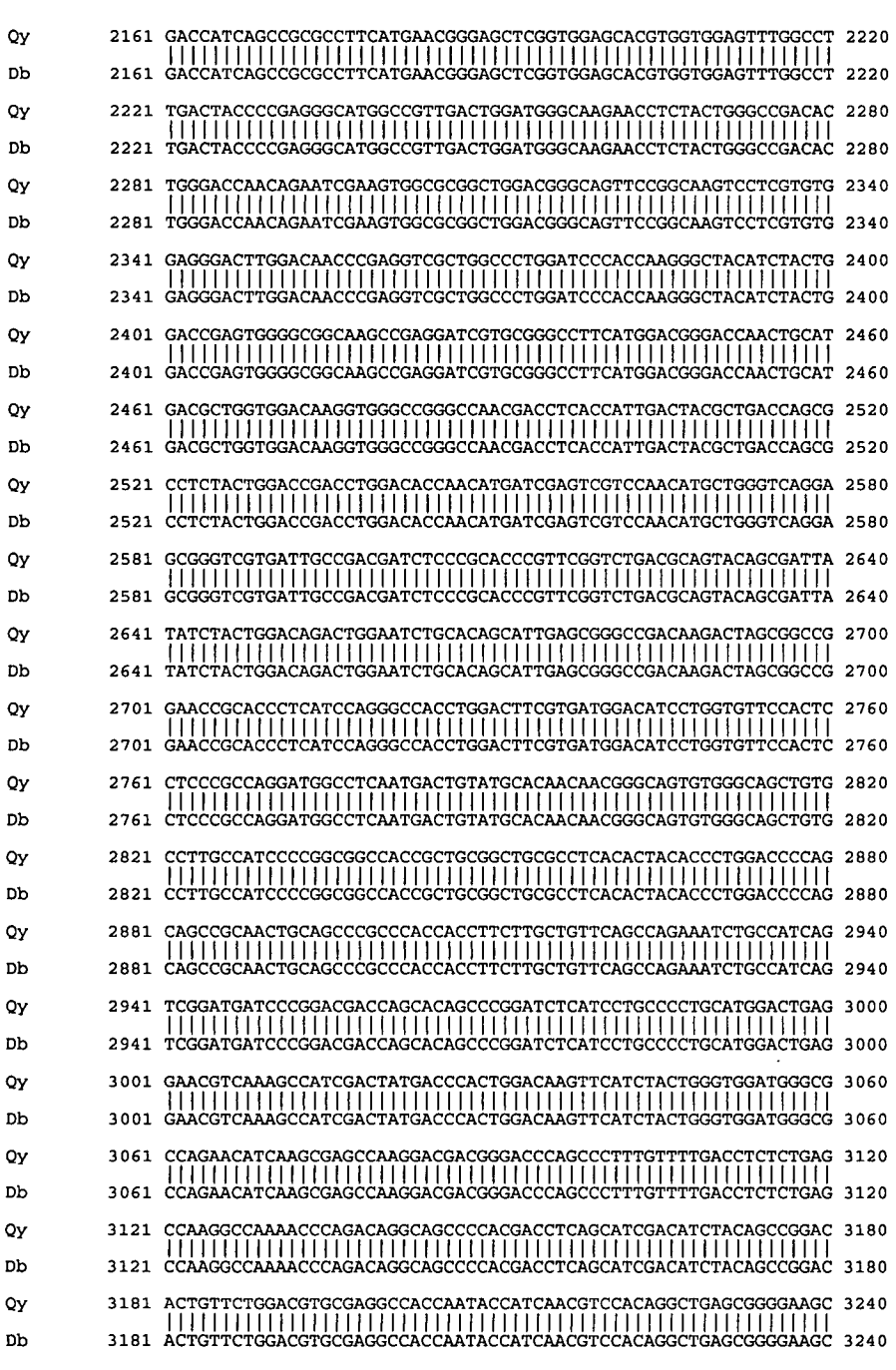
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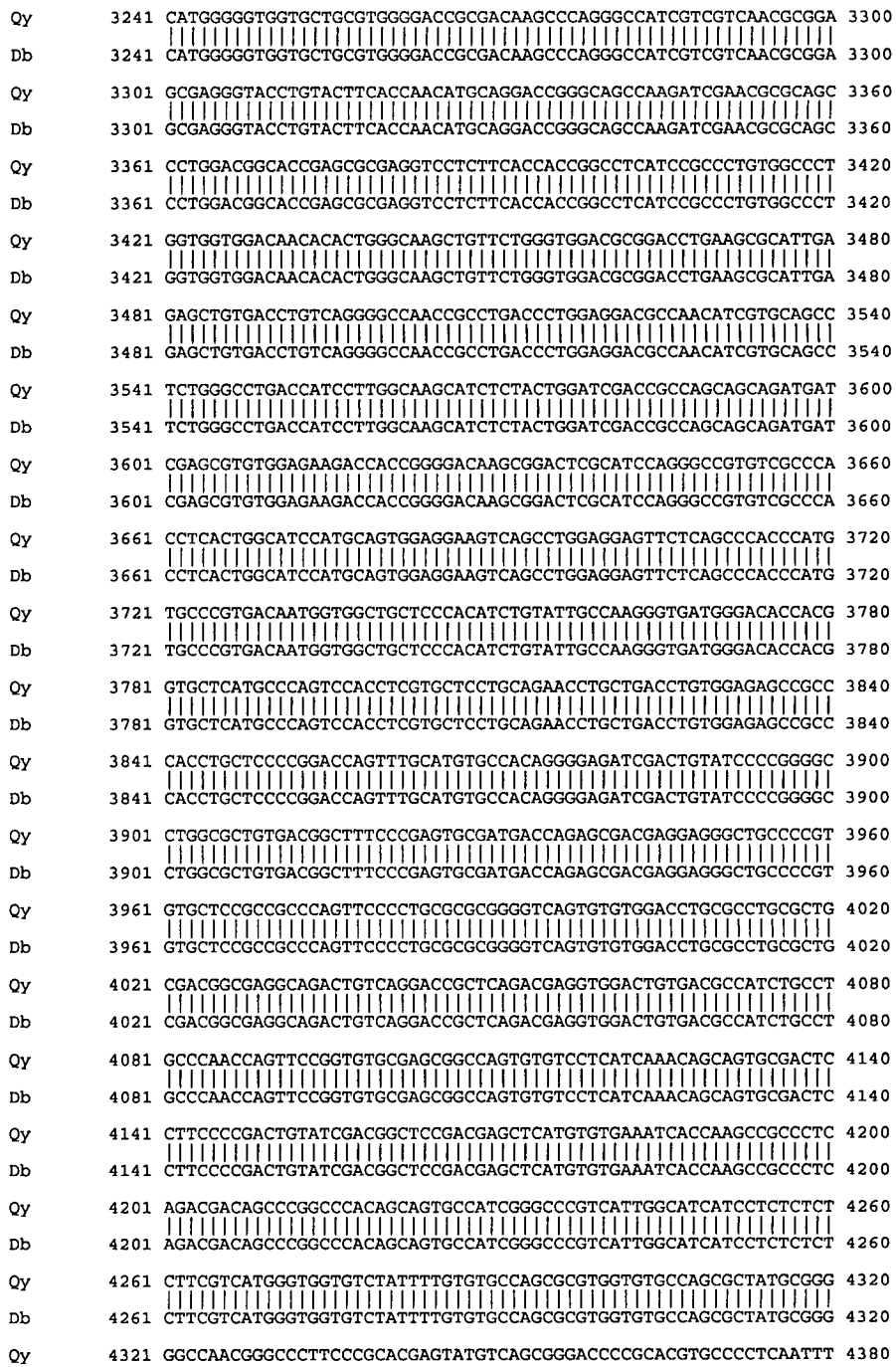
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RESULT 4
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; Sequence 1, Application US/09543771B
; Patent No. 6780609
; GENERAL INFORMATION:
;  APPLICANT: Carulli, John P.
;  APPLICANT:  Little, Randall D.
;  APPLICANT:  Recker, Robert R.
;  APPLICANT:  Johnson, Mark L.
;  TITLE OF INVENTION: High bone mass gene of 11q13.3
;  FILE REFERENCE: 032796-014
;  CURRENT APPLICATION NUMBER: US/09/543,771B
;  CURRENT FILING DATE:  2000-04-05
;  PRIOR APPLICATION NUMBER: US 09/229,319
;  PRIOR FILING DATE: 1999-01-13
;  PRIOR APPLICATION NUMBER: US 60/071,449
;  PRIOR FILING DATE: 1998-01-13
;  PRIOR APPLICATION NUMBER: US 60/105,511
;  PRIOR FILING DATE: 1998-10-23
;  NUMBER OF SEQ ID NOS: 641
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 5120
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-543-771B-1

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Qy       1501 CTGGGGAGAGAACCCTAAAATCGAGTGTGCCAACTTGGATGGGCAGGAGCGGCGTGTGCT 1560
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Qy       2761 CTCCCGCCAGGATGGCCTCAATGACTGTATGCACAACAACGGGCAGTGTGGGCAGCTGTG 2820
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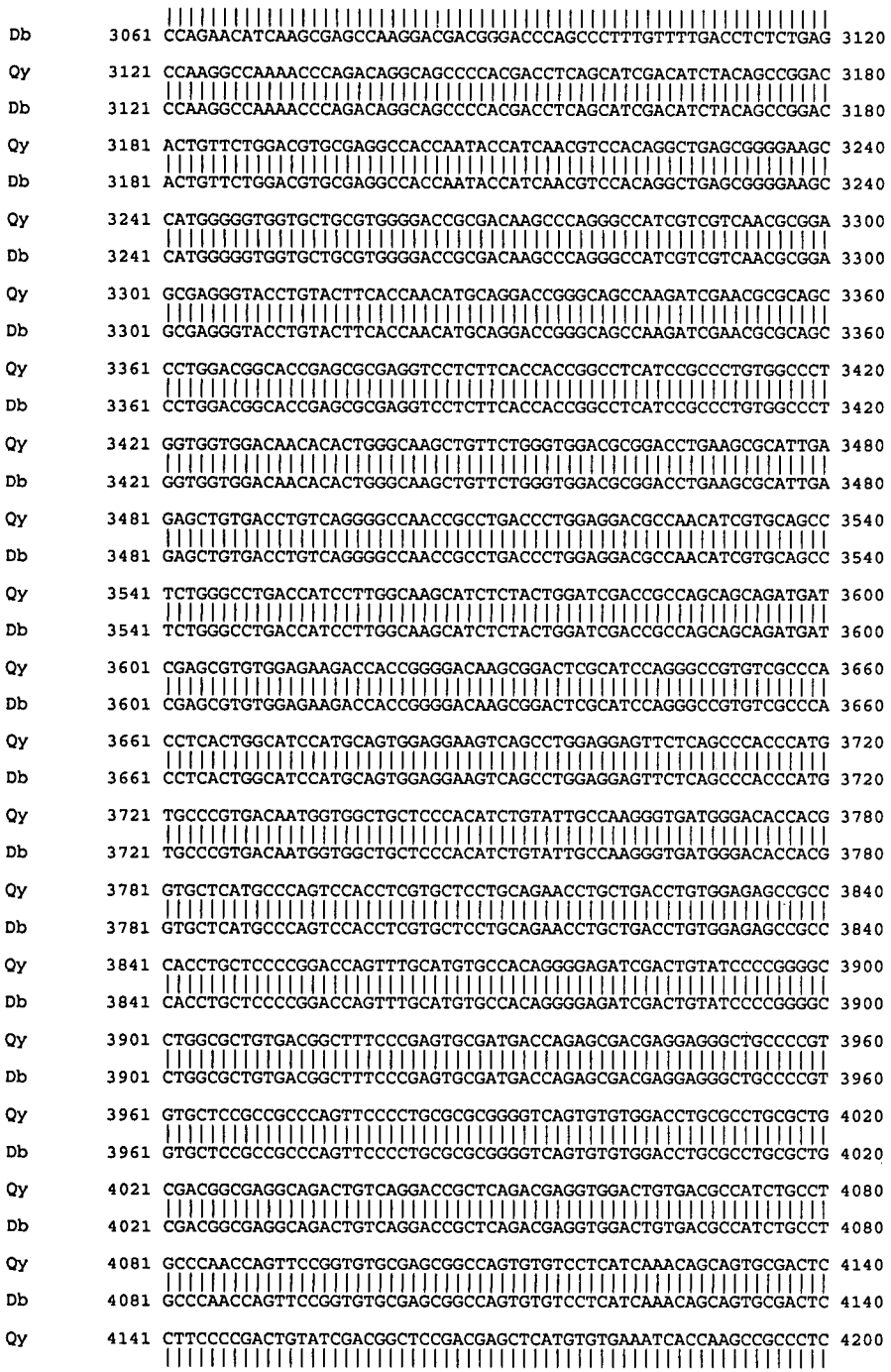
Qy       2821 CCTTGCCATCCCCGGCGGCCACCGCTGCGGCTGCGCCTCACACTACACCCTGGACCCCAG 2880
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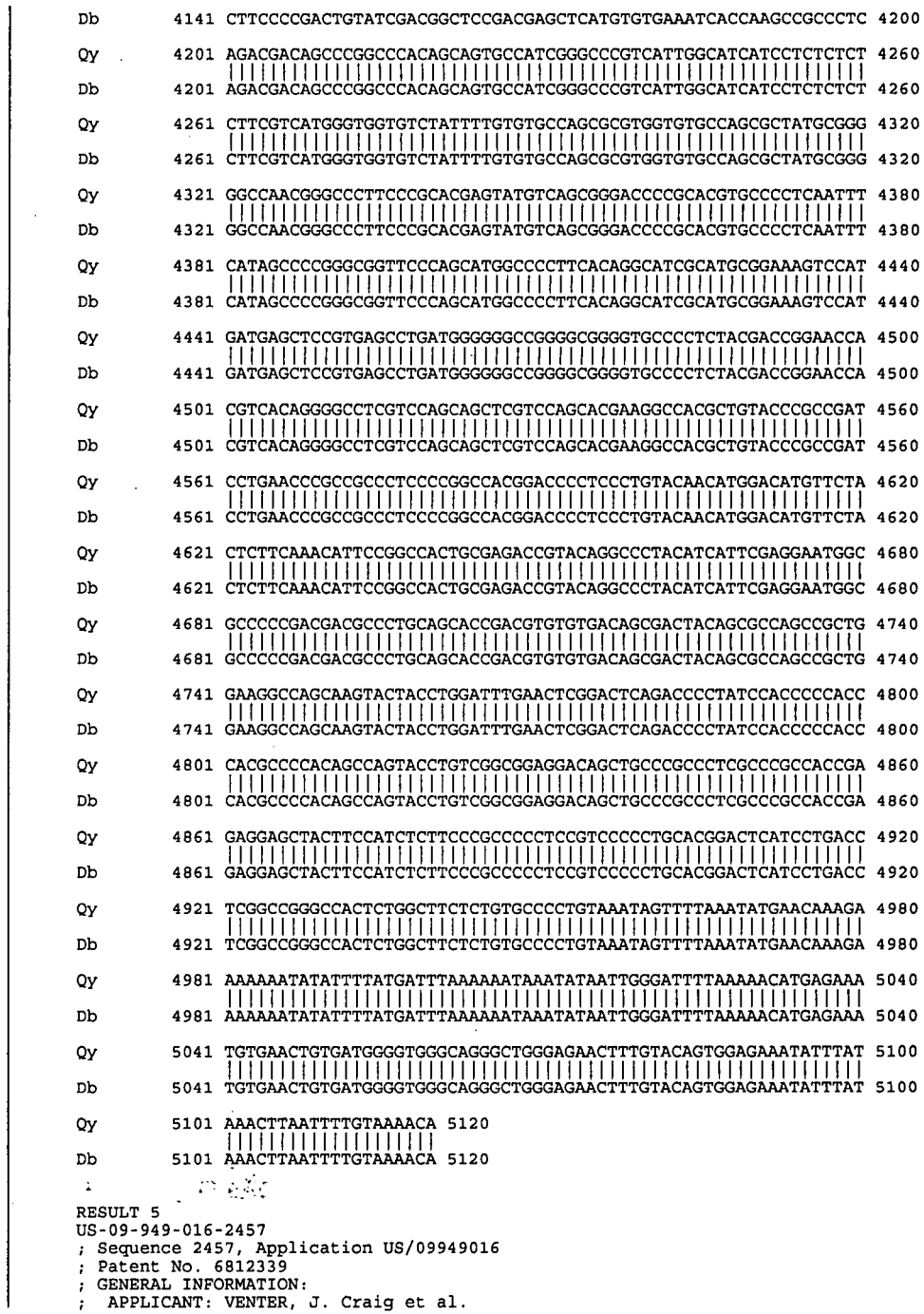
Qy       2881 CAGCCGCAACTGCAGCCCGCCCACCACCTTCTTGCTGTTCAGCCAGAAATCTGCCATCAG 2940
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Qy       2941 TCGGATGATCCCGGACGACCAGCACAGCCCGGATCTCATCCTGCCCCTGCATGGACTGAG 3000
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RESULT 5
US-09-949-016-2457
; Sequence 2457, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.

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;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2457
;   LENGTH: 5103
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-2457

  Query Match             99.2%;  Score 5080.8;  DB 4;  Length 5103;
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Qy      2423 AGGATCGTGCGGGCCTTCATGGACGGGACCAACTGCATGACGCTGGTGGACAAGGTGGGC 2482
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;    APPLICANT:  Todd, John A
;    APPLICANT:  Hess, John W
;    APPLICANT:  Caskey, Charles T
;    APPLICANT:  Cox, Roger D
;    APPLICANT:  Gerhold, David
;    APPLICANT:  Hammond, Holly
;    APPLICANT:  Hey, Patricia
;    APPLICANT:  Kawaguchi, Yoshihiko
;    APPLICANT:  Merriman, Tony R
;    APPLICANT:  Metzker, Michael L
;    TITLE OF INVENTION:  No. 6545137el Receptor
;    NUMBER OF SEQUENCES:  455
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Nixon and Vanderhye
;      STREET:  1100 No. 6545137th Glebe Road, Eighth Floor
;      CITY:  Arlington
;      STATE:  Virginia
;      COUNTRY:  US
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/060,299
;      FILING DATE:  15-APR-1998
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/043,553
;      FILING DATE:  15-APR-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/048,740
;      FILING DATE:  05-JUN-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  B.J.Sadoff
;      REGISTRATION NUMBER:  36,663
;      REFERENCE/DOCKET NUMBER:  620-35
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703)816-4091
;      TELEFAX:  (703)816-4100
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5098 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-060-299-1

  Query Match             98.7%;  Score 5053.4;  DB 4;  Length 5098;
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  Matches 5090;  Conservative    0;  Mismatches    6;  Indels    3;  Gaps    3;

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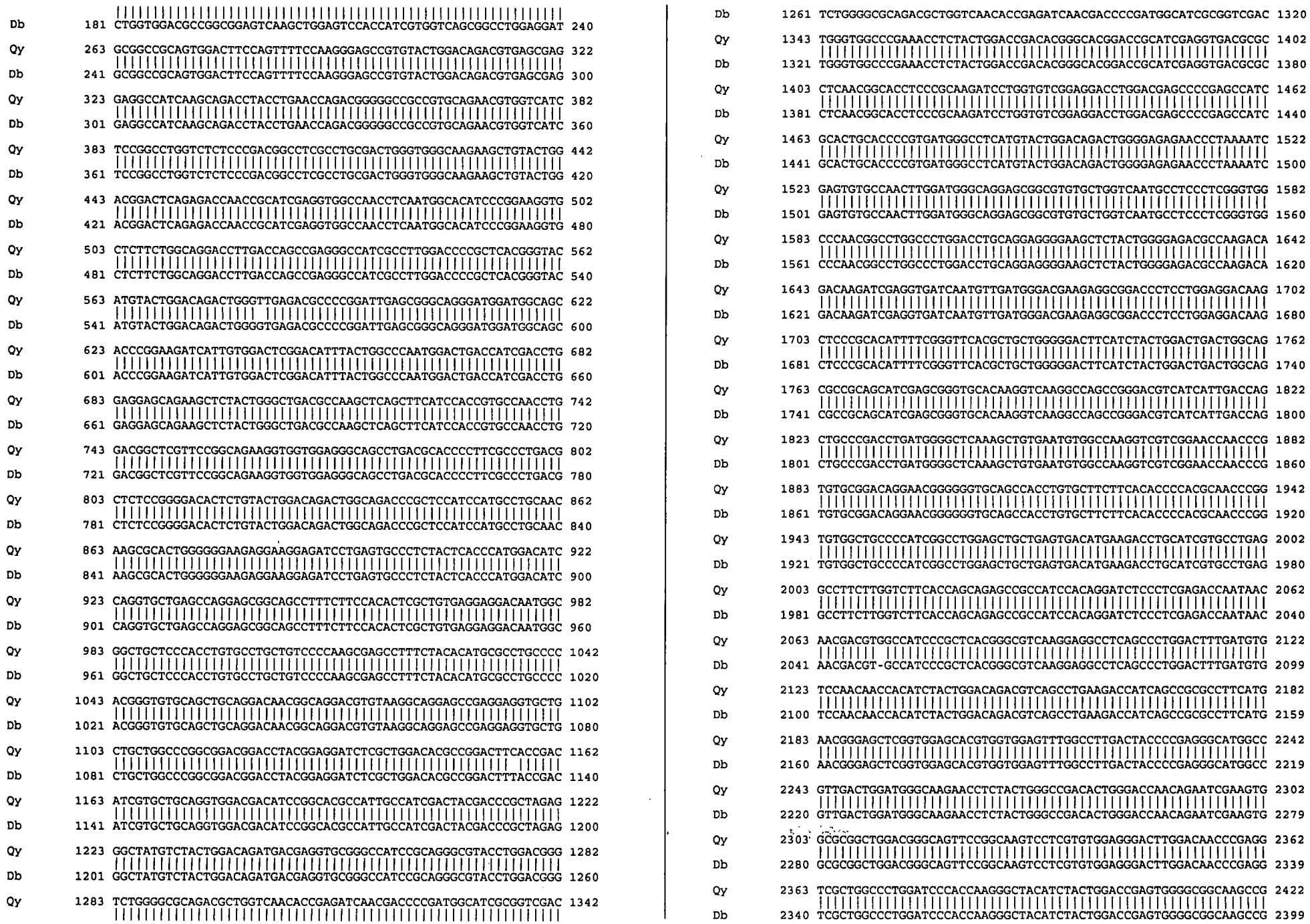
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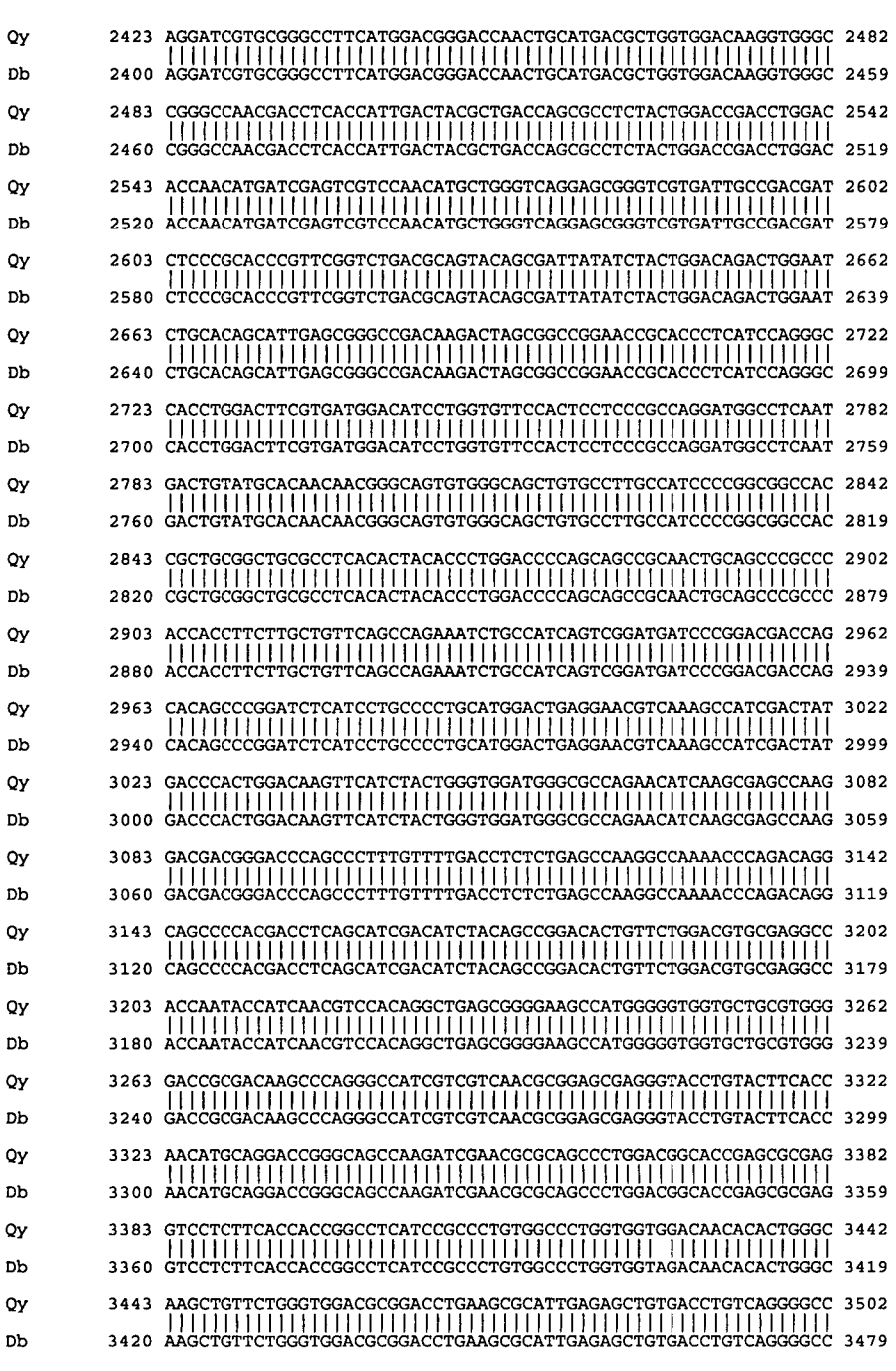
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RESULT 7
US-09-402-923A-1
; Sequence 1, Application US/09402923A
; Patent No. 6555654
;   GENERAL INFORMATION:
;        APPLICANT: Todd, John A
;                   Hess, John W
;                   Caskey, Charles T
;                   Cox, Roger D
;                   Gerhold, David
;                   Hammond, Holly
;                   Hey, Patricia
;                   Kawaguchi, Yoshihiko
;                   Merriman, Tony R
;                   Metzker, Michael L
;        TITLE OF INVENTION: No. 6555654el LDL-Receptor
;        NUMBER OF SEQUENCES: 455
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Nixon and Vanderhye
;             STREET: 1100 No. 6555654th Glebe Road, Eighth Floor
;             CITY: Arlington
;             STATE: Virginia
;             COUNTRY: US
;             ZIP: VA 22201-4714
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/402,923A
;             FILING DATE: 14-Feb-2001
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: PCT/GB98/01102
;             FILING DATE: 15-APR-1998
;             APPLICATION NUMBER: US 60/043,553
;             FILING DATE: 15-APR-1997
;             APPLICATION NUMBER: US 60/048,740
;             FILING DATE: 05-JUN-1997
;        ATTORNEY/AGENT INFORMATION:
;             NAME: B.J.Sadoff
;             REGISTRATION NUMBER: 36,663
;             REFERENCE/DOCKET NUMBER: 620-81
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (703)816-4091
;             TELEFAX: (703)816-4100
;   INFORMATION FOR SEQ ID NO: 1:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 5098 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-402-923A-1

  Query Match             98.7%;  Score 5053.4;  DB 4;  Length 5098;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 5090;  Conservative    0;  Mismatches    6;  Indels    3;  Gaps    3;

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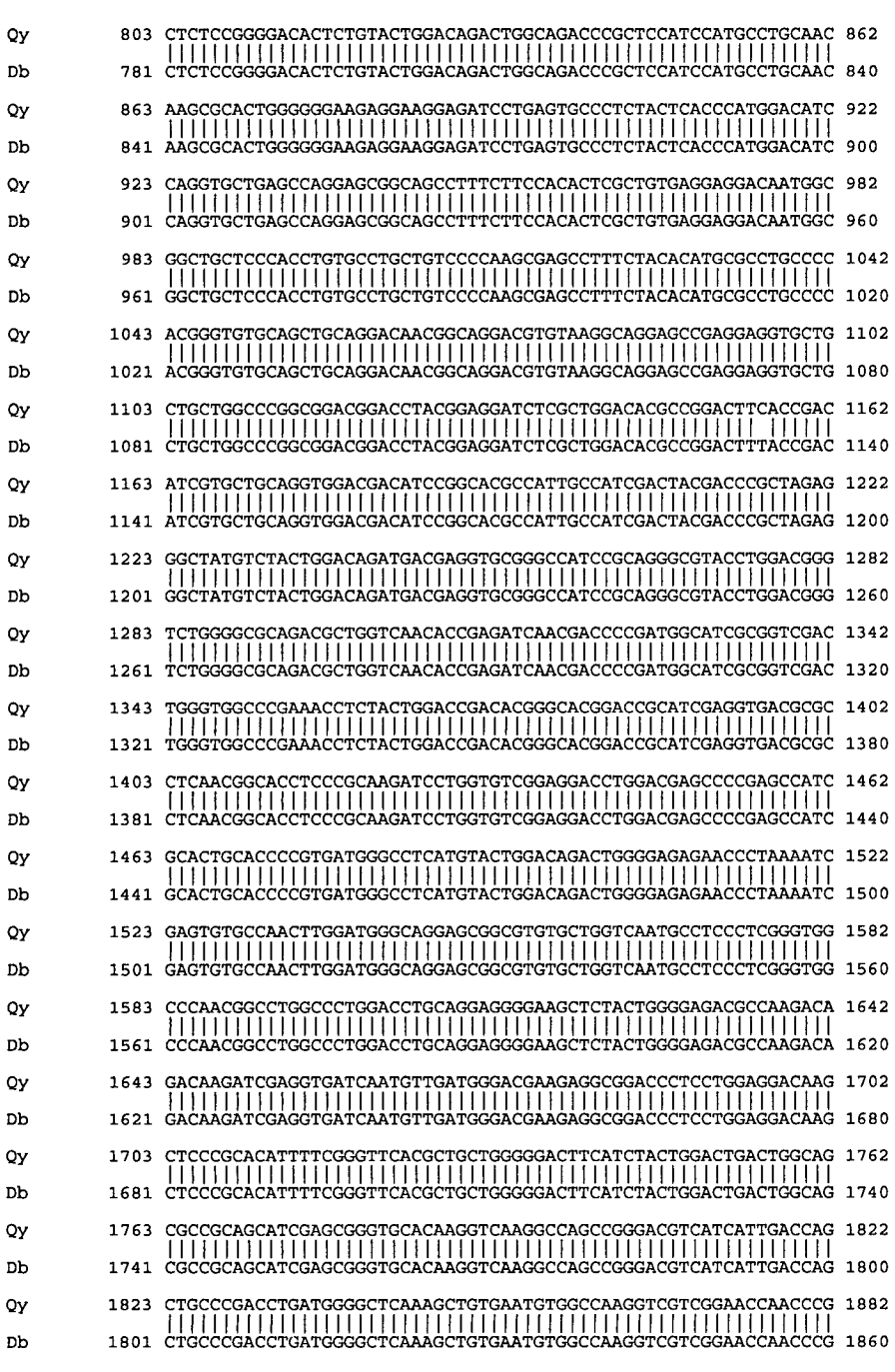
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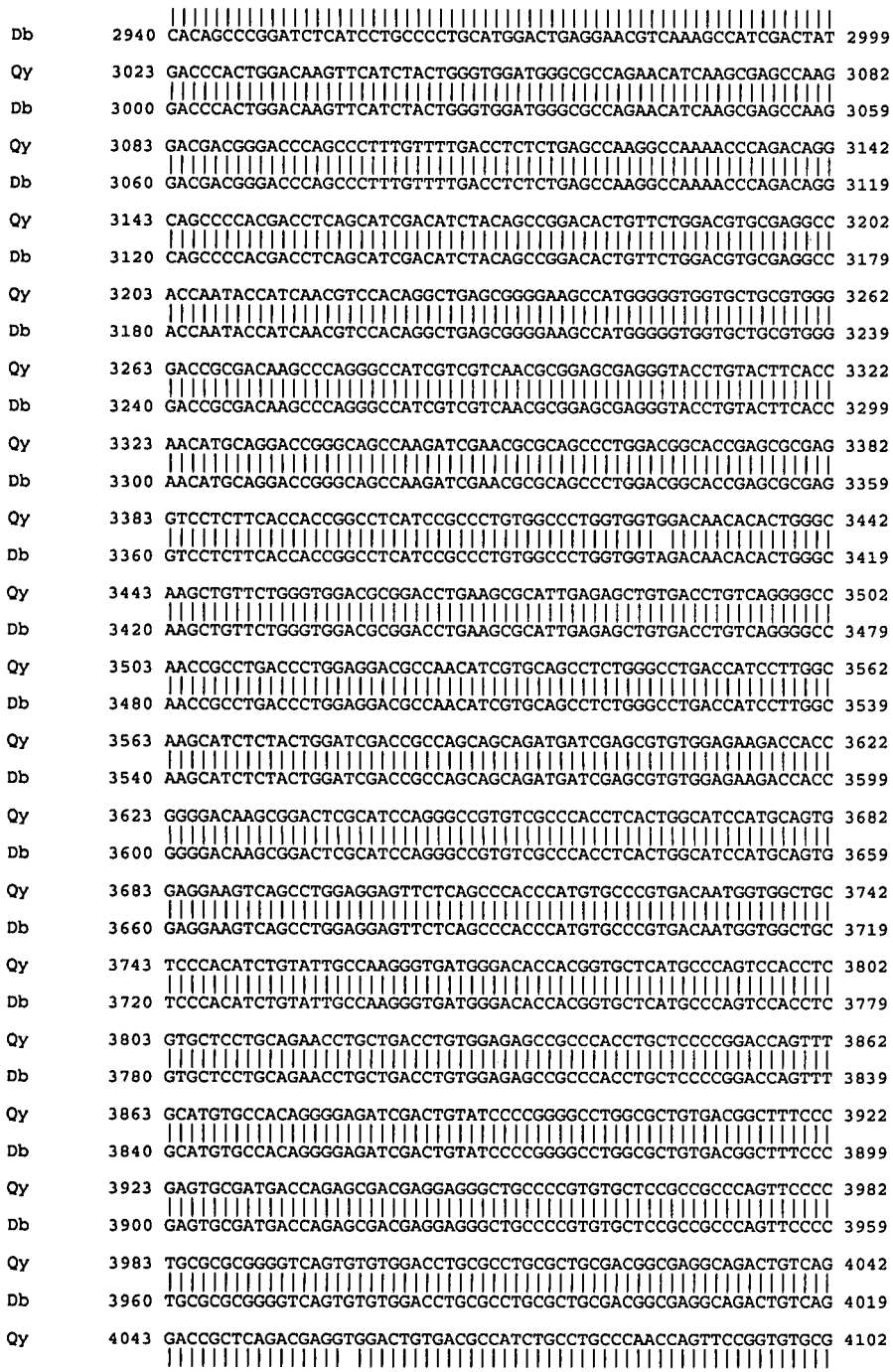
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Db        541 ATGTACTGGACAGACTGGGGTGAGACGCCCCGGATTGAGCGGGCAGGGATGGATGGCAGC 600

Qy        623 ACCCGGAAGATCATTGTGGACTCGGACATTTACTGGCCCAATGGACTGACCATCGACCTG 682
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Db        601 ACCCGGAAGATCATTGTGGACTCGGACATTTACTGGCCCAATGGACTGACCATCGACCTG 660

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Db        661 GAGGAGCAGAAGCTCTACTGGGCTGACGCCAAGCTCAGCTTCATCCACCGTGCCAACCTG 720

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Qy 923 CAGGTGCTGAGCCAGGAGCGGCAGCCTTTCTTCCACACTCGCTGTGAGGAGGACAATGGC 982
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RESULT 8
US-09-060-299-32

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; Sequence 32, Application US/09060299
; Patent No. 6545137
;  GENERAL INFORMATION:
;    APPLICANT:  Todd, John A
;    APPLICANT:  Hess, John W
;    APPLICANT:  Caskey, Charles T
;    APPLICANT:  Cox, Roger D
;    APPLICANT:  Gerhold, David
;    APPLICANT:  Hammond, Holly
;    APPLICANT:  Hey, Patricia
;    APPLICANT:  Kawaguchi, Yoshihiko
;    APPLICANT:  Merriman, Tony R
;    APPLICANT:  Metzker, Michael L
;    TITLE OF INVENTION:  No. 6545137el Receptor
;    NUMBER OF SEQUENCES:  455
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Nixon and Vanderhye
;      STREET:  1100 No. 6545137th Glebe Road, Eighth Floor
;      CITY:  Arlington
;      STATE:  Virginia
;      COUNTRY:  US
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/060,299
;      FILING DATE:  15-APR-1998
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/043,553
;      FILING DATE:  15-APR-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/048,740
;      FILING DATE:  05-JUN-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  B.J.Sadoff
;      REGISTRATION NUMBER:  36,663
;      REFERENCE/DOCKET NUMBER:  620-35
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703)816-4091
;      TELEFAX:  (703)816-4100
;  INFORMATION FOR SEQ ID NO:  32:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5022 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-060-299-32

  Query Match             96.2%;  Score 4927.4;  DB 4;  Length 5022;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 4953;  Conservative    0;  Mismatches    6;  Indels    2;  Gaps    2;

Qy        161 GCCTCGCCGCTCCTGCTATTTGCCAACCGCCGGGACGTACGGCTGGTGGACGCCGGCGGA 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 GCCTCGCCGCTCCTGCTATTTGCCAACCGCCGGGACGTACGGCTGGTGGACGCCGGCGGA 121

Qy        221 GTCAAGCTGGAGTCCACCATCGTGGTCAGCGGCCTGGAGGATGCGGCCGCAGTGGACTTC 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GTCAAGCTGGAGTCCACCATCGTGGTCAGCGGCCTGGAGGATGCGGCCGCAGTGGACTTC 181

Qy        281 CAGTTTTCCAAGGGAGCCGTGTACTGGACAGACGTGAGCGAGGAGGCCATCAAGCAGACC 340
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        182 CAGTTTTCCAAGGGAGCCGTGTACTGGACAGACG-GAGCGAGGAGGCCATCAAGCAGACC 240

Qy        341 TACCTGAACCAGACGGGGGCCGCCGTGCAGAACGTGGTCATCTCCGGCCTGGTCTCTCCC 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TACCTGAACCAGACGGGGGCCGCCGTGCAGAACGTGGTCATCTCCGGCCTGGTCTCTCCC 300

Qy        401 GACGGCCTCGCCTGCGACTGGGTGGGCAAGAAGCTGTACTGGACGGACTCAGAGACCAAC 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        301 GACGGCCTCGCCTGCGACTGGGTGGGCAAGAAGCTGTACTGGACGGACTCAGAGACCAAC 360

Qy        461 CGCATCGAGGTGGCCAACCTCAATGGCACATCCCGGAAGGTGCTCTTCTGGCAGGACCTT 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CGCATCGAGGTGGCCAACCTCAATGGCACATCCCGGAAGGTGCTCTTCTGGCAGGACCTT 420

Qy        521 GACCAGCCGAGGGCCATCGCCTTGGACCCCGCTCACGGGTACATGTACTGGACAGACTGG 580
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Db        421 GACCAGCCGAGGGCCATCGCCTTGGACCCCGCTCACGGGTACATGTACTGGACAGACTGG 480

Qy        581 GTTGAGACGCCCCGGATTGAGCGGGCAGGGATGGATGGCAGCACCCGGAAGATCATTGTG 640
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Db        481 GGTGAGACGCCCCGGATTGAGCGGGCAGGGATGGATGGCAGCACCCGGAAGATCATTGTG 540

Qy        641 GACTCGGACATTTACTGGCCCAATGGACTGACCATCGACCTGGAGGAGCAGAAGCTCTAC 700
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GACTCGGACATTTACTGGCCCAATGGACTGACCATCGACCTGGAGGAGCAGAAGCTCTAC 600

Qy        701 TGGGCTGACGCCAAGCTCAGCTTCATCCACCGTGCCAACCTGGACGGCTCGTTCCGGCAG 760
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TGGGCTGACGCCAAGCTCAGCTTCATCCACCGTGCCAACCTGGACGGCTCGTTCCGGCAG 660

Qy        761 AAGGTGGTGGAGGGCAGCCTGACGCACCCCTTCGCCCTGACGCTCTCCGGGGACACTCTG 820
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AAGGTGGTGGAGGGCAGCCTGACGCACCCCTTCGCCCTGACGCTCTCCGGGGACACTCTG 720

Qy        821 TACTGGACAGACTGGCAGACCCGCTCCATCCATGCCTGCAACAAGCGCACTGGGGGGAAG 880
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Db        721 TACTGGACAGACTGGCAGACCCGCTCCATCCATGCCTGCAACAAGCGCACTGGGGGGAAG 780

Qy        881 AGGAAGGAGATCCTGAGTGCCCTCTACTCACCCATGGACATCCAGGTGCTGAGCCAGGAG 940
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AGGAAGGAGATCCTGAGTGCCCTCTACTCACCCATGGACATCCAGGTGCTGAGCCAGGAG 840

Qy        941 CGGCAGCCTTTCTTCCACACTCGCTGTGAGGAGGACAATGGCGGCTGCTCCCACCTGTGC 1000
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CGGCAGCCTTTCTTCCACACTCGCTGTGAGGAGGACAATGGCGGCTGCTCCCACCTGTGC 900

Qy       1001 CTGCTGTCCCCAAGCGAGCCTTTCTACACATGCGCCTGCCCCACGGGTGTGCAGCTGCAG 1060
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CTGCTGTCCCCAAGCGAGCCTTTCTACACATGCGCCTGCCCCACGGGTGTGCAGCTGCAG 960

Qy       1061 GACAACGGCAGGACGTGTAAGGCAGGAGCCGAGGAGGTGCTGCTGCTGGCCCGGCGGACG 1120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GACAACGGCAGGACGTGTAAGGCAGGAGCCGAGGAGGTGCTGCTGCTGGCCCGGCGGACG 1020

Qy       1121 GACCTACGGAGGATCTCGCTGGACACGCCGGACTTCACCGACATCGTGCTGCAGGTGGAC 1180
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db       1021 GACCTACGGAGGATCTCGCTGGACACGCCGGACTTTACCGACATCGTGCTGCAGGTGGAC 1080

Qy       1181 GACATCCGGCACGCCATTGCCATCGACTACGACCCGCTAGAGGGCTATGTCTACTGGACA 1240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 GACATCCGGCACGCCATTGCCATCGACTACGACCCGCTAGAGGGCTATGTCTACTGGACA 1140

Qy       1241 GATGACGAGGTGCGGGCCATCCGCAGGGCGTACCTGGACGGGTCTGGGGCGCAGACGCTG 1300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GATGACGAGGTGCGGGCCATCCGCAGGGCGTACCTGGACGGGTCTGGGGCGCAGACGCTG 1200

Qy       1301 GTCAACACCGAGATCAACGACCCCGATGGCATCGCGGTCGACTGGGTGGCCCGAAACCTC 1360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GTCAACACCGAGATCAACGACCCCGATGGCATCGCGGTCGACTGGGTGGCCCGAAACCTC 1260

Qy       1361 TACTGGACCGACACGGGCACGGACCGCATCGAGGTGACGCGCCTCAACGGCACCTCCCGC 1420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 TACTGGACCGACACGGGCACGGACCGCATCGAGGTGACGCGCCTCAACGGCACCTCCCGC 1320

Qy       1421 AAGATCCTGGTGTCGGAGGACCTGGACGAGCCCCGAGCCATCGCACTGCACCCCGTGATG 1480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 AAGATCCTGGTGTCGGAGGACCTGGACGAGCCCCGAGCCATCGCACTGCACCCCGTGATG 1380

Qy       1481 GGCCTCATGTACTGGACAGACTGGGGAGAGAACCCTAAAATCGAGTGTGCCAACTTGGAT 1540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 GGCCTCATGTACTGGACAGACTGGGGAGAGAACCCTAAAATCGAGTGTGCCAACTTGGAT 1440
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Qy       1541 GGGCAGGAGCGGCGTGTGCTGGTCAATGCCTCCCTCGGGTGGCCCAACGGCCTGGCCCTG 1600
Db       1441 GGGCAGGAGCGGCGTGTGCTGGTCAATGCCTCCCTCGGGTGGCCCAACGGCCTGGCCCTG 1500

Qy       1601 GACCTGCAGGAGGGGAAGCTCTACTGGGGAGACGCCAAGACAGACAAGATCGAGGTGATC 1660
Db       1501 GACCTGCAGGAGGGGAAGCTCTACTGGGGAGACGCCAAGACAGACAAGATCGAGGTGATC 1560

Qy       1661 AATGTTGATGGGACGAAGAGGCGGACCCTCCTGGAGGACAAGCTCCCGCACATTTTCGGG 1720
Db       1561 AATGTTGATGGGACGAAGAGGCGGACCCTCCTGGAGGACAAGCTCCCGCACATTTTCGGG 1620

Qy       1721 TTCACGCTGCTGGGGGACTTCATCTACTGGACTGACTGGCAGCGCCGCAGCATCGAGCGG 1780
Db       1621 TTCACGCTGCTGGGGGACTTCATCTACTGGACTGACTGGCAGCGCCGCAGCATCGAGCGG 1680

Qy       1781 GTGCACAAGGTCAAGGCCAGCCGGGACGTCATCATTGACCAGCTGCCCGACCTGATGGGG 1840
Db       1681 GTGCACAAGGTCAAGGCCAGCCGGGACGTCATCATTGACCAGCTGCCCGACCTGATGGGG 1740

Qy       1841 CTCAAAGCTGTGAATGTGGCCAAGGTCGTCGGAACCAACCCGTGTGCGGACAGGAACGGG 1900
Db       1741 CTCAAAGCTGTGAATGTGGCCAAGGTCGTCGGAACCAACCCGTGTGCGGACAGGAACGGG 1800

Qy       1901 GGGTGCAGCCACCTGTGCTTCTTCACACCCCACGCAACCCGGTGTGGCTGCCCCATCGGC 1960
Db       1801 GGGTGCAGCCACCTGTGCTTCTTCACACCCCACGCAACCCGGTGTGGCTGCCCCATCGGC 1860

Qy       1961 CTGGAGCTGCTGAGTGACATGAAGACCTGCATCGTGCCTGAGGCCTTCTTGGTCTTCACC 2020
Db       1861 CTGGAGCTGCTGAGTGACATGAAGACCTGCATCGTGCCTGAGGCCTTCTTGGTCTTCACC 1920

Qy       2021 AGCAGAGCCGCCATCCACAGGATCTCCCTCGAGACCAATAACAACGACGTGGCCATCCCG 2080
Db       1921 AGCAGAGCCGCCATCCACAGGATCTCCCTCGAGACCAATAACAACGACGTGGCCATCCCG 1980

Qy       2081 CTCACGGGCGTCAAGGAGGCCTCAGCCCTGGACTTTGATGTGTCCAACAACCACATCTAC 2140
Db       1981 CTCACGGGCGTCAAGGAGGCCTCAGCCCTGGACTTTGATGTGTCCAACAACCACATCTAC 2040

Qy       2141 TGGACAGACGTCAGCCTGAAGACCATCAGCCGCGCCTTCATGAACGGGAGCTCGGTGGAG 2200
Db       2041 TGGACAGACGTCAGCCTGAAGACCATCAGCCGCGCCTTCATGAACGGGAGCTCGGTGGAG 2100

Qy       2201 CACGTGGTGGAGTTTGGCCTTGACTACCCCGAGGGCATGGCCGTTGACTGGATGGGCAAG 2260
Db       2101 CACGTGGTGGAGTTTGGCCTTGACTACCCCGAGGGCATGGCCGTTGACTGGATGGGCAAG 2160

Qy       2261 AACCTCTACTGGGCCGACACTGGGACCAACAGAATCGAAGTGGCGCGGCTGGACGGGCAG 2320
Db       2161 AACCTCTACTGGGCCGACACTGGGACCAACAGAATCGAAGTGGCGCGGCTGGACGGGCAG 2220

Qy       2321 TTCCGGCAAGTCCTCGTGTGGAGGGACTTGGACAACCCGAGGTCGCTGGCCCTGGATCCC 2380
Db       2221 TTCCGGCAAGTCCTCGTGTGGAGGGACTTGGACAACCCGAGGTCGCTGGCCCTGGATCCC 2280

Qy       2381 ACCAAGGGCTACATCTACTGGACCGAGTGGGGCGGCAAGCCGAGGATCGTGCGGGCCTTC 2440
Db       2281 ACCAAGGGCTACATCTACTGGACCGAGTGGGGCGGCAAGCCGAGGATCGTGCGGGCCTTC 2340

Qy       2441 ATGGACGGGACCAACTGCATGACGCTGGTGGACAAGGTGGGCCGGGCCAACGACCTCACC 2500
Db       2341 ATGGACGGGACCAACTGCATGACGCTGGTGGACAAGGTGGGCCGGGCCAACGACCTCACC 2400

Qy       2501 ATTGACTACGCTGACCAGCGCCTCTACTGGACCGACCTGGACACCAACATGATCGAGTCG 2560
Db       2401 ATTGACTACGCTGACCAGCGCCTCTACTGGACCGACCTGGACACCAACATGATCGAGTCG 2460

Qy       2561 TCCAACATGCTGGGTCAGGAGCGGGTCGTGATTGCCGACGATCTCCCGCACCCGTTCGGT 2620
Db       2461 TCCAACATGCTGGGTCAGGAGCGGGTCGTGATTGCCGACGATCTCCCGCACCCGTTCGGT 2520

Qy       2621 CTGACGCAGTACAGCGATTATATCTACTGGACAGACTGGAATCTGCACAGCATTGAGCGG 2680
Db       2521 CTGACGCAGTACAGCGATTATATCTACTGGACAGACTGGAATCTGCACAGCATTGAGCGG 2580

Qy       2681 GCCGACAAGACTAGCGGCCGGAACCGCACCCTCATCCAGGGCCACCTGGACTTCGTGATG 2740
Db       2581 GCCGACAAGACTAGCGGCCGGAACCGCACCCTCATCCAGGGCCACCTGGACTTCGTGATG 2640

Qy       2741 GACATCCTGGTGTTCCACTCCTCCCGCCAGGATGGCCTCAATGACTGTATGCACAACAAC 2800
Db       2641 GACATCCTGGTGTTCCACTCCTCCCGCCAGGATGGCCTCAATGACTGTATGCACAACAAC 2700

Qy       2801 GGGCAGTGTGGGCAGCTGTGCCTTGCCATCCCCGGCGGCCACCGCTGCGGCTGCGCCTCA 2860
Db       2701 GGGCAGTGTGGGCAGCTGTGCCTTGCCATCCCCGGCGGCCACCGCTGCGGCTGCGCCTCA 2760

Qy       2861 CACTACACCCTGGACCCCAGCAGCCGCAACTGCAGCCCGCCCACCACCTTCTTGCTGTTC 2920
Db       2761 CACTACACCCTGGACCCCAGCAGCCGCAACTGCAGCCCGCCCACCACCTTCTTGCTGTTC 2820

Qy       2921 AGCCAGAAATCTGCCATCAGTCGGATGATCCCGGACGACCAGCACAGCCCGGATCTCATC 2980
Db       2821 AGCCAGAAATCTGCCATCAGTCGGATGATCCCGGACGACCAGCACAGCCCGGATCTCATC 2880

Qy       2981 CTGCCCCTGCATGGACTGAGGAACGTCAAAGCCATCGACTATGACCCACTGGACAAGTTC 3040
Db       2881 CTGCCCCTGCATGGACTGAGGAACGTCAAAGCCATCGACTATGACCCACTGGACAAGTTC 2940

Qy       3041 ATCTACTGGGTGGATGGGCGCCAGAACATCAAGCGAGCCAAGGACGACGGGACCCAGCCC 3100
Db       2941 ATCTACTGGGTGGATGGGCGCCAGAACATCAAGCGAGCCAAGGACGACGGGACCCAGCCC 3000

Qy       3101 TTTGTTTTGACCTCTCTGAGCCAAGGCCAAAACCCAGACAGGCAGCCCCACGACCTCAGC 3160
Db       3001 TTTGTTTTGACCTCTCTGAGCCAAGGCCAAAACCCAGACAGGCAGCCCCACGACCTCAGC 3060

Qy       3161 ATCGACATCTACAGCCGGACACTGTTCTGGACGTGCGAGGCCACCAATACCATCAACGTC 3220
Db       3061 ATCGACATCTACAGCCGGACACTGTTCTGGACGTGCGAGGCCACCAATACCATCAACGTC 3120

Qy       3221 CACAGGCTGAGCGGGGAAGCCATGGGGGTGGTGCTGCGTGGGGACCGCGACAAGCCCAGG 3280
Db       3121 CACAGGCTGAGCGGGGAAGCCATGGGGGTGGTGCTGCGTGGGGACCGCGACAAGCCCAGG 3180

Qy       3281 GCCATCGTCGTCAACGCGGAGCGAGGGTACCTGTACTTCACCAACATGCAGGACCGGGCA 3340
Db       3181 GCCATCGTCGTCAACGCGGAGCGAGGGTACCTGTACTTCACCAACATGCAGGACCGGGCA 3240

Qy       3341 GCCAAGATCGAACGCGCAGCCCTGGACGGCACCGAGCGCGAGGTCCTCTTCACCACCGGC 3400
Db       3241 GCCAAGATCGAACGCGCAGCCCTGGACGGCACCGAGCGCGAGGTCCTCTTCACCACCGGC 3300

Qy       3401 CTCATCCGCCCTGTGGCCCTGGTGGTGGACAACACACTGGGCAAGCTGTTCTGGGTGGAC 3460
Db       3301 CTCATCCGCCCTGTGGCCCTGGTGGTAGACAACACACTGGGCAAGCTGTTCTGGGTGGAC 3360

Qy       3461 GCGGACCTGAAGCGCATTGAGAGCTGTGACCTGTCAGGGGCCAACCGCCTGACCCTGGAG 3520
Db       3361 GCGGACCTGAAGCGCATTGAGAGCTGTGACCTGTCAGGGGCCAACCGCCTGACCCTGGAG 3420

Qy       3521 GACGCCAACATCGTGCAGCCTCTGGGCCTGACCATCCTTGGCAAGCATCTCTACTGGATC 3580
Db       3421 GACGCCAACATCGTGCAGCCTCTGGGCCTGACCATCCTTGGCAAGCATCTCTACTGGATC 3480

Qy       3581 GACCGCCAGCAGCAGATGATCGAGCGTGTGGAGAAGACCACCGGGGACAAGCGGACTCGC 3640
Db       3481 GACCGCCAGCAGCAGATGATCGAGCGTGTGGAGAAGACCACCGGGGACAAGCGGACTCGC 3540

Qy       3641 ATCCAGGGCCGTGTCGCCCACCTCACTGGCATCCATGCAGTGGAGGAAGTCAGCCTGGAG 3700
Db       3541 ATCCAGGGCCGTGTCGCCCACCTCACTGGCATCCATGCAGTGGAGGAAGTCAGCCTGGAG 3600

Qy       3701 GAGTTCTCAGCCCACCCATGTGCCCGTGACAATGGTGGCTGCTCCCACATCTGTATTGCC 3760
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Db       3601 GAGTTCTCAGCCCACCCATGTGCCCGTGACAATGGTGGCTGCTCCCACATCTGTATTGCC 3660

Qy       3761 AAGGGTGATGGGACACCACGGTGCTCATGCCCAGTCCACCTCGTGCTCCTGCAGAACCTG 3820
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Db       3661 AAGGGTGATGGGACACCACGGTGCTCATGCCCAGTCCACCTCGTGCTCCTGCAGAACCTG 3720

Qy       3821 CTGACCTGTGGAGAGCCGCCCACCTGCTCCCCGGACCAGTTTGCATGTGCCACAGGGGAG 3880
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3721 CTGACCTGTGGAGAGCCGCCCACCTGCTCCCCGGACCAGTTTGCATGTGCCACAGGGGAG 3780

Qy       3881 ATCGACTGTATCCCCGGGGCCTGGCGCTGTGACGGCTTTCCCGAGTGCGATGACCAGAGC 3940
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Db       3781 ATCGACTGTATCCCCGGGGCCTGGCGCTGTGACGGCTTTCCCGAGTGCGATGACCAGAGC 3840

Qy       3941 GACGAGGAGGGCTGCCCCGTGTGCTCCGCCGCCCAGTTCCCCTGCGCGCGGGGTCAGTGT 4000
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3841 GACGAGGAGGGCTGCCCCGTGTGCTCCGCCGCCCAGTTCCCCTGCGCGCGGGGTCAGTGT 3900

Qy       4001 GTGGACCTGCGCCTGCGCTGCGACGGCGAGGCAGACTGTCAGGACCGCTCAGACGAGGTG 4060
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db       3901 GTGGACCTGCGCCTGCGCTGCGACGGCGAGGCAGACTGTCAGGACCGCTCAGACGAGGCG 3960

Qy       4061 GACTGTGACGCCATCTGCCTGCCCAACCAGTTCCGGTGTGCGAGCGGCCAGTGTGTCCTC 4120
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Db       3961 GACTGTGACGCCATCTGCCTGCCCAACCAGTTCCGGTGTGCGAGCGGCCAGTGTGTCCTC 4020

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Db       4021 ATCAAACAGCAGTGCGACTCCTTCCCCGACTGTATCGACGGCTCCGACGAGCTCATGTGT 4080

Qy       4181 GAAATCACCAAGCCGCCCTCAGACGACAGCCCGGCCCACAGCAGTGCCATCGGGCCCGTC 4240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4081 GAAATCACCAAGCCGCCCTCAGACGACAGCCCGGCCCACAGCAGTGCCATCGGGCCCGTC 4140

Qy       4241 ATTGGCATCATCCTCTCTCTCTTCGTCATGGGTGGTGTCTATTTTGTGTGCCAGCGCGTG 4300
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Db       4141 ATTGGCATCATCCTCTCTCTCTTCGTCATGGGTGGTGTCTATTTTGTGTGCCAGCGCGTG 4200

Qy       4301 GTGTGCCAGCGCTATGCGGGGGCCAACGGGCCCTTCCCGCACGAGTATGTCAGCGGGACC 4360
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Db       4201 GTGTGCCAGCGCTATGCGGGGGCCAACGGGCCCTTCCCGCACGAGTATGTCAGCGGGACC 4260

Qy       4361 CCGCACGTGCCCCTCAATTTCATAGCCCCGGGCGGTTCCCAGCATGGCCCCTTCACAGGC 4420
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Db       4261 CCGCACGTGCCCCTCAATTTCATAGCCCCGGGCGGTTCCCAGCATGGCCCCTTCACAGGC 4320

Qy       4421 ATCGCATGCGGAAAGTCCATGATGAGCTCCGTGAGCCTGATGGGGGGCCGGGGCGGGGTG 4480
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Db       4321 ATCGCATGCGGAAAGTCCATGATGAGCTCCGTGAGCCTGATGGGGGGCCGGGGCGGGGTG 4380

Qy       4481 CCCCTCTACGACCGGAACCACGTCACAGGGGCCTCGTCCAGCAGCTCGTCCAGCACGAAG 4540
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Db       4381 CCCCTCTACGACCGGAACCACGTCACAGGGGCCTCGTCCAGCAGCTCGTCCAGCACGAAG 4440

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Qy       4601 TACAACATGGACATGTTCTACTCTTCAAACATTCCGGCCACTGCGAGACCGTACAGGCCC 4660
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Db       4501 TACAACATGGACATGTTCTACTCTTCAAACATTCCGGCCACTGTGAGACCGTACAGGCCC 4560

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Db       4561 TACATCATTCGAGGAATGGCGCCCCCGACGACGCCCTGCAGCACCGACGTGTGTGACAGC 4620

Qy       4721 GACTACAGCGCCAGCCGCTGGAAGGCCAGCAAGTACTACCTGGATTTGAACTCGGACTCA 4780
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Db       4621 GACTACAGCGCCAGCCGCTGGAAGGCCAGCAAGTACTACCTGGATTTGAACTCGGACTCA 4680

Qy       4781 GACCCCTATCCACCCCCACCCACGCCCCACAGCCAGTACCTGTCGGCGGAGGACAGCTGC 4840
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Db       4681 GACCCCTATCCACCCCCACCCACGCCCCACAGCCAGTACCTGTCGGCGGAGGACAGCTGC 4740

Qy       4841 CCGCCCTCGCCCGCCACCGAGAGGAGCTACTTCCATCTCTTCCCGCCCCCTCCGTCCCCC 4900
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Db       4741 CCGCCCTCGCCCGCCACCGAGAGGAGCTACTTCCATCTCTTCCCGCCCCCTCCGTCCCCC 4800

Qy       4901 TGCACGGACTCATCCTGACCTCGGCCGGGCCACTCTGGCTTCTCTGTGCCCCTGTAAATA 4960
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Db       4801 TGCACGGACTCATCCTGACCTCGGCCGGGCCACTCTGGCTTCTCTGTGCCCCTGTAAATA 4860

Qy       4961 GTTTTAAATATGAACAAAGAAAAAAATATATTTTATGATTTAAAAAATAAATATAATTGG 5020
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Db       4861 GTTTTAAATATGAACAAAGAAAAAAATATATTTTATGATTTAAAAAATAAATATAATTGG 4920

Qy       5021 GATTTTAAAAACATGAGAAATGTGAACTGTGATGGGGTGGGCAGGGCTGGGAGAACTTTG 5080
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4921 GATTTTAAAAACATGAGAAATGTGAACTGTGATGGGGTGGGCAGGGCTGGGAGAACTTTG 4980

Qy       5081 TACAGTGG-AGAAATATTTATAAACTTAATTTTGTAAAACA 5120
                |||||||| | ||||||||||||||||||||||||||||
Db       4981 TACAGTGGAACAAATATTTATAAACTTAATTTTGTAAAACA 5021
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RESULT 9
US-09-402-923A-32
; Sequence 32, Application US/09402923A
; Patent No. 6555654
;   GENERAL INFORMATION:
;        APPLICANT: Todd, John A
;                   Hess, John W
;                   Caskey, Charles T
;                   Cox, Roger D
;                   Gerhold, David
;                   Hammond, Holly
;                   Hey, Patricia
;                   Kawaguchi, Yoshihiko
;                   Merriman, Tony R
;                   Metzker, Michael L
;        TITLE OF INVENTION: No. 6555654el LDL-Receptor
;        NUMBER OF SEQUENCES: 455
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Nixon and Vanderhye
;             STREET: 1100 No. 6555654th Glebe Road, Eighth Floor
;             CITY: Arlington
;             STATE: Virginia
;             COUNTRY: US
;             ZIP: VA 22201-4714
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/402,923A
;             FILING DATE: 14-Feb-2001
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: PCT/GB98/01102
;             FILING DATE: 15-APR-1998
;             APPLICATION NUMBER: US 60/043,553
;             FILING DATE: 15-APR-1997
;             APPLICATION NUMBER: US 60/048,740
;             FILING DATE: 05-JUN-1997
;        ATTORNEY/AGENT INFORMATION:
;             NAME: B.J.Sadoff
;             REGISTRATION NUMBER: 36,663
;             REFERENCE/DOCKET NUMBER: 620-81
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (703)816-4091
;             TELEFAX: (703)816-4100
;   INFORMATION FOR SEQ ID NO: 32:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 5022 base pairs
;             TYPE: nucleic acid
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;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 32:
US-09-402-923A-32

  Query Match             96.2%;  Score 4927.4;  DB 4;  Length 5022;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 4953;  Conservative    0;  Mismatches    6;  Indels    2;  Gaps    2;

Qy        161 GCCTCGCCGCTCCTGCTATTTGCCAACCGCCGGGACGTACGGCTGGTGGACGCCGGCGGA 220
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Qy       1481 GGCCTCATGTACTGGACAGACTGGGGAGAGAACCCTAAAATCGAGTGTGCCAACTTGGAT 1540
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Qy       1541 GGGCAGGAGCGGCGTGTGCTGGTCAATGCCTCCCTCGGGTGGCCCAACGGCCTGGCCCTG 1600
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Qy       1781 GTGCACAAGGTCAAGGCCAGCCGGGACGTCATCATTGACCAGCTGCCCGACCTGATGGGG 1840
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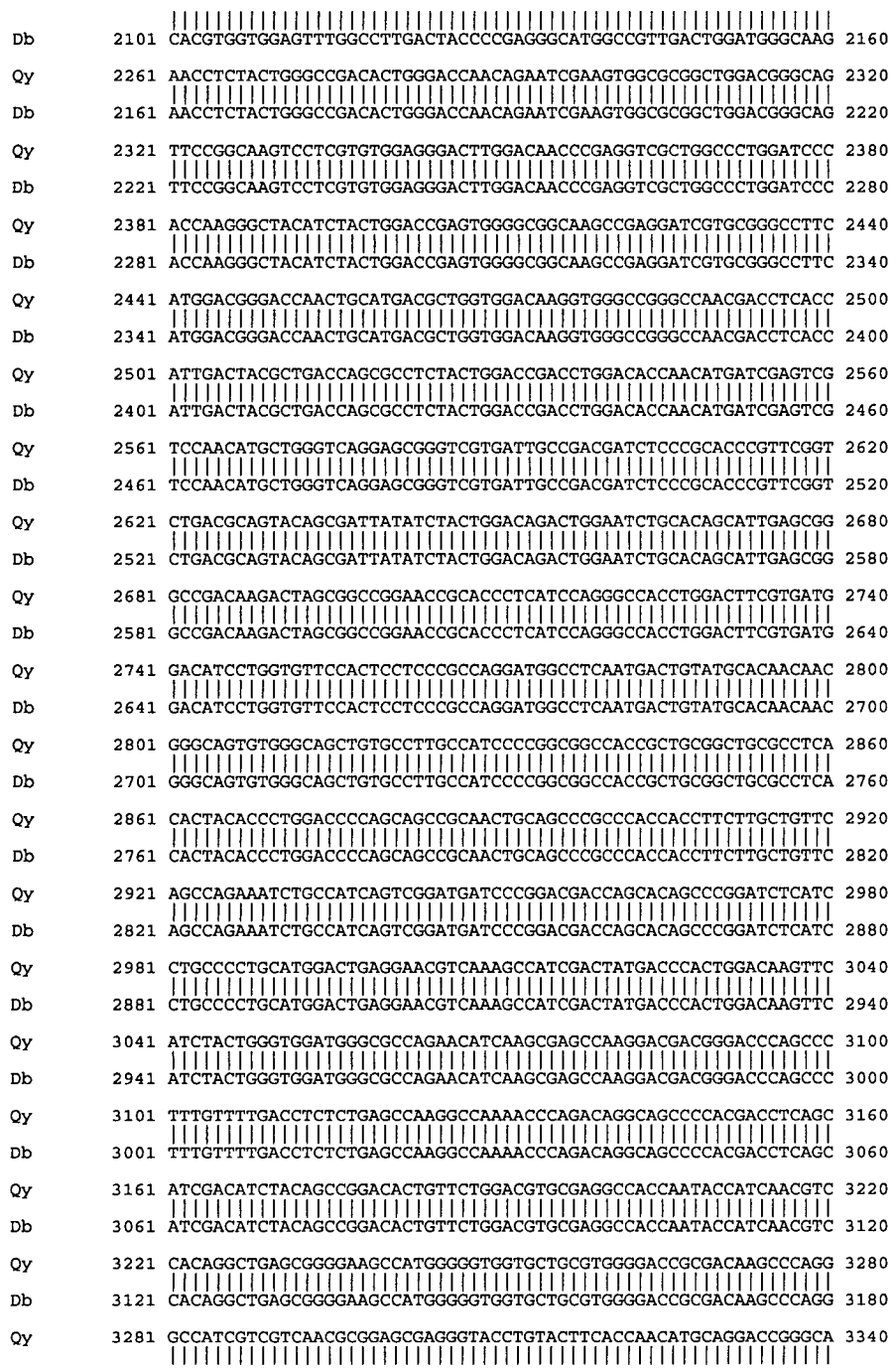
Qy       1961 CTGGAGCTGCTGAGTGACATGAAGACCTGCATCGTGCCTGAGGCCTTCTTGGTCTTCACC 2020
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Db       1861 CTGGAGCTGCTGAGTGACATGAAGACCTGCATCGTGCCTGAGGCCTTCTTGGTCTTCACC 1920

Qy       2021 AGCAGAGCCGCCATCCACAGGATCTCCCTCGAGACCAATAACAACGACGTGGCCATCCCG 2080
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Db       1921 AGCAGAGCCGCCATCCACAGGATCTCCCTCGAGACCAATAACAACGACGTGGCCATCCCG 1980

Qy       2081 CTCACGGGCGTCAAGGAGGCCTCAGCCCTGGACTTTGATGTGTCCAACAACCACATCTAC 2140
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Db       1981 CTCACGGGCGTCAAGGAGGCCTCAGCCCTGGACTTTGATGTGTCCAACAACCACATCTAC 2040

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Db       2041 TGGACAGACGTCAGCCTGAAGACCATCAGCCGCGCCTTCATGAACGGGAGCTCGGTGGAG 2100

Qy       2201 CACGTGGTGGAGTTTGGCCTTGACTACCCCGAGGGCATGGCCGTTGACTGGATGGGCAAG 2260
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Db 2101 CACGTGGTGGAGTTTGGCCTTGACTACCCCGAGGGCATGGCCGTTGACTGGATGGGCAAG 2160
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Qy 2981 CTGCCCCTGCATGGACTGAGGAACGTCAAAGCCATCGACTATGACCCACTGGACAAGTTC 3040
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Db       4981 TACAGTGGAACAAATATTTATAAACTTAATTTTGTAAAACA 5021
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RESULT 10
US-09-060-299-31
; Sequence 31, Application US/09060299
; Patent No. 6545137
;  GENERAL INFORMATION:
;    APPLICANT:  Todd, John A
;    APPLICANT:  Hess, John W
;    APPLICANT:  Caskey, Charles T
;    APPLICANT:  Cox, Roger D
;    APPLICANT:  Gerhold, David
;    APPLICANT:  Hammond, Holly
;    APPLICANT:  Hey, Patricia
;    APPLICANT:  Kawaguchi, Yoshihiko
;    APPLICANT:  Merriman, Tony R
;    APPLICANT:  Metzker, Michael L
;    TITLE OF INVENTION:  No. 6545137el Receptor
;    NUMBER OF SEQUENCES:  455
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Nixon and Vanderhye
;      STREET:  1100 No. 6545137th Glebe Road, Eighth Floor
;      CITY:  Arlington
;      STATE:  Virginia
;      COUNTRY:  US
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/060,299
;      FILING DATE:  15-APR-1998
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/043,553
;      FILING DATE:  15-APR-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/048,740
;      FILING DATE:  05-JUN-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  B.J.Sadoff
;      REGISTRATION NUMBER:  36,663
;      REFERENCE/DOCKET NUMBER:  620-35
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703)816-4091
;      TELEFAX:  (703)816-4100
;  INFORMATION FOR SEQ ID NO:  31:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5263 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-060-299-31

  Query Match             96.1%;  Score 4919.8;  DB 4;  Length 5263;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 4957;  Conservative    0;  Mismatches    7;  Indels    3;  Gaps    3;

Qy        155 GCCGCGGCCTCGCCGCTCCTGCTATTTGCCAACCGCCGGGACGTACGGCTGGTGGACGCC 214
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Db        358 GGCGGAGTCAAGCTGGAGTCCACCATCGTGGTCAGCGGCCTGGAGGATGCGGCCGCAGTG 417

Qy        275 GACTTCCAGTTTTCCAAGGGAGCCGTGTACTGGACAGACGTGAGCGAGGAGGCCATCAAG 334
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Db        418 GACTTCCAGTTTTCCAAGGGAGCCGTGTACTGGACAGACGTGAGCGAGGAGGCCATCAAG 477

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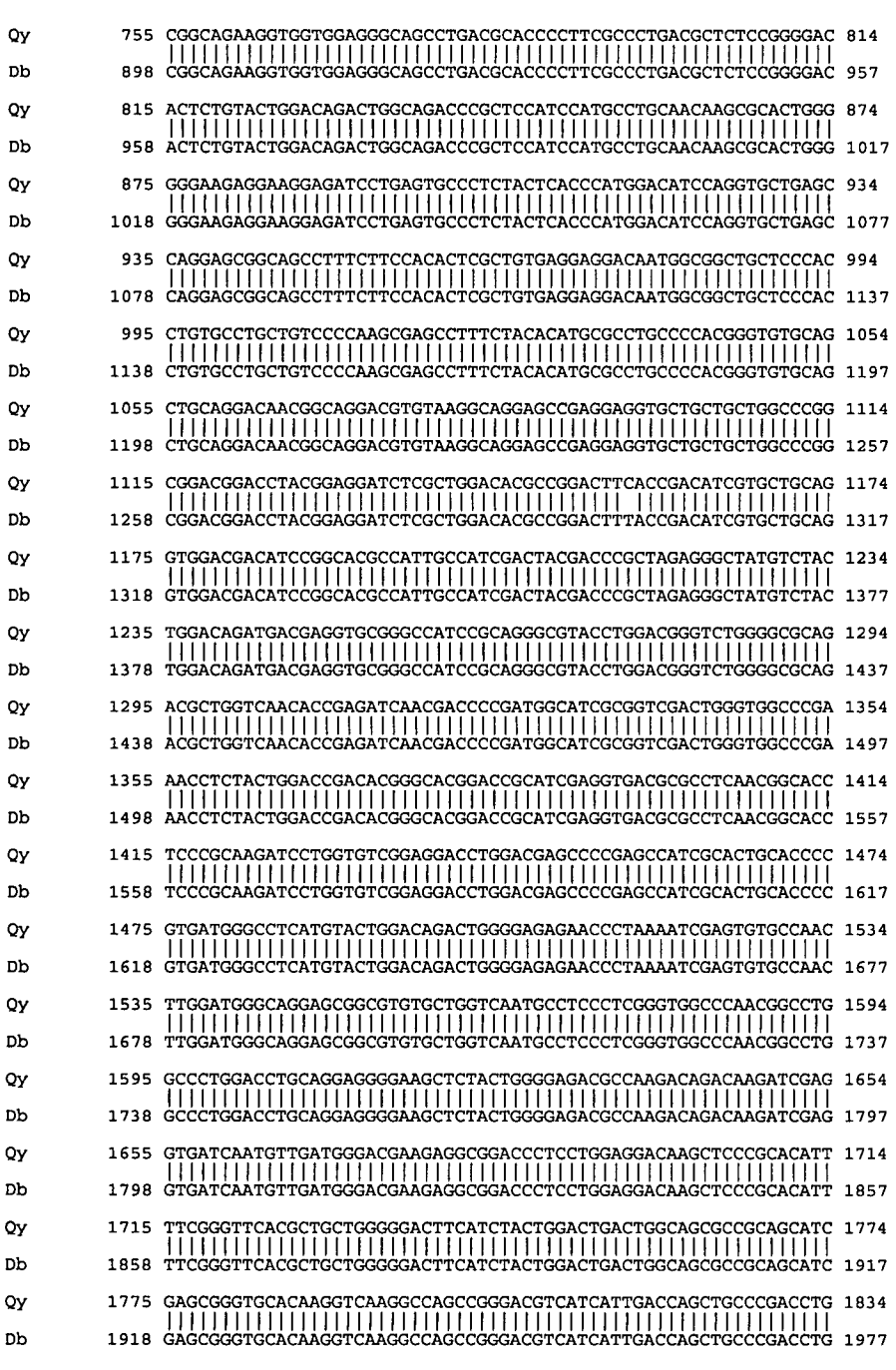
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Db        658 GACCTTGACCAGCCGAGGGCCATCGCCTTGGACCCCGCTCACGGGTACATGTACTGGACA 717

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Db        718 GACTGGGGTGAGACGCCCCGGATTGAGCGGGCAGGGATGGATGGCAGCACCCGGAAGATC 777

Qy        635 ATTGTGGACTCGGACATTTACTGGCCCAATGGACTGACCATCGACCTGGAGGAGCAGAAG 694
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Db        778 ATTGTGGACTCGGACATTTACTGGCCCAATGGACTGACCATCGACCTGGAGGAGCAGAAG 837

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Qy 1235 TGGACAGATGACGAGGTGCGGGCCATCCGCAGGGCGTACCTGGACGGGTCTGGGGCGCAG 1294
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Db      3597 GTGGACGCGGACCTGAAGCGCATTGAGAGCTGTGACCTGTCAGGGGCCAACCGCCTGACC 3656
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Qy      3695 CTGGAGGAGTTCTCAGCCCACCCATGTGCCCGTGACAATGGTGGCTGCTCCCACATCTGT 3754
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Db      4496 GGGACCCCGCACGTGCCCCTCAATTTCATAGCCCCGGGCGGTTCCCAGCATGGCCCCTTC 4555
Qy      4415 ACAGGCATCGCATGCGGAAAGTCCATGATGAGCTCCGTGAGCCTGATGGGGGGCCGGGGC 4474
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Qy      4475 GGGGTGCCCCTCTACGACCGGAACCACGTCACAGGGGCCTCGTCCAGCAGCTCGTCCAGC 4534
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Qy      4595 TCCCTGTACAACATGGACATGTTCTACTCTTCAAACATTCCGGCCACTGCGAGACCGTAC 4654
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Db      5216 ACTTTGTACAGTGGAACAAATATTTATAAACTTAATTTTGTAAAACA 5262
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RESULT 11
US-09-402-923A-31
; Sequence 31, Application US/09402923A
; Patent No. 6555654
;   GENERAL INFORMATION:
;        APPLICANT: Todd, John A
;                   Hess, John W
;                   Caskey, Charles T
;                   Cox, Roger D
;                   Gerhold, David
;                   Hammond, Holly
;                   Hey, Patricia
;                   Kawaguchi, Yoshihiko
;                   Merriman, Tony R
;                   Metzker, Michael L
;        TITLE OF INVENTION: No. 6555654el LDL-Receptor
;        NUMBER OF SEQUENCES: 455
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Nixon and Vanderhye
;             STREET: 1100 No. 6555654th Glebe Road, Eighth Floor
;             CITY: Arlington
;             STATE: Virginia
;             COUNTRY: US
;             ZIP: VA 22201-4714
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/402,923A
;             FILING DATE: 14-Feb-2001
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: PCT/GB98/01102
;             FILING DATE: 15-APR-1998
;             APPLICATION NUMBER: US 60/043,553
;             FILING DATE: 15-APR-1997
;             APPLICATION NUMBER: US 60/048,740
;             FILING DATE: 05-JUN-1997
;        ATTORNEY/AGENT INFORMATION:
;             NAME: B.J.Sadoff
;             REGISTRATION NUMBER: 36,663
;             REFERENCE/DOCKET NUMBER: 620-81
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (703)816-4091
;             TELEFAX: (703)816-4100
;   INFORMATION FOR SEQ ID NO: 31:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 5263 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 31:
US-09-402-923A-31

  Query Match             96.1%;  Score 4919.8;  DB 4;  Length 5263;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 4957;  Conservative    0;  Mismatches    7;  Indels    3;  Gaps    3;

Qy        155 GCCGCGGCCTCGCCGCTCCTGCTATTTGCCAACCGCCGGGACGTACGGCTGGTGGACGCC 214
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Db        298 GCCGCAGCCTCGCCGCTCCTGCTATTTGCCAACCGCCGGGACGTACGGCTGGTGGACGCC 357

Qy        215 GGCGGAGTCAAGCTGGAGTCCACCATCGTGGTCAGCGGCCTGGAGGATGCGGCCGCAGTG 274
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        358 GGCGGAGTCAAGCTGGAGTCCACCATCGTGGTCAGCGGCCTGGAGGATGCGGCCGCAGTG 417

Qy        275 GACTTCCAGTTTTCCAAGGGAGCCGTGTACTGGACAGACGTGAGCGAGGAGGCCATCAAG 334
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        418 GACTTCCAGTTTTCCAAGGGAGCCGTGTACTGGACAGACGTGAGCGAGGAGGCCATCAAG 477

Qy        335 CAGACCTACCTGAACCAGACGGGGGCCGCCGTGCAGAACGTGGTCATCTCCGGCCTGGTC 394
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        478 CAGACCTACCTGAACCAGACGGGGGCCGCCGTGCAGAACGTGGTCATCTCCGGCCTGGTC 537

Qy        395 TCTCCCGACGGCCTCGCCTGCGACTGGGTGGGCAAGAAGCTGTACTGGACGGACTCAGAG 454
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        538 TCTCCCGACGGCCTCGCCTGCGACTGGGTGGGCAAGAAGCTGTACTGGACGGACTCAGAG 597

Qy        455 ACCAACCGCATCGAGGTGGCCAACCTCAATGGCACATCCCGGAAGGTGCTCTTCTGGCAG 514
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        598 ACCAACCGCATCGAGGTGGCCAACCTCAATGGCACATCCCGGAAGGTGCTCTTCTGGCAG 657

Qy        515 GACCTTGACCAGCCGAGGGCCATCGCCTTGGACCCCGCTCACGGGTACATGTACTGGACA 574
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        658 GACCTTGACCAGCCGAGGGCCATCGCCTTGGACCCCGCTCACGGGTACATGTACTGGACA 717

Qy        575 GACTGGGTTGAGACGCCCCGGATTGAGCGGGCAGGGATGGATGGCAGCACCCGGAAGATC 634
              ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        718 GACTGGGGTGAGACGCCCCGGATTGAGCGGGCAGGGATGGATGGCAGCACCCGGAAGATC 777

Qy        635 ATTGTGGACTCGGACATTTACTGGCCCAATGGACTGACCATCGACCTGGAGGAGCAGAAG 694
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        778 ATTGTGGACTCGGACATTTACTGGCCCAATGGACTGACCATCGACCTGGAGGAGCAGAAG 837

Qy        695 CTCTACTGGGCTGACGCCAAGCTCAGCTTCATCCACCGTGCCAACCTGGACGGCTCGTTC 754
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        838 CTCTACTGGGCTGACGCCAAGCTCAGCTTCATCCACCGTGCCAACCTGGACGGCTCGTTC 897

Qy        755 CGGCAGAAGGTGGTGGAGGGCAGCCTGACGCACCCCTTCGCCCTGACGCTCTCCGGGGAC 814
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        898 CGGCAGAAGGTGGTGGAGGGCAGCCTGACGCACCCCTTCGCCCTGACGCTCTCCGGGGAC 957

Qy        815 ACTCTGTACTGGACAGACTGGCAGACCCGCTCCATCCATGCCTGCAACAAGCGCACTGGG 874
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        958 ACTCTGTACTGGACAGACTGGCAGACCCGCTCCATCCATGCCTGCAACAAGCGCACTGGG 1017

Qy        875 GGGAAGAGGAAGGAGATCCTGAGTGCCCTCTACTCACCCATGGACATCCAGGTGCTGAGC 934
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Db       1018 GGGAAGAGGAAGGAGATCCTGAGTGCCCTCTACTCACCCATGGACATCCAGGTGCTGAGC 1077

Qy        935 CAGGAGCGGCAGCCTTTCTTCCACACTCGCTGTGAGGAGGACAATGGCGGCTGCTCCCAC 994
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1078 CAGGAGCGGCAGCCTTTCTTCCACACTCGCTGTGAGGAGGACAATGGCGGCTGCTCCCAC 1137

Qy        995 CTGTGCCTGCTGTCCCCAAGCGAGCCTTTCTACACATGCGCCTGCCCCACGGGTGTGCAG 1054
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1138 CTGTGCCTGCTGTCCCCAAGCGAGCCTTTCTACACATGCGCCTGCCCCACGGGTGTGCAG 1197

Qy       1055 CTGCAGGACAACGGCAGGACGTGTAAGGCAGGAGCCGAGGAGGTGCTGCTGCTGGCCCGG 1114
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1198 CTGCAGGACAACGGCAGGACGTGTAAGGCAGGAGCCGAGGAGGTGCTGCTGCTGGCCCGG 1257

Qy       1115 CGGACGGACCTACGGAGGATCTCGCTGGACACGCCGGACTTCACCGACATCGTGCTGCAG 1174
              |||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db       1258 CGGACGGACCTACGGAGGATCTCGCTGGACACGCCGGACTTTACCGACATCGTGCTGCAG 1317

Qy       1175 GTGGACGACATCCGGCACGCCATTGCCATCGACTACGACCCGCTAGAGGGCTATGTCTAC 1234
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1318 GTGGACGACATCCGGCACGCCATTGCCATCGACTACGACCCGCTAGAGGGCTATGTCTAC 1377

Qy       1235 TGGACAGATGACGAGGTGCGGGCCATCCGCAGGGCGTACCTGGACGGGTCTGGGGCGCAG 1294
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1378 TGGACAGATGACGAGGTGCGGGCCATCCGCAGGGCGTACCTGGACGGGTCTGGGGCGCAG 1437

Qy       1295 ACGCTGGTCAACACCGAGATCAACGACCCCGATGGCATCGCGGTCGACTGGGTGGCCCGA 1354
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1438 ACGCTGGTCAACACCGAGATCAACGACCCCGATGGCATCGCGGTCGACTGGGTGGCCCGA 1497

Qy       1355 AACCTCTACTGGACCGACACGGGCACGGACCGCATCGAGGTGACGCGCCTCAACGGCACC 1414
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1498 AACCTCTACTGGACCGACACGGGCACGGACCGCATCGAGGTGACGCGCCTCAACGGCACC 1557

Qy       1415 TCCCGCAAGATCCTGGTGTCGGAGGACCTGGACGAGCCCCGAGCCATCGCACTGCACCCC 1474
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Db      1558 TCCCGCAAGATCCTGGTGTCGGAGGACCTGGACGAGCCCCGAGCCATCGCACTGCACCCC 1617
Qy      1475 GTGATGGGCCTCATGTACTGGACAGACTGGGGAGAGAACCCTAAAATCGAGTGTGCCAAC 1534
Db      1618 GTGATGGGCCTCATGTACTGGACAGACTGGGGAGAGAACCCTAAAATCGAGTGTGCCAAC 1677
Qy      1535 TTGGATGGGCAGGAGCGGCGTGTGCTGGTCAATGCCTCCCTCGGGTGGCCCAACGGCCTG 1594
Db      1678 TTGGATGGGCAGGAGCGGCGTGTGCTGGTCAATGCCTCCCTCGGGTGGCCCAACGGCCTG 1737
Qy      1595 GCCCTGGACCTGCAGGAGGGGAAGCTCTACTGGGGAGACGCCAAGACAGACAAGATCGAG 1654
Db      1738 GCCCTGGACCTGCAGGAGGGGAAGCTCTACTGGGGAGACGCCAAGACAGACAAGATCGAG 1797
Qy      1655 GTGATCAATGTTGATGGGACGAAGAGGCGGACCCTCCTGGAGGACAAGCTCCCGCACATT 1714
Db      1798 GTGATCAATGTTGATGGGACGAAGAGGCGGACCCTCCTGGAGGACAAGCTCCCGCACATT 1857
Qy      1715 TTCGGGTTCACGCTGCTGGGGGACTTCATCTACTGGACTGACTGGCAGCGCCGCAGCATC 1774
Db      1858 TTCGGGTTCACGCTGCTGGGGGACTTCATCTACTGGACTGACTGGCAGCGCCGCAGCATC 1917
Qy      1775 GAGCGGGTGCACAAGGTCAAGGCCAGCCGGGACGTCATCATTGACCAGCTGCCCGACCTG 1834
Db      1918 GAGCGGGTGCACAAGGTCAAGGCCAGCCGGGACGTCATCATTGACCAGCTGCCCGACCTG 1977
Qy      1835 ATGGGGCTCAAAGCTGTGAATGTGGCCAAGGTCGTCGGAACCAACCCGTGTGCGGACAGG 1894
Db      1978 ATGGGGCTCAAAGCTGTGAATGTGGCCAAGGTCGTCGGAACCAACCCGTGTGCGGACAGG 2037
Qy      1895 AACGGGGGGTGCAGCCACCTGTGCTTCTTCACACCCCACGCAACCCGGTGTGGCTGCCCC 1954
Db      2038 AACGGGGGGTG-AGCCACCTGTGCTTCTTCACACCCCACGCAACCCGGTGTGGCTGCCCC 2096
Qy      1955 ATCGGCCTGGAGCTGCTGAGTGACATGAAGACCTGCATCGTGCCTGAGGCCTTCTTGGTC 2014
Db      2097 ATCGGCCTGGAGCTGCTGAGTGACATGAAGACCTGCATCGTGCCTGAGGCCTTCTTGGTC 2156
Qy      2015 TTCACCAGCAGAGCCGCCATCCACAGGATCTCCCTCGAGACCAATAACAACGACGTGGCC 2074
Db      2157 TTCACCAGCAGAGCCGCCATCCACAGGATCTCCCTCGAGACCAATAACAACGACGTGGCC 2216
Qy      2075 ATCCCGCTCACGGGCGTCAAGGAGGCCTCAGCCCTGGACTTTGATGTGTCCAACAACCAC 2134
Db      2217 ATCCCGCTCACGGGCGTCAAGGAGGCCTCAGCCCTGGACTTTGATGTGTCCAACAACCAC 2276
Qy      2135 ATCTACTGGACAGACGTCAGCCTGAAGACCATCAGCCGCGCCTTCATGAACGGGAGCTCG 2194
Db      2277 ATCTACTGGACAGACGTCAGCCTGAAGACCATCAGCCGCGCCTTCATGAACGGGAGCTCG 2336
Qy      2195 GTGGAGCACGTGGTGGAGTTTGGCCTTGACTACCCCGAGGGCATGGCCGTTGACTGGATG 2254
Db      2337 GTGGAGCACGTGGTGGAGTTTGGCCTTGACTACCCCGAGGGCATGGCCGTTGACTGGATG 2396
Qy      2255 GGCAAGAACCTCTACTGGGCCGACACTGGGACCAACAGAATCGAAGTGGCGCGGCTGGAC 2314
Db      2397 GGCAAGAACCTCTACTGGGCCGACACTGGGACCAACAGAATCGAAGTGGCGCGGCTGGAC 2456
Qy      2315 GGGCAGTTCCGGCAAGTCCTCGTGTGGAGGGACTTGGACAACCCGAGGTCGCTGGCCCTG 2374
Db      2457 GGGCAGTTCCGGCAAGTCCTCGTGTGGAGGGACTTGGACAACCCGAGGTCGCTGGCCCTG 2516
Qy      2375 GATCCCACCAAGGGCTACATCTACTGGACCGAGTGGGGCGGCAAGCCGAGGATCGTGCGG 2434
Db      2517 GATCCCACCAAGGGCTACATCTACTGGACCGAGTGGGGCGGCAAGCCGAGGATCGTGCGG 2576
Qy      2435 GCCTTCATGGACGGGACCAACTGCATGACGCTGGTGGACAAGGTGGGCCGGGCCAACGAC 2494
Db      2577 GCCTTCATGGACGGGACCAACTGCATGACGCTGGTGGACAAGGTGGGCCGGGCCAACGAC 2636
Qy      2495 CTCACCATTGACTACGCTGACCAGCGCCTCTACTGGACCGACCTGGACACCAACATGATC 2554
Db      2637 CTCACCATTGACTACGCTGACCAGCGCCTCTACTGGACCGACCTGGACACCAACATGATC 2696
Qy      2555 GAGTCGTCCAACATGCTGGGTCAGGAGCGGGTCGTGATTGCCGACGATCTCCCGCACCCG 2614
Db      2697 GAGTCGTCCAACATGCTGGGTCAGGAGCGGGTCGTGATTGCCGACGATCTCCCGCACCCG 2756
Qy      2615 TTCGGTCTGACGCAGTACAGCGATTATATCTACTGGACAGACTGGAATCTGCACAGCATT 2674
Db      2757 TTCGGTCTGACGCAGTACAGCGATTATATCTACTGGACAGACTGGAATCTGCACAGCATT 2816
Qy      2675 GAGCGGGCCGACAAGACTAGCGGCCGGAACCGCACCCTCATCCAGGGCCACCTGGACTTC 2734
Db      2817 GAGCGGGCCGACAAGACTAGCGGCCGGAACCGCACCCTCATCCAGGGCCACCTGGACTTC 2876
Qy      2735 GTGATGGACATCCTGGTGTTCCACTCCTCCCGCCAGGATGGCCTCAATGACTGTATGCAC 2794
Db      2877 GTGATGGACATCCTGGTGTTCCACTCCTCCCGCCAGGATGGCCTCAATGACTGTATGCAC 2936
Qy      2795 AACAACGGGCAGTGTGGGCAGCTGTGCCTTGCCATCCCCGGCGGCCACCGCTGCGGCTGC 2854
Db      2937 AACAACGGGCAGTGTGGGCAGCTGTGCCTTGCCATCCCCGGCGGCCACCGCTGCGGCTGC 2996
Qy      2855 GCCTCACACTACACCCTGGACCCCAGCAGCCGCAACTGCAGCCCGCCCACCACCTTCTTG 2914
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Qy      2915 CTGTTCAGCCAGAAATCTGCCATCAGTCGGATGATCCCGGACGACCAGCACAGCCCGGAT 2974
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Qy      2975 CTCATCCTGCCCCTGCATGGACTGAGGAACGTCAAAGCCATCGACTATGACCCACTGGAC 3034
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Qy      3035 AAGTTCATCTACTGGGTGGATGGGCGCCAGAACATCAAGCGAGCCAAGGACGACGGGACC 3094
Db      3177 AAGTTCATCTACTGGGTGGATGGGCGCCAGAACATCAAGCGAGCCAAGGACGACGGGACC 3236
Qy      3095 CAGCCCTTTGTTTTGACCTCTCTGAGCCAAGGCCAAAACCCAGACAGGCAGCCCCACGAC 3154
Db      3237 CAGCCCTTTGTTTTGACCTCTCTGAGCCAAGGCCAAAACCCAGACAGGCAGCCCCACGAC 3296
Qy      3155 CTCAGCATCGACATCTACAGCCGGACACTGTTCTGGACGTGCGAGGCCACCAATACCATC 3214
Db      3297 CTCAGCATCGACATCTACAGCCGGACACTGTTCTGGACGTGCGAGGCCACCAATACCATC 3356
Qy      3215 AACGTCCACAGGCTGAGCGGGGAAGCCATGGGGGTGGTGCTGCGTGGGGACCGCGACAAG 3274
Db      3357 AACGTCCACAGGCTGAGCGGGGAAGCCATGGGGGTGGTGCTGCGTGGGGACCGCGACAAG 3416
Qy      3275 CCCAGGGCCATCGTCGTCAACGCGGAGCGAGGGTACCTGTACTTCACCAACATGCAGGAC 3334
Db      3417 CCCAGGGCCATCGTCGTCAACGCGGAGCGAGGGTACCTGTACTTCACCAACATGCAGGAC 3476
Qy      3335 CGGGCAGCCAAGATCGAACGCGCAGCCCTGGACGGCACCGAGCGCGAGGTCCTCTTCACC 3394
Db      3477 CGGGCAGCCAAGATCGAACGCGCAGCCCTGGACGGCACCGAGCGCGAGGTCCTCTTCACC 3536
Qy      3395 ACCGGCCTCATCCGCCCTGTGGCCCTGGTGGTGGACAACACACTGGGCAAGCTGTTCTGG 3454
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Qy      3455 GTGGACGCGGACCTGAAGCGCATTGAGAGCTGTGACCTGTCAGGGGCCAACCGCCTGACC 3514
Db      3597 GTGGACGCGGACCTGAAGCGCATTGAGAGCTGTGACCTGTCAGGGGCCAACCGCCTGACC 3656
Qy      3515 CTGGAGGACGCCAACATCGTGCAGCCTCTGGGCCTGACCATCCTTGGCAAGCATCTCTAC 3574
Db      3657 CTGGAGGACGCCAACATCGTGCAGCCTCTGGGCCTGACCATCCTTGGCAAGCATCTCTAC 3716
Qy      3575 TGGATCGACCGCCAGCAGCAGATGATCGAGCGTGTGGAGAAGACCACCGGGGACAAGCGG 3634
Db      3717 TGGATCGACCGCCAGCAGCAGATGATCGAGCGTGTGGAGAAGACCACCGGGGACAAGCGG 3776
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Qy       3635 ACTCGCATCCAGGGCCGTGTCGCCCACCTCACTGGCATCCATGCAGTGGAGGAAGTCAGC 3694
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3777 ACTCGCATCCAGGGCCGTGTCGCCCACCTCACTGGCATCCATGCAGTGGAGGAAGTCAGC 3836

Qy       3695 CTGGAGGAGTTCTCAGCCCACCCATGTGCCCGTGACAATGGTGGCTGCTCCCACATCTGT 3754
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3837 CTGGAGGAGTTCTCAGCCCACCCATGTGCCCGTGACAATGGTGGCTGCTCCCACATCTGT 3896

Qy       3755 ATTGCCAAGGGTGATGGGACACCACGGTGCTCATGCCCAGTCCACCTCGTGCTCCTGCAG 3814
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3897 ATTGCCAAGGGTGATGGGACACCACGGTGCTCATGCCCAGTCCACCTCGTGCTCCTGCAG 3956

Qy       3815 AACCTGCTGACCTGTGGAGAGCCGCCCACCTGCTCCCCGGACCAGTTTGCATGTGCCACA 3874
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Db       3957 AACCTGCTGACCTGTGGAGAGCCGCCCACCTGCTCCCCGGACCAGTTTGCATGTGCCACA 4016

Qy       3875 GGGGAGATCGACTGTATCCCCGGGGCCTGGCGCTGTGACGGCTTTCCCGAGTGCGATGAC 3934
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4017 GGGGAGATCGACTGTATCCCCGGGGCCTGGCGCTGTGACGGCTTTCCCGAGTGCGATGAC 4076

Qy       3935 CAGAGCGACGAGGAGGGCTGCCCCGTGTGCTCCGCCGCCCAGTTCCCCTGCGCGCGGGGT 3994
             |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db       4077 CAGAGCGACGAGGAGGGCTGCCCCGTG-GCTCCGCCGCCCAGTTCCCCTGCGCGCGGGGT 4135

Qy       3995 CAGTGTGTGGACCTGCGCCTGCGCTGCGACGGCGAGGCAGACTGTCAGGACCGCTCAGAC 4054
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4136 CAGTGTGTGGACCTGCGCCTGCGCTGCGACGGCGAGGCAGACTGTCAGGACCGCTCAGAC 4195

Qy       4055 GAGGTGGACTGTGACGCCATCTGCCTGCCCAACCAGTTCCGGTGTGCGAGCGGCCAGTGT 4114
             |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4196 GAGGCGGACTGTGACGCCATCTGCCTGCCCAACCAGTTCCGGTGTGCGAGCGGCCAGTGT 4255

Qy       4115 GTCCTCATCAAACAGCAGTGCGACTCCTTCCCCGACTGTATCGACGGCTCCGACGAGCTC 4174
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4256 GTCCTCATCAAACAGCAGTGCGACTCCTTCCCCGACTGTATCGACGGCTCCGACGAGCTC 4315

Qy       4175 ATGTGTGAAATCACCAAGCCGCCCTCAGACGACAGCCCGGCCCACAGCAGTGCCATCGGG 4234
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Db       4316 ATGTGTGAAATCACCAAGCCGCCCTCAGACGACAGCCCGGCCCACAGCAGTGCCATCGGG 4375

Qy       4235 CCCGTCATTGGCATCATCCTCTCTCTCTTCGTCATGGGTGGTGTCTATTTTGTGTGCCAG 4294
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Db       4376 CCCGTCATTGGCATCATCCTCTCTCTCTTCGTCATGGGTGGTGTCTATTTTGTGTGCCAG 4435

Qy       4295 CGCGTGGTGTGCCAGCGCTATGCGGGGGCCAACGGGCCCTTCCCGCACGAGTATGTCAGC 4354
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Qy       4355 GGGACCCCGCACGTGCCCCTCAATTTCATAGCCCCGGGCGGTTCCCAGCATGGCCCCTTC 4414
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Qy       4415 ACAGGCATCGCATGCGGAAAGTCCATGATGAGCTCCGTGAGCCTGATGGGGGGCCGGGGC 4474
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Qy       4475 GGGGTGCCCCTCTACGACCGGAACCACGTCACAGGGGCCTCGTCCAGCAGCTCGTCCAGC 4534
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Qy       4535 ACGAAGGCCACGCTGTACCCGCCGATCCTGAACCCGCCGCCCTCCCCGGCCACGGACCCC 4594
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Qy       4595 TCCCTGTACAACATGGACATGTTCTACTCTTCAAACATTCCGGCCACTGCGAGACCGTAC 4654
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Qy       4655 AGGCCCTACATCATTCGAGGAATGGCGCCCCCGACGACGCCCTGCAGCACCGACGTGTGT 4714
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4796 AGGCCCTACATCATTCGAGGAATGGCGCCCCCGACGACGCCCTGCAGCACCGACGTGTGT 4855

Qy       4715 GACAGCGACTACAGCGCCAGCCGCTGGAAGGCCAGCAAGTACTACCTGGATTTGAACTCG 4774
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4856 GACAGCGACTACAGCGCCAGCCGCTGGAAGGCCAGCAAGTACTACCTGGATTTGAACTCG 4915

Qy       4775 GACTCAGACCCCTATCCACCCCCACCCACGCCCCACAGCCAGTACCTGTCGGCGGAGGAC 4834
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Db       4916 GACTCAGACCCCTATCCACCCCCACCCACGCCCCACAGCCAGTACCTGTCGGCGGAGGAC 4975

Qy       4835 AGCTGCCCGCCCTCGCCCGCCACCGAGAGGAGCTACTTCCATCTCTTCCCGCCCCCTCCG 4894
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Db       4976 AGCTGCCCGCCCTCGCCCGCCACCGAGAGGAGCTACTTCCATCTCTTCCCGCCCCCTCCG 5035

Qy       4895 TCCCCCTGCACGGACTCATCCTGACCTCGGCCGGGCCACTCTGGCTTCTCTGTGCCCCTG 4954
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Db       5036 TCCCCCTGCACGGACTCATCCTGACCTCGGCCGGGCCACTCTGGCTTCTCTGTGCCCCTG 5095

Qy       4955 TAAATAGTTTTAAATATGAACAAAGAAAAAAATATATTTTATGATTTAAAAAATAAATAT 5014
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5096 TAAATAGTTTTAAATATGAACAAAGAAAAAAATATATTTTATGATTTAAAAAATAAATAT 5155

Qy       5015 AATTGGGATTTTAAAAACATGAGAAATGTGAACTGTGATGGGGTGGGCAGGGCTGGGAGA 5074
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Db       5156 AATTGGGATTTTAAAAACATGAGAAATGTGAACTGTGATGGGGTGGGCAGGGCTGGGAGA 5215

Qy       5075 ACTTTGTACAGTGG-AGAAATATTTATAAACTTAATTTTGTAAAACA 5120
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Db       5216 ACTTTGTACAGTGGAACAAATATTTATAAACTTAATTTTGTAAAACA 5262
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RESULT 12
US-09-060-299-26
; Sequence 26, Application US/09060299
; Patent No. 6545137
; GENERAL INFORMATION:
; APPLICANT: Todd, John A
; APPLICANT: Hess, John W
; APPLICANT: Caskey, Charles T
; APPLICANT: Cox, Roger D
; APPLICANT: Gerhold, David
; APPLICANT: Hammond, Holly
; APPLICANT: Hey, Patricia
; APPLICANT: Kawaguchi, Yoshihiko
; APPLICANT: Merriman, Tony R
; APPLICANT: Metzker, Michael L
; TITLE OF INVENTION: No. 6545137el Receptor
; NUMBER OF SEQUENCES: 455
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon and Vanderhye
; STREET: 1100 No. 6545137th Glebe Road, Eighth Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: US
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/060,299
; FILING DATE: 15-APR-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/043,553
; FILING DATE: 15-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/048,740
; FILING DATE: 05-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: B.J.Sadoff
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 620-35
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)816-4091

```
;      TELEFAX:  (703)816-4100
;  INFORMATION FOR SEQ ID NO:  26:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5125 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-060-299-26

  Query Match             96.0%;  Score 4916;  DB 4;  Length 5125;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 4952;  Conservative    0;  Mismatches    5;  Indels    3;  Gaps    3;

Qy       162 CCTCGCCGCTCCTGCTATTTGCCAACCGCCGGGACGTACGGCTGGTGGACGCCGGCGGAG 221
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       167 CCTCGCCGCTCCTGCTATTTGCCAACCGCCGGGACGTACGGCTGGTGGACGCCGGCGGAG 226

Qy       222 TCAAGCTGGAGTCCACCATCGTGGTCAGCGGCCTGGAGGATGCGGCCGCAGTGGACTTCC 281
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Qy       282 AGTTTTCCAAGGGAGCCGTGTACTGGACAGACGTGAGCGAGGAGGCCATCAAGCAGACCT 341
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Qy       342 ACCTGAACCAGACGGGGGCCGCCGTGCAGAACGTGGTCATCTCCGGCCTGGTCTCTCCCG 401
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Db       347 ACCTGAACCAGACGGGGGCCGCCGTGCAGAACGTGGTCATCTCCGGCCTGGTCTCTCCCG 406

Qy       402 ACGGCCTCGCCTGCGACTGGGTGGGCAAGAAGCTGTACTGGACGGACTCAGAGACCAACC 461
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Db       407 ACGGCCTCGCCTGCGACTGGGTGGGCAAGAAGCTGTACTGGACGGACTCAGAGACCAACC 466

Qy       462 GCATCGAGGTGGCCAACCTCAATGGCACATCCCGGAAGGTGCTCTTCTGGCAGGACCTTG 521
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Db       467 GCATCGAGGTGGCCAACCTCAATGGCACATCCCGGAAGGTGCTCTTCTGGCAGGACCTTG 526

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Qy       582 TTGAGACGCCCCGGATTGAGCGGGCAGGGATGGATGGCAGCACCCGGAAGATCATTGTGG 641
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Qy       642 ACTCGGACATTTACTGGCCCAATGGACTGACCATCGACCTGGAGGAGCAGAAGCTCTACT 701
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Qy       702 GGGCTGACGCCAAGCTCAGCTTCATCCACCGTGCCAACCTGGACGGCTCGTTCCGGCAGA 761
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Db       767 AGGTGGTGGAGGGCAGCCTGACGCACCCCTTCGCCCTGACGCTCTCCGGGGACACTCTGT 826

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Qy       942 GGCAGCCTTTCTTCCACACTCGCTGTGAGGAGGACAATGGCGGCTGCTCCCACCTGTGCC 1001
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Qy      1002 TGCTGTCCCCAAGCGAGCCTTTCTACACATGCGCCTGCCCCACGGGTGTGCAGCTGCAGG 1061
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Qy      1062 ACAACGGCAGGACGTGTAAGGCAGGAGCCGAGGAGGTGCTGCTGCTGGCCCGGCGGACGG 1121
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Db      1067 ACAACGGCAGGACGTGTAAGGCAGGAGCCGAGGAGGTGCTGCTGCTGGCCCGGCGGACGG 1126

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Db      1127 ACCTACGGAGGATCTCGCTGGACACGCCGGACTTTACCGACATCGTGCTGCAGGTGGACG 1186

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Db      1247 ATGACGAGGTGCGGGCCATCCGCAGGGCGTACCTGGACGGGTCTGGGGCGCAGACGCTGG 1306

Qy      1302 TCAACACCGAGATCAACGACCCCGATGGCATCGCGGTCGACTGGGTGGCCCGAAACCTCT 1361
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Db      1307 TCAACACCGAGATCAACGACCCCGATGGCATCGCGGTCGACTGGGTGGCCCGAAACCTCT 1366

Qy      1362 ACTGGACCGACACGGGCACGGACCGCATCGAGGTGACGCGCCTCAACGGCACCTCCCGCA 1421
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Db      1367 ACTGGACCGACACGGGCACGGACCGCATCGAGGTGACGCGCCTCAACGGCACCTCCCGCA 1426

Qy      1422 AGATCCTGGTGTCGGAGGACCTGGACGAGCCCCGAGCCATCGCACTGCACCCCGTGATGG 1481
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1427 AGATCCTGGTGTCGGAGGACCTGGACGAGCCCCGAGCCATCGCACTGCACCCCGTGATGG 1486

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Db      1487 GCCTCATGTACTGGACAGACTGGGGAGAGAACCCTAAAATCGAGTGTGCCAACTTGGATG 1546

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Db      1547 GGCAGGAGCGGCGTGTGCTGGTCAATGCCTCCCTCGGGTGGCCCAACGGCCTGGCCCTGG 1606

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Db      1607 ACCTGCAGGAGGGGAAGCTCTACTGGGGAGACGCCAAGACAGACAAGATCGAGGTGATCA 1666

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Db      1667 ATGTTGATGGGACGAAGAGGCGGACCCTCCTGGAGGACAAGCTCCCGCACATTTTCGGGT 1726

Qy      1722 TCACGCTGCTGGGGGACTTCATCTACTGGACTGACTGGCAGCGCCGCAGCATCGAGCGGG 1781
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Db      1727 TCACGCTGCTGGGGGACTTCATCTACTGGACTGACTGGCAGCGCCGCAGCATCGAGCGGG 1786

Qy      1782 TGCACAAGGTCAAGGCCAGCCGGGACGTCATCATTGACCAGCTGCCCGACCTGATGGGGC 1841
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Db      1787 TGCACAAGGTCAAGGCCAGCCGGGACGTCATCATTGACCAGCTGCCCGACCTGATGGGGC 1846

Qy      1842 TCAAAGCTGTGAATGTGGCCAAGGTCGTCGGAACCAACCCGTGTGCGGACAGGAACGGGG 1901
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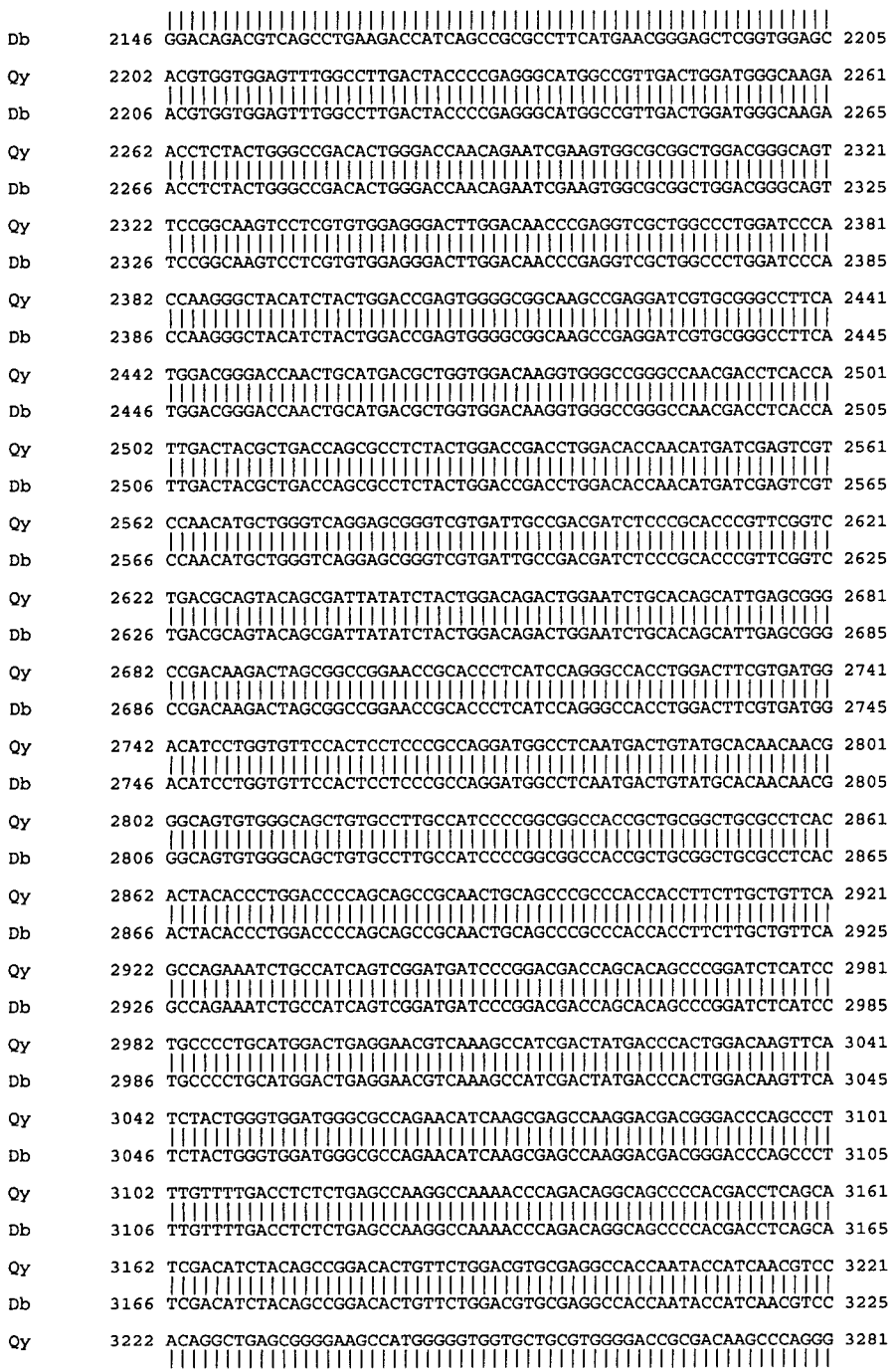
Qy      1902 GGTGCAGCCACCTGTGCTTCTTCACACCCCACGCAACCCGGTGTGGCTGCCCCATCGGCC 1961
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Db      1907 GGTGCAGCCACCTGTGCTTCTTCACACCCCACGCAACCCGGTGTGGCTGCCCCATCGGCC 1966

Qy      1962 TGGAGCTGCTGAGTGACATGAAGACCTGCATCGTGCCTGAGGCCTTCTTGGTCTTCACCA 2021
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1967 TGGAGCTGCTGAGTGACATGAAGACCTGCATCGTGCCTGAGGCCTTCTTGGTCTTCACCA 2026

Qy      2022 GCAGAGCCGCCATCCACAGGATCTCCCTCGAGACCAATAACAACGACGTGGCCATCCCGC 2081
            |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db      2027 GCAGAGCCGCCATCCACAGGAT-TCCCTCGAGACCAATAACAACGACGTGGCCATCCCGC 2085

Qy      2082 TCACGGGCGTCAAGGAGGCCTCAGCCCTGGACTTTGATGTGTCCAACAACCACATCTACT 2141
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Db      2086 TCACGGGCGTCAAGGAGGCCTCAGCCCTGGACTTTGATGTGTCCAACAACCACATCTACT 2145

Qy      2142 GGACAGACGTCAGCCTGAAGACCATCAGCCGCGCCTTCATGAACGGGAGCTCGGTGGAGC 2201
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Db 2146 GGACAGACGTCAGCCTGAAGACCATCAGCCGCGCCTTCATGAACGGGAGCTCGGTGGAGC 2205
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Qy 2262 ACCTCTACTGGGCCGACACTGGGACCAACAGAATCGAAGTGGCGCGGCTGGACGGGCAGT 2321
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Qy 2382 CCAAGGGCTACATCTACTGGACCGAGTGGGGCGGCAAGCCGAGGATCGTGCGGGCCTTCA 2441
Db 2386 CCAAGGGCTACATCTACTGGACCGAGTGGGGCGGCAAGCCGAGGATCGTGCGGGCCTTCA 2445
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Db 2446 TGGACGGGACCAACTGCATGACGCTGGTGGACAAGGTGGGCCGGGCCAACGACCTCACCA 2505
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Db 2806 GGCAGTGTGGGCAGCTGTGCCTTGCCATCCCCGGCGGCCACCGCTGCGGCTGCGCCTCAC 2865
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Qy 2922 GCCAGAAATCTGCCATCAGTCGGATGATCCCGGACGACCAGCACAGCCCGGATCTCATCC 2981
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Db 2986 TGCCCCTGCATGGACTGAGGAACGTCAAAGCCATCGACTATGACCCACTGGACAAGTTCA 3045
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Db 3046 TCTACTGGGTGGATGGGCGCCAGAACATCAAGCGAGCCAAGGACGACGGGACCCAGCCCT 3105
Qy 3102 TTGTTTTGACCTCTCTGAGCCAAGGCCAAAACCCAGACAGGCAGCCCCACGACCTCAGCA 3161
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Db 3526 ACGCCAACATCGTGCAGCCTCTGGGCCTGACCATCCTTGGCAAGCATCTCTACTGGATCG 3585
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Qy 3642 TCCAGGGCCGTGTCGCCCACCTCACTGGCATCCATGCAGTGGAGGAAGTCAGCCTGGAGG 3701
Db 3646 TCCAGGGCCGTGTCGCCCACCTCACTGGCATCCATGCAGTGGAGGAAGTCAGCCTGGAGG 3705
Qy 3702 AGTTCTCAGCCCACCCATGTGCCCGTGACAATGGTGGCTGCTCCCACATCTGTATTGCCA 3761
Db 3706 AGTTCTCAGCCCACCCATGTGCCCGTGACAATGGTGGCTGCTCCCACATCTGTATTGCCA 3765
Qy 3762 AGGGTGATGGGACACCACGGTGCTCATGCCCAGTCCACCTCGTGCTCCTGCAGAACCTGC 3821
Db 3766 AGGGTGATGGGACACCACGGTGCTCATGCCCAGTCCACCTCGTGCTCCTGCAGAACCTGC 3825
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Db 3826 TGACCTGTGGAGAGCCGCCCACCTGCTCCCCGGACCAGTTTGCATGTGCCACAGGGGAGA 3885
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Db       4545 CCACGCTGTACCCGCCGATCCTGAACCCGCCGCCCTCCCCGGCCACGGACCCCTCCCTGT 4604

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Db       4605 ACAACATGGACATGTTCTACTCTTCAAACATTCCGGCCACTGCGAGACCGTACAGGCCCT 4664

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Qy       4842 CGCCCTCGCCCGCCACCGAGAGGAGCTACTTCCATCTCTTCCCGCCCCCTCCGTCCCCCT 4901
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Db       4845 CGCCCTCGCCCGCCACCGAGAGGAGCTACTTCCATCTCTTCCCGCCCCCTCCGTCCCCCT 4904

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RESULT 13
US-09-402-923A-26
; Sequence 26, Application US/09402923A
; Patent No. 6555654
;   GENERAL INFORMATION:
;        APPLICANT: Todd, John A
;                   Hess, John W
;                   Caskey, Charles T
;                   Cox, Roger D
;                   Gerhold, David
;                   Hammond, Holly
;                   Hey, Patricia
;                   Kawaguchi, Yoshihiko
;                   Merriman, Tony R
;                   Metzker, Michael L
;        TITLE OF INVENTION: No. 6555654el LDL-Receptor
;        NUMBER OF SEQUENCES: 455
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Nixon and Vanderhye
;             STREET: 1100 No. 6555654th Glebe Road, Eighth Floor
;             CITY: Arlington
;             STATE: Virginia
;             COUNTRY: US
;             ZIP: VA 22201-4714
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/402,923A
;             FILING DATE: 14-Feb-2001
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: PCT/GB98/01102
;             FILING DATE: 15-APR-1998
;             APPLICATION NUMBER: US 60/043,553
;             FILING DATE: 15-APR-1997
;             APPLICATION NUMBER: US 60/048,740
;             FILING DATE: 05-JUN-1997
;        ATTORNEY/AGENT INFORMATION:
;             NAME: B.J.Sadoff
;             REGISTRATION NUMBER: 36,663
;             REFERENCE/DOCKET NUMBER: 620-81
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (703)816-4091
;             TELEFAX: (703)816-4100
;   INFORMATION FOR SEQ ID NO: 26:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 5125 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-09-402-923A-26

  Query Match             96.0%;  Score 4916;  DB 4;  Length 5125;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 4952;  Conservative    0;  Mismatches    5;  Indels    3;  Gaps    3;

Qy        162 CCTCGCCGCTCCTGCTATTTGCCAACCGCCGGGACGTACGGCTGGTGGACGCCGGCGGAG 221
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Db        167 CCTCGCCGCTCCTGCTATTTGCCAACCGCCGGGACGTACGGCTGGTGGACGCCGGCGGAG 226

Qy        222 TCAAGCTGGAGTCCACCATCGTGGTCAGCGGCCTGGAGGATGCGGCCGCAGTGGACTTCC 281
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Db        227 TCAAGCTGGAGTCCACCATCGTGGTCAGCGGCCTGGAGGATGCGGCCGCAGTGGACTTCC 286

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Qy        342 ACCTGAACCAGACGGGGGCCGCCGTGCAGAACGTGGTCATCTCCGGCCTGGTCTCTCCCG 401
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        347 ACCTGAACCAGACGGGGGCCGCCGTGCAGAACGTGGTCATCTCCGGCCTGGTCTCTCCCG 406

Qy        402 ACGGCCTCGCCTGCGACTGGGTGGGCAAGAAGCTGTACTGGACGGACTCAGAGACCAACC 461
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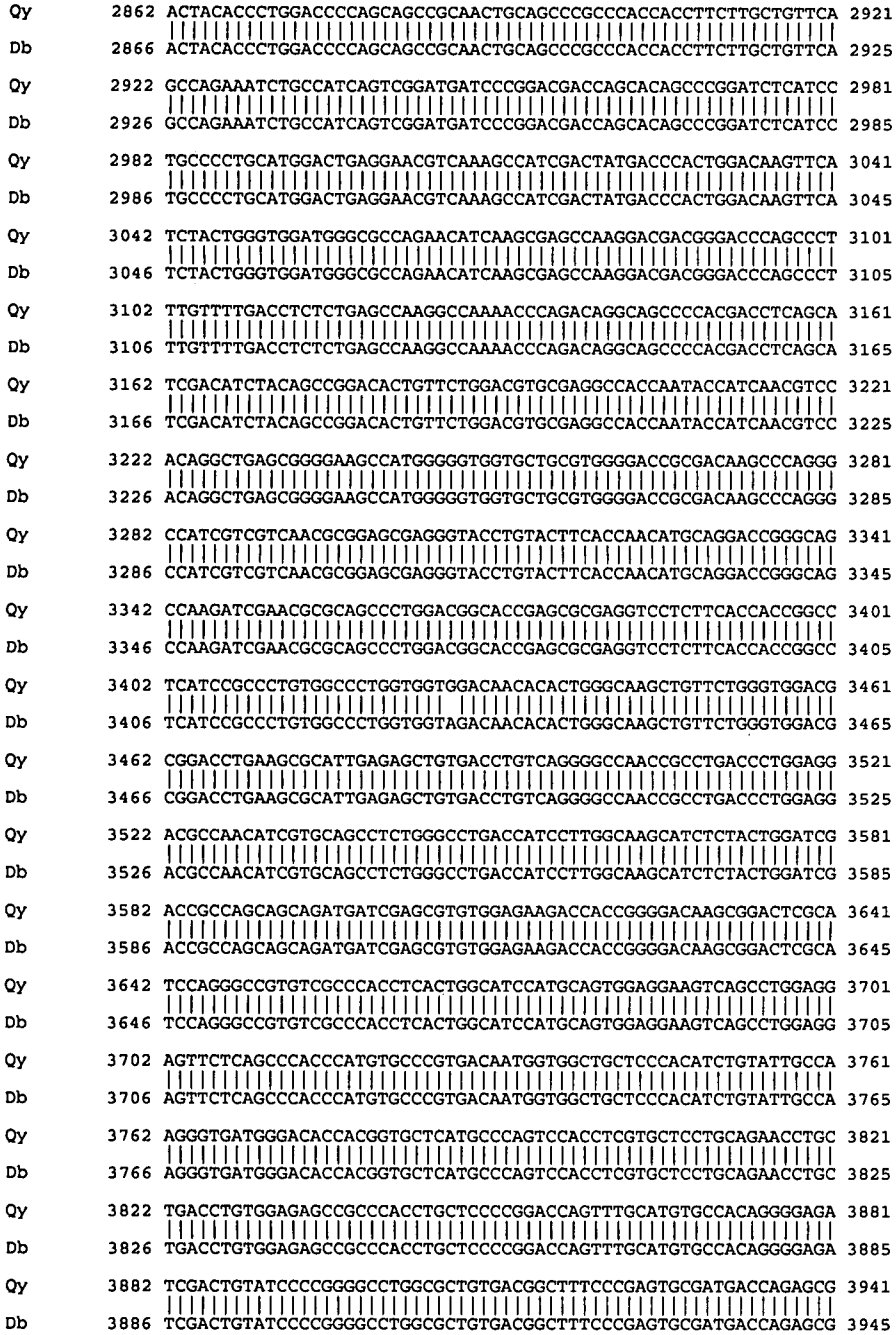
Qy        462 GCATCGAGGTGGCCAACCTCAATGGCACATCCCGGAAGGTGCTCTTCTGGCAGGACCTTG 521
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Qy        522 ACCAGCCGAGGGCCATCGCCTTGGACCCCGCTCACGGGTACATGTACTGGACAGACTGGG 581
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Db        527 ACCAGCCGAGGGCCATCGCCTTGGACCCCGCTCACGGGTACATGTACTGGACAGACTGGG 586

Qy        582 TTGAGACGCCCCGGATTGAGCGGGCAGGGATGGATGGCAGCACCCGGAAGATCATTGTGG 641
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Db        587 GTGAGACGCCCCGGATTGAGCGGGCAGGGATGGATGGCAGCACCCGGAAGATCATTGTGG 646

Qy        642 ACTCGGACATTTACTGGCCCAATGGACTGACCATCGACCTGGAGGAGCAGAAGCTCTACT 701
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Db       647 ACTCGGACATTTACTGGCCCAATGGACTGACCATCGACCTGGAGGAGCAGAAGCTCTACT 706
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Db       767 AGGTGGTGGAGGGCAGCCTGACGCACCCCTTCGCCCTGACGCTCTCCGGGGACACTCTGT 826
Qy       822 ACTGGACAGACTGGCAGACCCGCTCCATCCATGCCTGCAACAAGCGCACTGGGGGGAAGA 881
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Db       947 GGCAGCCTTTCTTCCACACTCGCTGTGAGGAGGACAATGGCGGCTGCTCCCACCTGTGCC 1006
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Db 4785 ACCCCTATCCACCCCCACCCACGCCCCACAGCCAGTACCTGTCGGCGGAGGACAGCTGCC 4844
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Qy       5082 ACAGTGG-AGAAATATTTATAAACTTAATTTTGTAAAACA 5120
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RESULT 14
US-09-060-299-33
; Sequence 33, Application US/09060299
; Patent No. 6545137
;  GENERAL INFORMATION:
;    APPLICANT:  Todd, John A
;    APPLICANT:  Hess, John W
;    APPLICANT:  Caskey, Charles T
;    APPLICANT:  Cox, Roger D
;    APPLICANT:  Gerhold, David
;    APPLICANT:  Hammond, Holly
;    APPLICANT:  Hey, Patricia
;    APPLICANT:  Kawaguchi, Yoshihiko
;    APPLICANT:  Merriman, Tony R
;    APPLICANT:  Metzker, Michael L
;    TITLE OF INVENTION:  No. 6545137el Receptor
;    NUMBER OF SEQUENCES:  455
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Nixon and Vanderhye
;      STREET:  1100 No. 6545137th Glebe Road, Eighth Floor
;      CITY:  Arlington
;      STATE:  Virginia
;      COUNTRY:  US
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/060,299
;      FILING DATE:  15-APR-1998
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/043,553
;      FILING DATE:  15-APR-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/048,740
;      FILING DATE:  05-JUN-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  B.J.Sadoff
;      REGISTRATION NUMBER:  36,663
;      REFERENCE/DOCKET NUMBER:  620-35
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703)816-4091
;      TELEFAX:  (703)816-4100
;  INFORMATION FOR SEQ ID NO:  33:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5162 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-060-299-33

  Query Match             96.0%;  Score 4915;  DB 4;  Length 5162;
  Best Local Similarity   99.7%;  Pred. No. 0;
  Matches 4954;  Conservative    0;  Mismatches   10;  Indels    3;  Gaps    3;

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Qy        695 CTCTACTGGGCTGACGCCAAGCTCAGCTTCATCCACCGTGCCAACCTGGACGGCTCGTTC 754
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Db        737 CTCTACTGGGCTGACGCCAAGCTCAGCTTCATCCACCGTGCCAACCTGGACGGCTCGTTC 796

Qy        755 CGGCAGAAGGTGGTGGAGGGCAGCCTGACGCACCCCTTCGCCCTGACGCTCTCCGGGGAC 814
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        797 CGGCAGAAGGTGGTGGAGGGCAGCCTGACGCACCCCTTCGCCCTGACGCTCTCCGGGGAC 856

Qy        815 ACTCTGTACTGGACAGACTGGCAGACCCGCTCCATCCATGCCTGCAACAAGCGCACTGGG 874
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        857 ACTCTGTACTGGACAGACTGGCAGACCCGCTCCATCCATGCCTGCAACAAGCGCACTGGG 916

Qy        875 GGGAAGAGGAAGGAGATCCTGAGTGCCCTCTACTCACCCATGGACATCCAGGTGCTGAGC 934
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        917 GGGAAGAGGAAGGAGATCCTGAGTGCCCTCTACTCACCCATGGACATCCAGGTGCTGAGC 976

Qy        935 CAGGAGCGGCAGCCTTTCTTCCACACTCGCTGTGAGGAGGACAATGGCGGCTGCTCCCAC 994
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        977 CAGGAGCGGCAGCCTTTCTTCCACACTCGCTGTGAGGAGGACAATGGCGGCTGCTCCCAC 1036

Qy        995 CTGTGCCTGCTGTCCCCAAGCGAGCCTTTCTACACATGCGCCTGCCCCACGGGTGTGCAG 1054
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1037 CTGTGCCTGCTGTCCCCAAGCGAGCCTTTCTACACATGCGCCTGCCCCACGGGTGTGCAG 1096

Qy       1055 CTGCAGGACAACGGCAGGACGTGTAAGGCAGGAGCCGAGGAGGTGCTGCTGCTGGCCCGG 1114
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1097 CTGCAGGACAACGGCAGGACGTGTAAGGCAGGAGCCGAGGAGGTGCTGCTGCTGGCCCGG 1156

Qy       1115 CGGACGGACCTACGGAGGATCTCGCTGGACACGCCGGACTTCACCGACATCGTGCTGCAG 1174
                |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db       1157 CGGACGGACCTACGGAGGATCTCGCTGGACACGCCGGACTTTACCGACATCGTGCTGCAG 1216

Qy       1175 GTGGACGACATCCGGCACGCCATTGCCATCGACTACGACCCGCTAGAGGGCTATGTCTAC 1234
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1217 GTGGACGACATCCGGCACGCCATTGCCATCGACTACGACCCGCTAGAGGGCTATGTCTAC 1276

Qy       1235 TGGACAGATGACGAGGTGCGGGCCATCCGCAGGGCGTACCTGGACGGGTCTGGGGCGCAG 1294
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1277 TGGACAGATGACGAGGTGCGGGCCATCCGCAGGGCGTACCTGGACGGGTCTGGGGCGCAG 1336

Qy       1295 ACGCTGGTCAACACCGAGATCAACGACCCCGATGGCATCGCGGTCGACTGGGTGGCCCGA 1354
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1337 ACGCTGGTCAACACCGAGATCAACGACCCCGATGGCATCGCGGTCGACTGGGTGGCCCGA 1396

Qy       1355 AACCTCTACTGGACCGACACGGGCACGGACCGCATCGAGGTGACGCGCCTCAACGGCACC 1414
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Db      1397 AACCTCTACTGGACCGACACGGGCACGGACCGCATCGAGGTGACGCGCCTCAACGGCACC 1456
Qy      1415 TCCCGCAAGATCCTGGTGTCGGAGGACCTGGACGAGCCCCGAGCCATCGCACTGCACCCC 1474
Db      1457 TCCCGCAAGATCCTGGTGTCGGAGGACCTGGACGAGCCCCGAGCCATCGCACTGCACCCC 1516
Qy      1475 GTGATGGGCCTCATGTACTGGACAGACTGGGGAGAGAACCCTAAAATCGAGTGTGCCAAC 1534
Db      1517 GTGATGGGCCTCATGTACTGGACAGACTGGGGAGAGAACCCTAAAATCGAGTGTGCCAAC 1576
Qy      1535 TTGGATGGGCAGGAGCGGCGTGTGCTGGTCAATGCCTCCCTCGGGTGGCCCAACGGCCTG 1594
Db      1577 TTGGATGGGCAGGAGCGGCGTGTGCTGGTCAATGCCTCCCTCGGGTGGCCCAACGGCCTG 1636
Qy      1595 GCCCTGGACCTGCAGGAGGGGAAGCTCTACTGGGGAGACGCCAAGACAGACAAGATCGAG 1654
Db      1637 GCCCTGGACCTGCAGGAGGGGAAGCTCTACTGGGGAGACGCCAAGACAGACAAGATCGAG 1696
Qy      1655 GTGATCAATGTTGATGGGACGAAGAGGCGGACCCTCCTGGAGGACAAGCTCCCGCACATT 1714
Db      1697 GTGATCAATGTTGATGGGACGAAGAGGCGGACCCTCCTGGAGGACAAGCTCCCGCACATT 1756
Qy      1715 TTCGGGTTCACGCTGCTGGGGGACTTCATCTACTGGACTGACTGGCAGCGCCGCAGCATC 1774
Db      1757 TTCGGGTTCACGCTGCTGGGGGACTTCATCTACTGGACTGACTGGCAGCGCCGCAGCATC 1816
Qy      1775 GAGCGGGTGCACAAGGTCAAGGCCAGCCGGGACGTCATCATTGACCAGCTGCCCGACCTG 1834
Db      1817 GAGCGGGTGCACAAGGTCAAGGCCAGCCGGGACGTCATCATTGACCAGCTGCCCGACCTG 1876
Qy      1835 ATGGGGCTCAAAGCTGTGAATGTGGCCAAGGTCGTCGGAACCAACCCGTGTGCGGACAGG 1894
Db      1877 ATGGGGCTCAAAGCTGTGAATGTGGCCAAGGTCGTCGGAACCAACCCGTGTGCGGACAGG 1936
Qy      1895 AACGGGGGGGTGCAGCCACCTGTGCTTCTTCACACCCCACGCAACCCGGTGTGGCTGCCCC 1954
Db      1937 AACGGGGGGGTGCAGCCACCTGTGCTTCTTCACACCCCACGCAACCCGGTGTGGCTGCCCC 1996
Qy      1955 ATCGGCCTGGAGCTGCTGAGTGACATGAAGACCTGCATCGTGCCTGAGGCCTTCTTGGTC 2014
Db      1997 ATCGGCCTGGAGCTGCTGAGTGACATGAAGACCTGCATCGTGCCTGAGGCC-TCTTGGTC 2055
Qy      2015 TTCACCAGCAGAGCCGCCATCCACAGGATCTCCCTCGAGACCAATAACAACGACGTGGCC 2074
Db      2056 TTCACCAGCAGAGCCGCCATCCACAGGATCTCCCTCGAGACCAATAACAACGACGTGGCC 2115
Qy      2075 ATCCCGCTCACGGGCGTCAAGGAGGCCTCAGCCCTGGACTTTGATGTGTCCAACAACCAC 2134
Db      2116 ATCCCGCTCACGGGCGTCAAGGAGGCCTCAGCCCTGGACTTTGATGTGTCCAACAACCAC 2175
Qy      2135 ATCTACTGGACAGACGTCAGCCTGAAGACCATCAGCCGCGCCTTCATGAACGGGAGCTCG 2194
Db      2176 ATCTACTGGACAGACGTCAGCCTGAAGACCATCAGCCGCGCCTTCATGAACGGGAGCTCG 2235
Qy      2195 GTGGAGCACGTGGTGGAGTTTGGCCTTGACTACCCCGAGGGCATGGCCGTTGACTGGATG 2254
Db      2236 GTGGAGCACGTGGTGGAGTTTGGCCTTGACTACCCCGAGGGCATGGCCGTTGACTGGATG 2295
Qy      2255 GGCAAGAACCTCTACTGGGCCGACACTGGGACCAACAGAATCGAAGTGGCGCGGCTGGAC 2314
Db      2296 GGCAAGAACCTCTACTGGGCCGACACTGGGACCAACAGAATCGAAGTGGCGCGGCTGGAC 2355
Qy      2315 GGGCAGTTCCGGCAAGTCCTCGTGTGGAGGGACTTGGACAACCCGAGGTCGCTGGCCCTG 2374
Db      2356 GGGCAGTTCCGGCAAGTCCTCGTGTGGAGGGACTTGGACAACCCGAGGTCGCTGGCCCTG 2415
Qy      2375 GATCCCACCAAGGGCTACATCTACTGGACCGAGTGGGGCGGCAAGCCGAGGATCGTGCGG 2434
Db      2416 GATCCCACCAAGGGCTACATCTACTGGACCGAGTGGGGCGGCAAGCCGAGGATCGTGCGG 2475
Qy      2435 GCCTTCATGGACGGGACCAACTGCATGACGCTGGTGGACAAGGTGGGCCGGGCCAACGAC 2494
Db      2476 GCCTTCATGGACGGGACCAACTGCATGACGCTGGTGGACAAGGTGGGCCGGGCCAACGAC 2535
Qy      2495 CTCACCATTGACTACGCTGACCAGCGCCTCTACTGGACCGACCTGGACACCAACATGATC 2554
Db      2536 CTCACCATTGACTACGCTGACCAGCGCCTCTACTGGACCGACCTGGACACCAACATGATC 2595
Qy      2555 GAGTCGTCCAACATGCTGGGTCAGGAGCGGGTCGTGATTGCCGACGATCTCCCGCACCCG 2614
Db      2596 GAGTCGTCCAACATGCTGGGTCAGGAGCGGGTCGTGATTGCCGACGATCTCCCGCACCCG 2655
Qy      2615 TTCGGTCTGACGCAGTACAGCGATTATATCTACTGGACAGACTGGAATCTGCACAGCATT 2674
Db      2656 TTCGGTCTGACGCAGTACAGCGATTATATCTACTGGACAGACTGGAATCTGCACAGCATT 2715
Qy      2675 GAGCGGGCCGACAAGACTAGCGGCCGGAACCGCACCCTCATCCAGGGCCACCTGGACTTC 2734
Db      2716 GAGCGGGCCGACAAGACTAGCGGCCGGAACCGCACCCTCATCCAGGGCCACCTGGACTTC 2775
Qy      2735 GTGATGGACATCCTGGTGTTCCACTCCTCCCGCCAGGATGGCCTCAATGACTGTATGCAC 2794
Db      2776 GTGATGGACATCCTGGTGTTCCACTCCTCCCGCCAGGATGGCCTCAATGACTGTATGCAC 2835
Qy      2795 AACAACGGGCAGTGTGGGCAGCTGTGCCTTGCCATCCCCGGCGGCCACCGCTGCGGCTGC 2854
Db      2836 AACAACGGGCAGTGTGGGCAGCTGTGCCTTGCCATCCCCGGCGGCCACCGCTGCGGCTGC 2895
Qy      2855 GCCTCACACTACACCCTGGACCCCAGCAGCCGCAACTGCAGCCCGCCCACCACCTTCTTG 2914
Db      2896 GCCTCACACTACACCCTGGACCCCAGCAGCCGCAACTGCAGCCCGCCCACCACCTTCTTG 2955
Qy      2915 CTGTTCAGCCAGAAATCTGCCATCAGTCGGATGATCCCCGGACGACCAGCACAGCCCGGAT 2974
Db      2956 CTGTTCAGCCAGAAATCTGCCATCAGTCGGATGATCCCCGGACGACCAGCACAGCCCGGAT 3015
Qy      2975 CTCATCCTGCCCCCTGCATGGACTGAGGAACGTCAAAGCCATCGACTATGACCCACTGGAC 3034
Db      3016 CTCATCCTGCCCCCTGCATGGACTGAGGAACGTCAAAGCCATCGACTATGACCCACTGGAC 3075
Qy      3035 AAGTTCATCTACTGGGTGGATGGGCGCCAGAACATCAAGCGAGCCAAGGACGACGGGACC 3094
Db      3076 AAGTTCATCTACTGGGTGGATGGGCGCCAGAACATCAAGCGAGCCAAGGACGACGGGACC 3135
Qy      3095 CAGCCCTTTGTTTTGACCTCTCTGAGCCAAGGCCAAAACCCAGACAGGCAGCCCCACGAC 3154
Db      3136 CAGCCCTTTGTTTTGACCTCTCTGAGCCAAGGCCAAAACCCAGACAGGCAGCCCCACGAC 3195
Qy      3155 CTCAGCATCGACATCTACAGCCGGACACTGTTCTGGACGTGCGAGGCCACCAATACCATC 3214
Db      3196 CTCAGCATCGACATCTACAGCCGGACACTGTTCTGGACGTGCGAGGCCACCAATACCATC 3255
Qy      3215 AACGTCCACAGGCTGAGCGGGGAAGCCATGGGGGTGGTGCTGCGTGGGGACCGCGACAAG 3274
Db      3256 AACGTCCACAGGCTGAGCGGGGAAGCCATGGGGGTGGTGCTGCGTGGGGACCGCGACAAG 3315
Qy      3275 CCCAGGGCCATCGTCGTCAACGCGGAGCGAGGGTACCTGTACTTCACCAACATGCAGGAC 3334
Db      3316 CCCAGGGCCATCGTCGTCAACGCGGAGCGAGGGTACCTGTACTTCACCAACATGCAGGAC 3375
Qy      3335 CGGGCAGCCAAGATCGAACGCGCAGCCCTGGACGGCACCGAGCGCGAGGTCCTCTTCACC 3394
Db      3376 CGGGCAGCCAAGATCGAACGCGCAGCCCTGGACGGCACCGAGCGCGAGGTCCTCTTCACC 3435
Qy      3395 ACCGGCCTCATCCGCCCTGTGGCCCTGGTGGTGGACAACACACTGGGCAAGCTGTTCTGG 3454
Db      3436 ACCGGCCTCATCCGCCCTGTGGCCCTGGTGGTAGACAACACACTGGGCAAGCTGTTCTGG 3495
Qy      3455 GTGGACGCGGACCTGAAGCGCATTGAGAGCTGTGACCTGTCAGGGGCCAACCGCCTGACC 3514
Db      3496 GTGGACGCGGACCTGAAGCGCATTGAGAGCTGTGACCTGTCAGGGGCCAACCGCCTGACC 3555
Qy      3515 CTGGAGGACGCCAACATCGTGCAGCCTCTGGGCCTGACCATCCTTGGCAAGCATCTCTAC 3574
Db      3556 CTGGAGGACGCCAACATCGTGCAGCCTCTGGGCCTGACCATCCTTGGCAAGCATCTCTAC 3615
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Qy       3575 TGGATCGACCGCCAGCAGCAGATGATCGAGCGTGTGGAGAAGACCACCGGGGACAAGCGG 3634
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3616 TGGATCGACCGCCAGCAGCAGATGATCGAGCGTGTGGAGAAGACCACCGGGGACAAGCGG 3675

Qy       3635 ACTCGCATCCAGGGCCGTGTCGCCCACCTCACTGGCATCCATGCAGTGGAGGAAGTCAGC 3694
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3676 ACTCGCATCCAGGGCCGTGTCGCCCACCTCACTGGCATCCATGCAGTGGAGGAAGTCAGC 3735

Qy       3695 CTGGAGGAGTTCTCAGCCCACCCATGTGCCCGTGACAATGGTGGCTGCTCCCACATCTGT 3754
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Db       3736 CTGGAGGAGTTCTCAGCCCACCCATGTGCCCGTGACAATGGTGGCTGCTCCCACATCTGT 3795

Qy       3755 ATTGCCAAGGGTGATGGGACACCACGGTGCTCATGCCCAGTCCACCTCGTGCTCCTGCAG 3814
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3796 ATTGCCAAGGGTGATGGGACACCACGGTGCTCATGCCCAGTCCACCTCGTGCTCCTGCAG 3855

Qy       3815 AACCTGCTGACCTGTGGAGAGCCGCCCACCTGCTCCCCGGACCAGTTTGCATGTGCCACA 3874
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3856 AACCTGCTGACCTGTGGAGAGCCGCCCACCTGCTCCCCGGACCAGTTTGCATGTGCCACA 3915

Qy       3875 GGGGAGATCGACTGTATCCCCGGGGCCTGGCGCTGTGACGGCTTTCCCGAGTGCGATGAC 3934
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3916 GGGGAGATCGACTGTATCCCCGGGGCCTGGCGCTGTGACGGCTTTCCCGAGTGCGATGAC 3975

Qy       3935 CAGAGCGACGAGGAGGGCTGCCCCGTGTGCTCCGCCGCCCAGTTCCCCTGCGCGCGGGGT 3994
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3976 CAGAGCGACGAGGAGGGCTGCCCCGTGTGCTCCGCCGCCCAGTTCCCCTGCGCGCGGGGT 4035

Qy       3995 CAGTGTGTGGACCTGCGCCTGCGCTGCGACGGCGAGGCAGACTGTCAGGACCGCTCAGAC 4054
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4036 CAGTGTGTGGACCTGCGCCTGCGCTGCGACGGCGAGGCAGACTGTCAGGACCGCTCAGAC 4095

Qy       4055 GAGGTGGACTGTGACGCCATCTGCCTGCCCAACCAGTTCCGGTGTGCGAGCGGCCAGTGT 4114
             |||| |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db       4096 GAGGCGGACTGTGACGCCATC-GCCTGCCCAACCAGTTCCGGTGTGCGAGCGGCCAGTGT 4154

Qy       4115 GTCCTCATCAAACAGCAGTGCGACTCCTTCCCCGACTGTATCGACGGCTCCGACGAGCTC 4174
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4155 GTCCTCATCAAACAGCAGTGCGACTCCTTCCCCGACTGTATCGACGGCTCCGACGAGCTC 4214

Qy       4175 ATGTGTGAAATCACCAAGCCGCCCTCAGACGACAGCCCGGCCCACAGCAGTGCCATCGGG 4234
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Db       4215 ATGTGTGAAATCACCAAGCCGCCCTCAGACGACAGCCCGGCCCACAGCAGTGCCATCGGG 4274

Qy       4235 CCCGTCATTGGCATCATCCTCTCTCTCTTCGTCATGGGTGGTGTCTATTTTGTGTGCCAG 4294
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Qy       4295 CGCGTGGTGTGCCAGCGCTATGCGGGGGCCAACGGGCCCTTCCCGCACGAGTATGTCAGC 4354
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Qy       4355 GGGACCCCGCACGTGCCCCTCAATTTCATAGCCCCGGGCGGTTCCCAGCATGGCCCCTTC 4414
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Qy       4415 ACAGGCATCGCATGCGGAAAGTCCATGATGAGCTCCGTGAGCCTGATGGGGGGCCGGGGC 4474
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Qy       4475 GGGGTGCCCCCTCTACGACCGGAACCACGTCACAGGGGCCTCGTCCAGCAGCTCGTCCAGC 4534
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Qy       4535 ACGAAGGCCACGCTGTACCCGCCGATCCTGAACCCGCCGCCCTCCCCGGCCACGGACCCC 4594
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Qy       4595 TCCCTGTACAACATGGACATGTTCTACTCTTCAAACATTCCGGCCACTGCGAGACCGTAC 4654
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Db       4635 TCCCTGTACAACATGGACATGTTCTACTCTTCAAACATTCCGGCCACTGCGAGACCGTAC 4694

Qy       4655 AGGCCCTACATCATTCGAGGAATGGCGCCCCCGACGACGCCCTGCAGCACCGACGTGTGT 4714
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4695 AGGCCCTACATCATTCGAGGAATGGCGCCCCCGACGACGCCCTGCAGCACCGACGTGTGT 4754

Qy       4715 GACAGCGACTACAGCGCCAGCCGCTGGAAGGCCAGCAAGTACTACCTGGATTTGAACTCG 4774
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4755 GACAGCGACTACAGCGCCAGCCGCTGGAAGGCCAGCAAGTACTACCTGGATTTGAACTCG 4814

Qy       4775 GACTCAGACCCCTATCCACCCCCACCCACGCCCCACAGCCAGTACCTGTCGGCGGAGGAC 4834
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Db       4815 GACTCAGACCCCTATCCACCCCCACCCACGCCCCACAGCCAGTACCTGTCGGCGGAGGAC 4874

Qy       4835 AGCTGCCCGCCCTCGCCCGCCACCGAGAGGAGCTACTTCCATCTCTTCCCGCCCCCTCCG 4894
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4875 AGCTGCCCGCCCTCGCCCGCCACCGAGAGGAGCTACTTCCATCTCTTCCCGCCCCCTCCG 4934

Qy       4895 TCCCCCTGCACGGACTCATCCTGACCTCGGCCGGGCCACTCTGGCTTCTCTGTGCCCCTG 4954
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4935 TCCCCCTGCACGGACTCATCCTGACCTCGGCCGGGCCACTCTGGCTTCTCTGTGCCCCTG 4994

Qy       4955 TAAATAGTTTTAAATATGAACAAAGAAAAAAATATATTTTATGATTTAAAAAATAAATAT 5014
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Db       4995 TAAATAGTTTTAAATATGAACAAAGAAAAAAATATATTTTATGATTTAAAAAATAAATAT 5054

Qy       5015 AATTGGGATTTTAAAAACATGAGAAATGTGAACTGTGATGGGGTGGGCAGGGCTGGGAGA 5074
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Qy       5075 ACTTTGTACAGTGG-AGAAATATTTATAAACTTAATTTTGTAAAACA 5120
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Db       5115 ACTTTGTACAGTGGAACAAATATTTATAAACTTAATTTTGTAAAACA 5161
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RESULT 15
US-09-402-923A-33
; Sequence 33, Application US/09402923A
; Patent No. 6555654
; GENERAL INFORMATION:
; APPLICANT: Todd, John A
; Hess, John W
; Caskey, Charles T
; Cox, Roger D
; Gerhold, David
; Hammond, Holly
; Hey, Patricia
; Kawaguchi, Yoshihiko
; Merriman, Tony R
; Metzker, Michael L
; TITLE OF INVENTION: No. 6555654el LDL-Receptor
; NUMBER OF SEQUENCES: 455
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon and Vanderhye
; STREET: 1100 No. 6555654th Glebe Road, Eighth Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: US
; ZIP: VA 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/402,923A
; FILING DATE: 14-Feb-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB98/01102
; FILING DATE: 15-APR-1998
; APPLICATION NUMBER: US 60/043,553
; FILING DATE: 15-APR-1997
; APPLICATION NUMBER: US 60/048,740
; FILING DATE: 05-JUN-1997
; ATTORNEY/AGENT INFORMATION:

```
;             NAME: B.J.Sadoff
;             REGISTRATION NUMBER: 36,663
;             REFERENCE/DOCKET NUMBER: 620-81
;       TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (703)816-4091
;             TELEFAX: (703)816-4100
;   INFORMATION FOR SEQ ID NO: 33:
;       SEQUENCE CHARACTERISTICS:
;             LENGTH: 5162 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 33:
US-09-402-923A-33

  Query Match             96.0%;  Score 4915;  DB 4;  Length 5162;
  Best Local Similarity   99.7%;  Pred. No. 0;
  Matches 4954;  Conservative    0;  Mismatches   10;  Indels    3;  Gaps    3;

Qy        155 GCCGCGGCCTCGCCGCTCCTGCTATTTGCCAACCGCCGGGACGTACGGCTGGTGGACGCC 214
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Db        197 GCCTACCCCTCGCCGCTCCTGCTATTTGCCAACCGCCGGGACGTACGGCTGGTGGACGCC 256

Qy        215 GGCGGAGTCAAGCTGGAGTCCACCATCGTGGTCAGCGGCCTGGAGGATGCGGCCGCAGTG 274
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Db        257 GGCGGAGTCAAGCTGGAGTCCACCATCGTGGTCAGCGGCCTGGAGGATGCGGCCGCAGTG 316

Qy        275 GACTTCCAGTTTTCCAAGGGAGCCGTGTACTGGACAGACGTGAGCGAGGAGGCCATCAAG 334
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Db        317 GACTTCCAGTTTTCCAAGGGAGCCGTGTACTGGACAGACGTGAGCGAGGAGGCCATCAAG 376

Qy        335 CAGACCTACCTGAACCAGACGGGGGCCGCCGTGCAGAACGTGGTCATCTCCGGCCTGGTC 394
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        377 CAGACCTACCTGAACCAGACGGGGGCCGCCGTGCAGAACGTGGTCATCTCCGGCCTGGTC 436

Qy        395 TCTCCCGACGGCCTCGCCTGCGACTGGGTGGGCAAGAAGCTGTACTGGACGGACTCAGAG 454
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        437 TCTCCCGACGGCCTCGCCTGCGACTGGGTGGGCAAGAAGCTGTACTGGACGGACTCAGAG 496

Qy        455 ACCAACCGCATCGAGGTGGCCAACCTCAATGGCACATCCCGGAAGGTGCTCTTCTGGCAG 514
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        497 ACCAACCGCATCGAGGTGGCCAACCTCAATGGCACATCCCGGAAGGTGCTCTTCTGGCAG 556

Qy        515 GACCTTGACCAGCCGAGGGCCATCGCCTTGGACCCCGCTCACGGGTACATGTACTGGACA 574
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        557 GACCTTGACCAGCCGAGGGCCATCGCCTTGGACCCCGCTCACGGGTACATGTACTGGACA 616

Qy        575 GACTGGGTTGAGACGCCCCGGATTGAGCGGGCAGGGATGGATGGCAGCACCCGGAAGATC 634
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Db        617 GACTGGGGTGAGACGCCCCGGATTGAGCGGGCAGGGATGGATGGCAGCACCCGGAAGATC 676

Qy        635 ATTGTGGACTCGGACATTTACTGGCCCAATGGACTGACCATCGACCTGGAGGAGCAGAAG 694
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Qy        695 CTCTACTGGGCTGACGCCAAGCTCAGCTTCATCCACCGTGCCAACCTGGACGGCTCGTTC 754
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Qy        875 GGGAAGAGGAAGGAGATCCTGAGTGCCCTCTACTCACCCATGGACATCCAGGTGCTGAGC 934
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Qy        995 CTGTGCCTGCTGTCCCCAAGCGAGCCTTTCTACACATGCGCCTGCCCCACGGGTGTGCAG 1054
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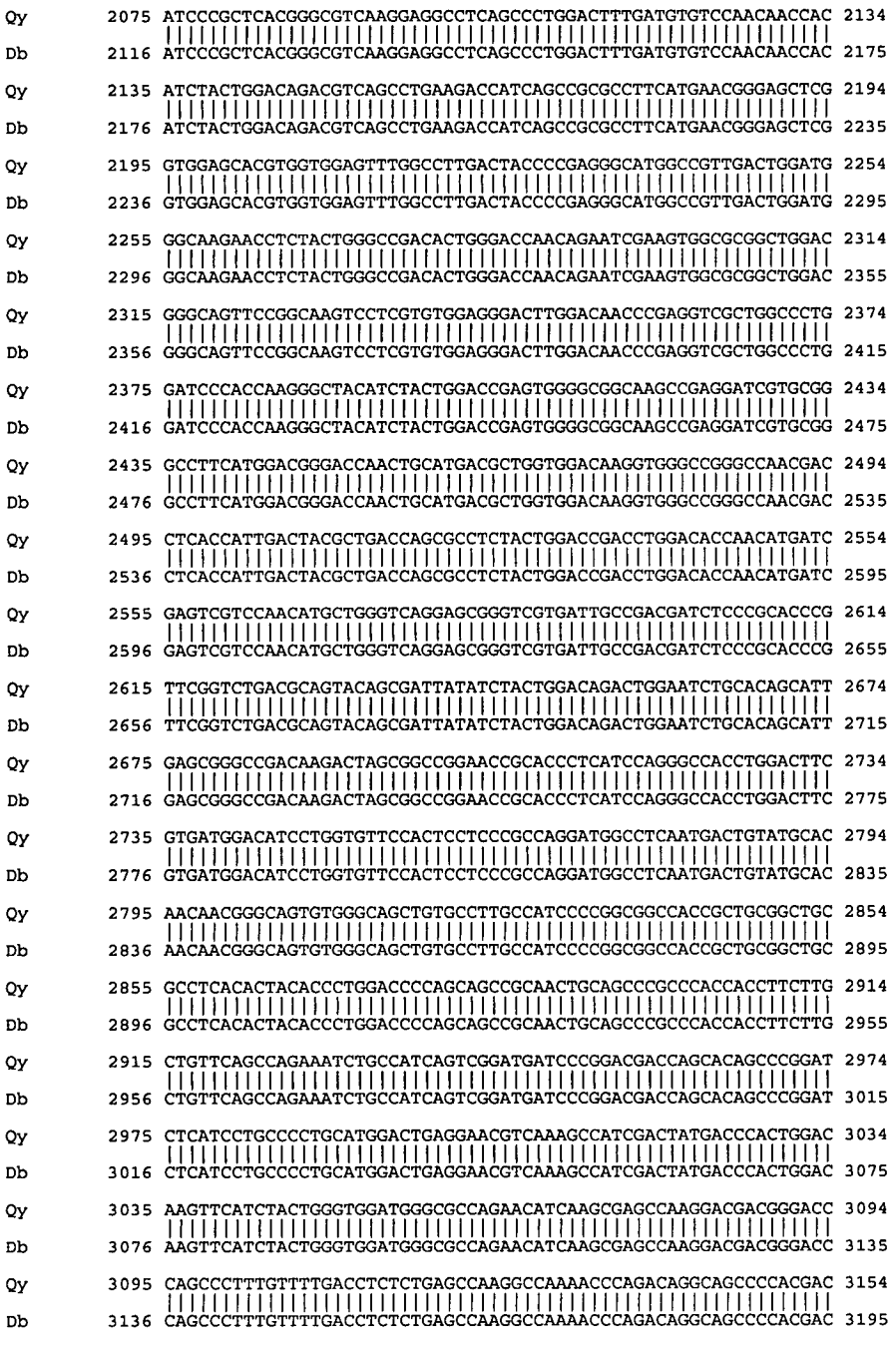
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